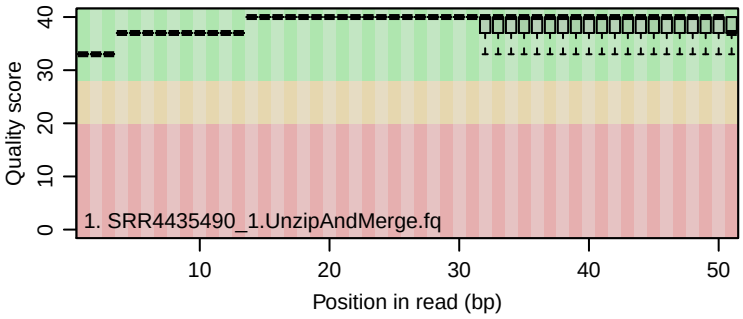
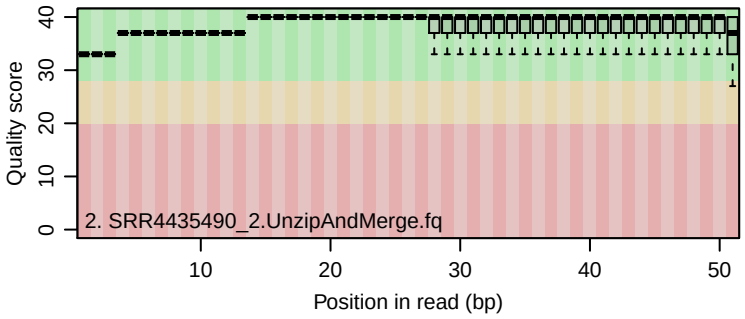
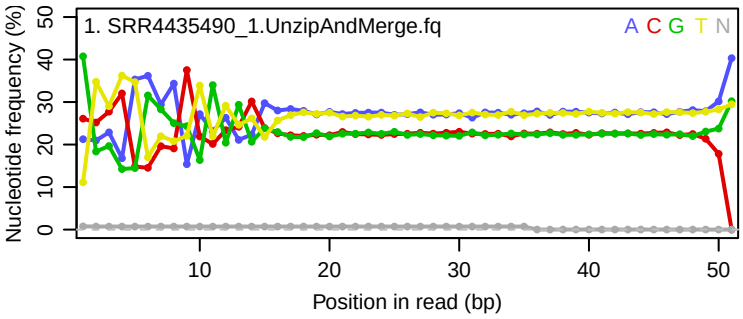
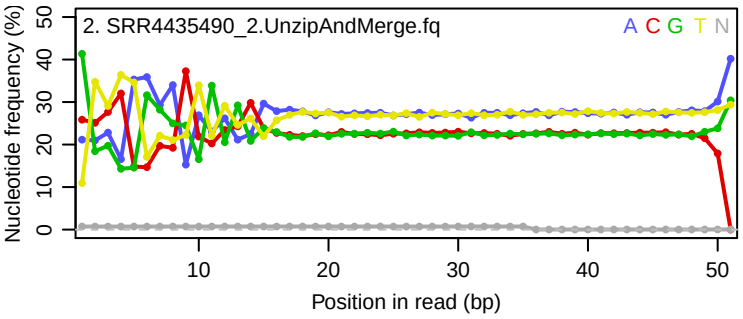
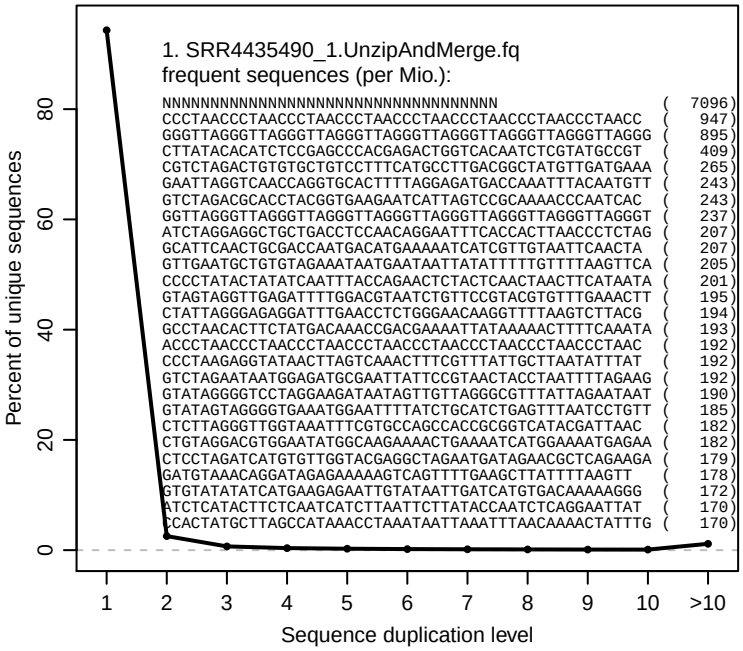
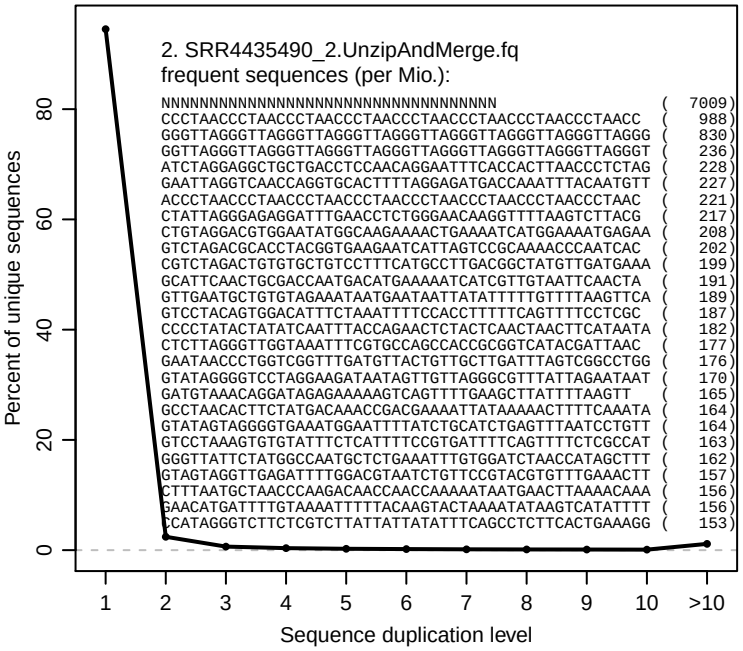

Quality score
0
10
20
30
40
1. SRR4435490_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


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 (7096)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (947)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (895)
CTTATACACATCTCCGAGCCCACGAGACTGGTCACAATCTCGTATGCCGT (409)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (265)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (243)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (243)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (237)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (207)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (207)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (205)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (201)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (195)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (194)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (193)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (192)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (192)
GTCTAGAATAATGGAGATGCGAATTATTCCGTAACTACCTAATTTTAGAAG (192)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (190)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (185)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (182)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (182)
CTCCTAGATCATGTGTTGGTACGAGGCTAGAATGATAGAACGCTCAGAAGA (179)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (178)
GTGTATATATCATGAAGAGAATTGTATAATTGATCATGTGACAAAAAGGG (172)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (170)
CCACTATGCTTAGCCATAAACCTAAATAATTAAATTTAACAAAACTATTTG (170)
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 (7009)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (988)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (830)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGT (236)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (228)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (227)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (221)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (217)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (208)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (202)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (199)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (191)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (189)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (187)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (182)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (177)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (176)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (170)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (165)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (164)
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GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (157)
CTTTAATGCTAACCCAAGACAACCAACCAAAAATAATGAACTTAAAACAAA (156)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT (156)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG (153)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level