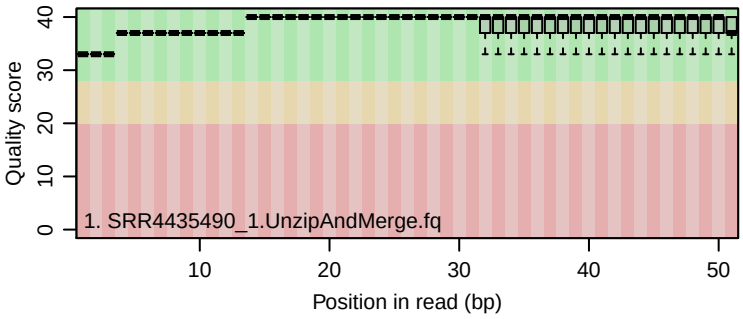
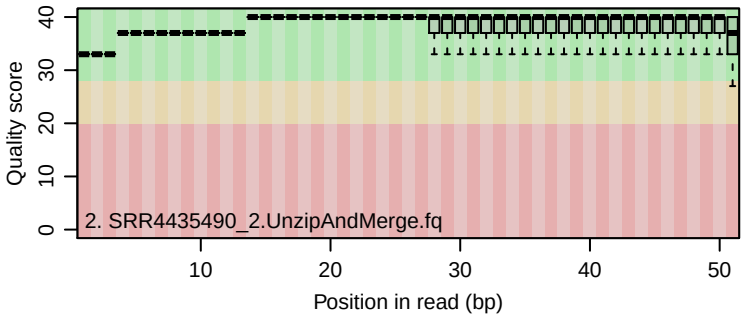
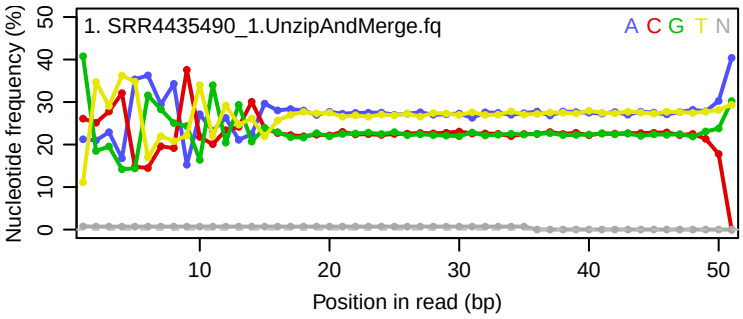
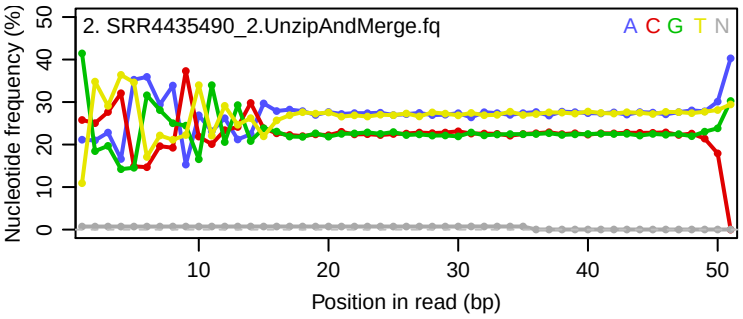
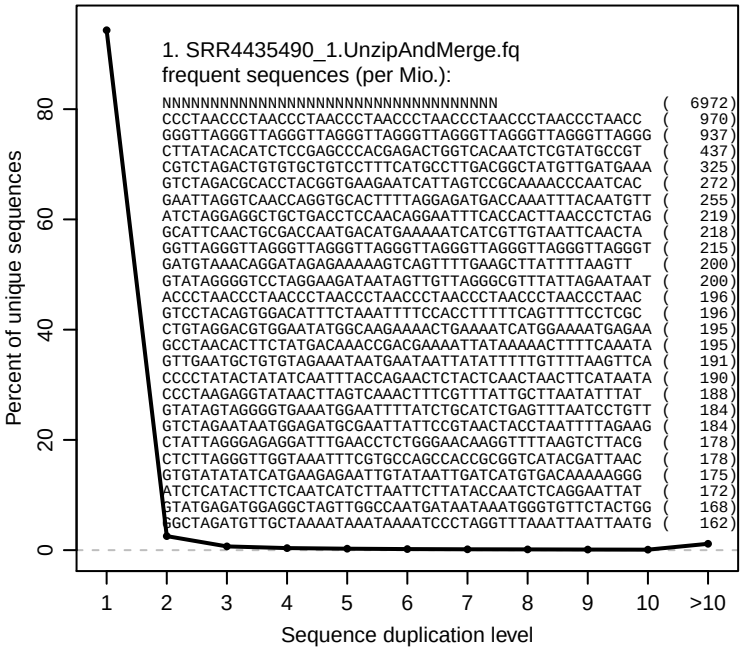
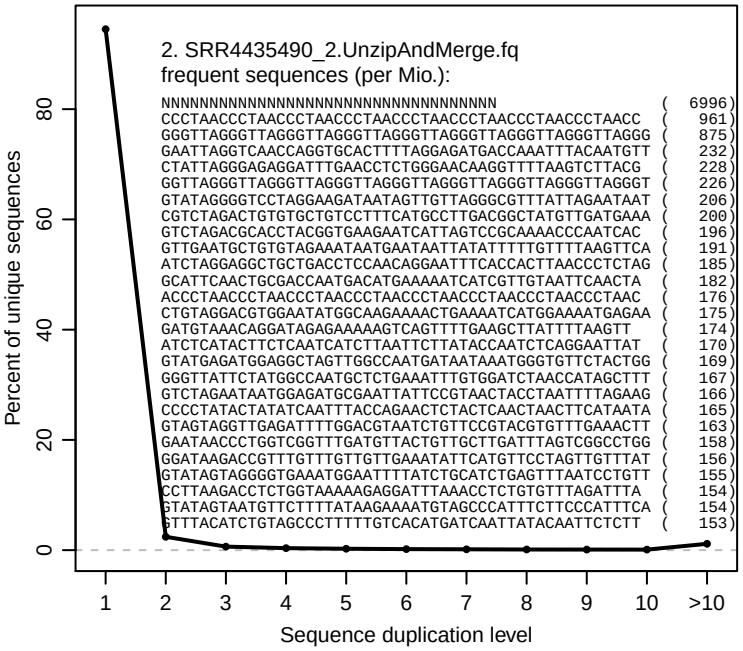

Quality score
0
10
20
30
40
1. SRR4435490_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


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 (6972)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (970)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (937)
CTTATACACATCTCCGAGCCCACGAGACTGGTCACAATCTCGTATGCCGT (437)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (325)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (272)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (255)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (219)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (218)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (215)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (200)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (200)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (196)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (196)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (195)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (195)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (191)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (190)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (188)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (184)
GTCTAGAATAATGGAGATGCGAATTATTCCGTAACTACCTAATTTTAGAAG (184)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (178)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (178)
GTGTATATATCATGAAGAGAATTGTATAATTGATCATGTGACAAAAAGGG (175)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (172)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (168)
GGCTAGATGTTGCTAAAATAAATAAAATCCCTAGGTTTAAATTAATTAATG (162)
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.):
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GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (232)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (228)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (226)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (206)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (200)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (196)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (191)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (185)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (182)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (176)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (175)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (174)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (170)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (169)
GGGTTATTCTATGGCCAATGCTCTGAAATTTGTGGATCTAACCATAGCTTT (167)
GTCTAGAATAATGGAGATGCGAATTATTCCGTAACTACCTAATTTTAGAAG (166)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (165)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (163)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (158)
GGATAAGACCGTTTGTTTGTTGTTGAAATATTCATGTTCCTAGTTGTTTAT (156)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (155)
CCTTAAGACCTCTGGTAAAAAGAGGATTTAAACCTCTGTGTTTAGATTTA (154)
GTATAGTAATGTTCTTTTATAAGAAAATGTAGCCCATTTCTTCCCATTTCA (154)
GTTTACATCTGTAGCCCTTTTTGTCACATGATCAATTATACAATTCTCTT (153)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level