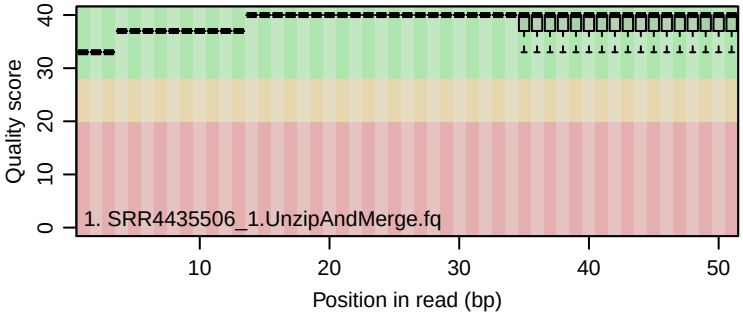
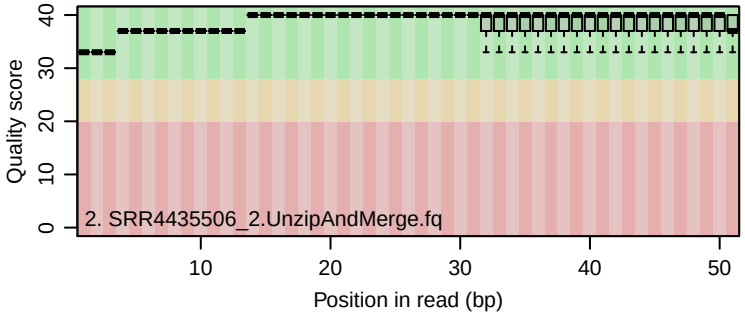
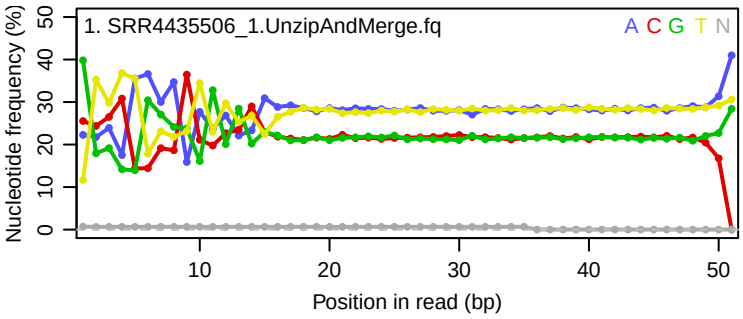
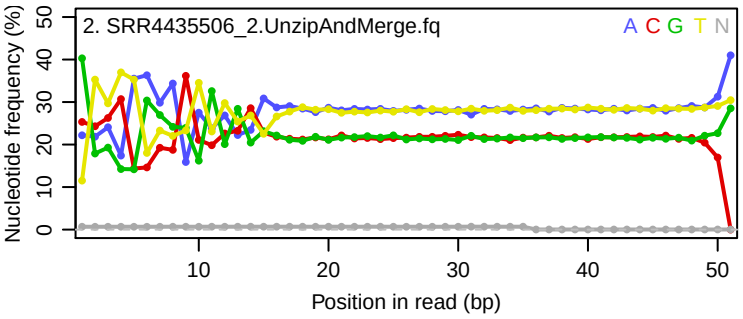
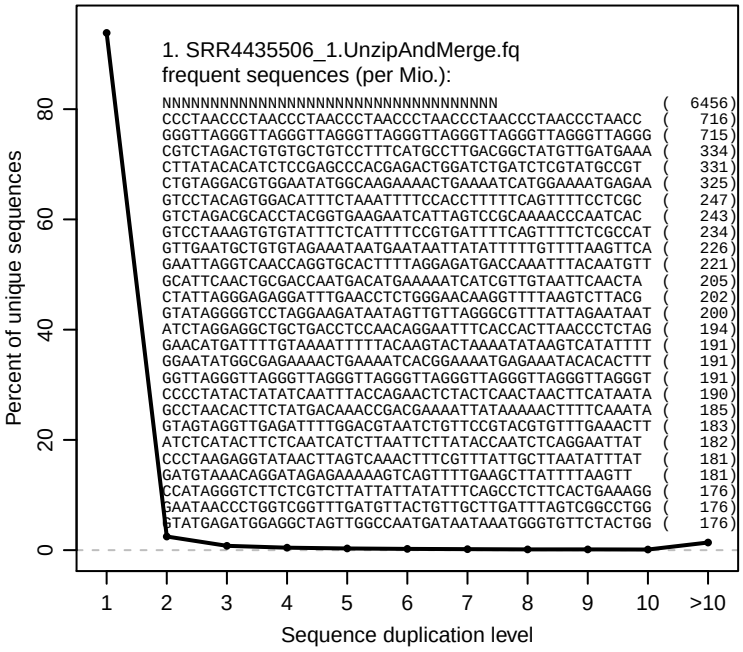
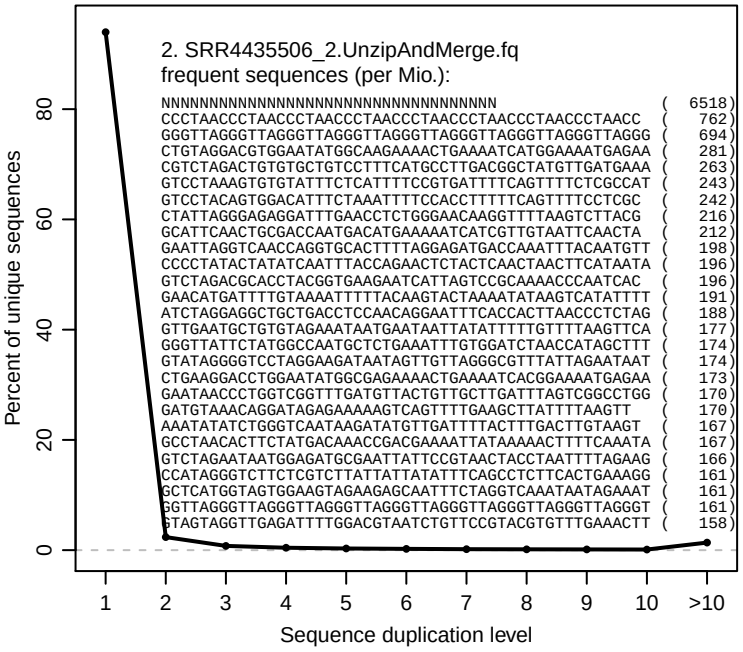

Quality score
0
10
20
30
40
1. SRR4435506_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR4435506_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR4435506_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. SRR4435506_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. SRR4435506_1.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (6456)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (716)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (715)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (334)
CTTATACACATCTCCGAGCCCACGAGACTGGATCTGATCTCGTATGCCGT (331)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (325)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (247)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (243)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (234)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (226)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (221)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (205)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (202)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (200)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (194)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT (191)
GGAATATGGCGAGAAAACTGAAAATCACGGAAAATGAGAAATACACACTTT (191)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (191)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (190)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (185)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (183)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (182)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (181)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (181)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG (176)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (176)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (176)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR4435506_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (6518)
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GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (694)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (281)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (263)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (243)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (242)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (216)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (212)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (198)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (196)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (196)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT (191)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (188)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (177)
GGGTTATTCTATGGCCAATGCTCTGAAATTTGTGGATCTAACCATAGCTTT (174)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (174)
CTGAAGGACCTGGAATATGGCGAGAAAACTGAAAATCACGGAAAATGAGAA (173)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (170)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (170)
AAATATATCTGGGTCAATAAGATATGTTGATTTTACTTTGACTTGTAAGT (167)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (167)
GTCTAGAATAATGGAGATGCGAATTATTCCGTAACTACCTAATTTTAGAAG (166)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG (161)
GCTCATGGTAGTGGAAGTAGAAGAGCAATTTCTAGGTCAAATAATAGAAAT (161)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (161)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (158)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level