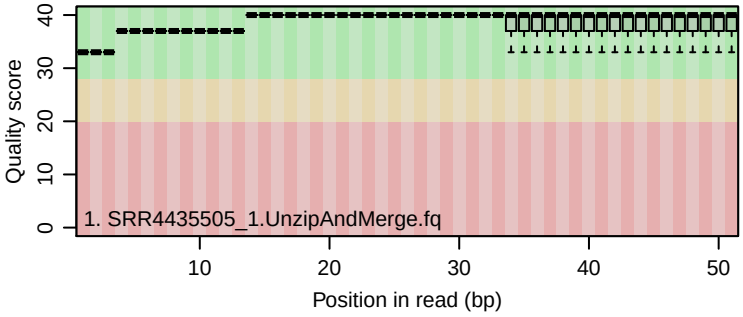
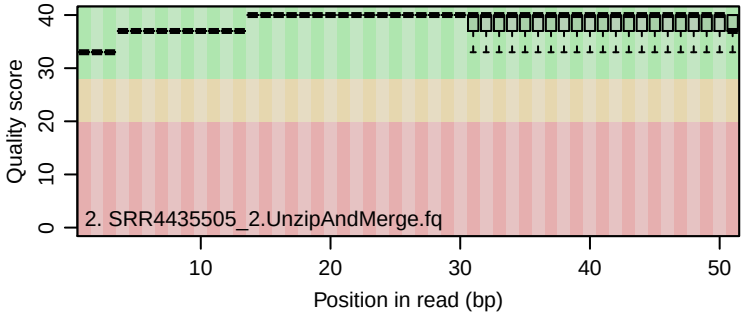
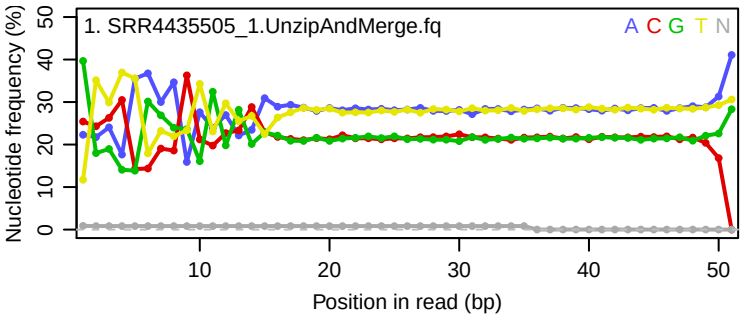
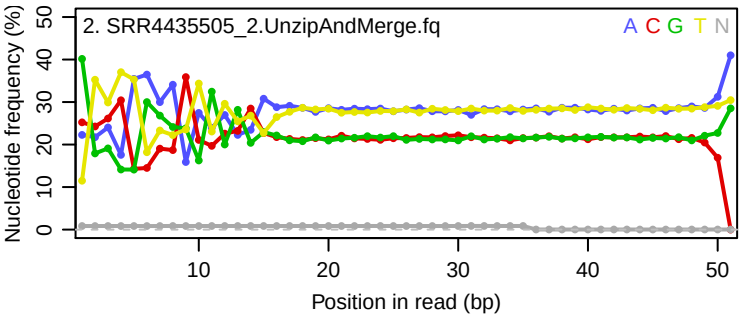
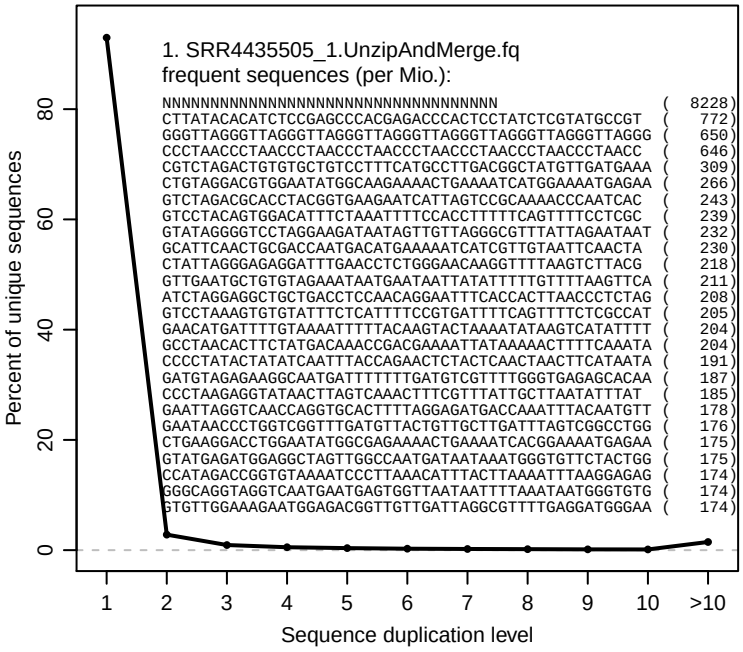
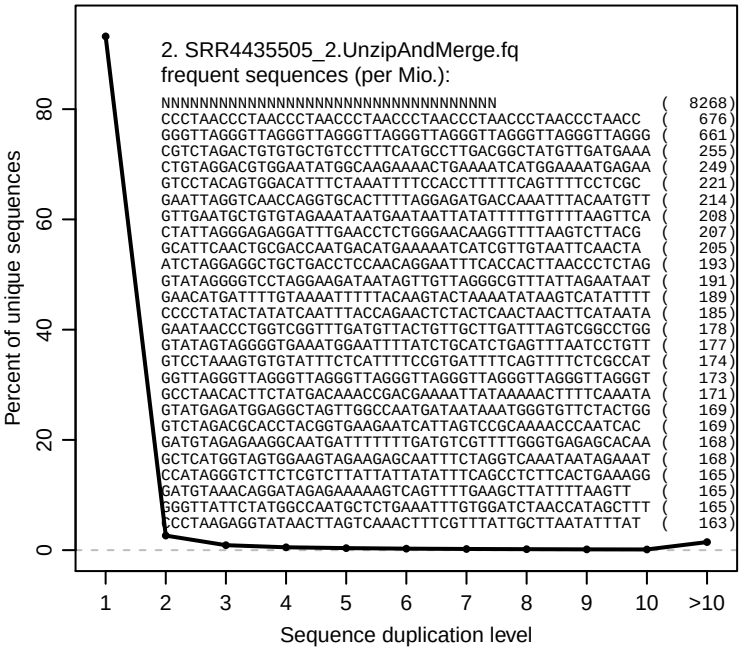

Quality score
0
10
20
30
40
1. SRR4435505_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


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 ( 8228)
CTTATACACATCTCCGAGCCCACGAGACCCACTCCTATCTCGTATGCCGT ( 772)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG ( 650)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC ( 646)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA ( 309)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA ( 266)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC ( 243)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC ( 239)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT ( 232)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA ( 230)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG ( 218)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA ( 211)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG ( 208)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT ( 205)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT ( 204)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA ( 204)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA ( 191)
GATGTAGAGAAGGCAATGATTTTTTTGATGTCGTTTTGGGTGAGAGCACAA ( 187)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT ( 185)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT ( 178)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG ( 176)
CTGAAGGACCTGGAATATGGCGAGAAAACTGAAAATCACGGAAAATGAGAA ( 175)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG ( 175)
CCATAGACCGGTGTAAAATCCCTTAAACATTTACTTAAAATTTAAGGAGAG ( 174)
GGGCAGGTAGGTCAATGAATGAGTGGTTAATAATTTTAAATAATGGGTGTG ( 174)
GTGTTGGAAAGAATGGAGACGGTTGTTGATTAGGCGTTTTGAGGATGGGAA ( 174)
Percent of unique sequences
0
20
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 ( 8268)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC ( 676)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG ( 661)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA ( 255)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA ( 249)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC ( 221)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT ( 214)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA ( 208)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG ( 207)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA ( 205)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG ( 193)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT ( 191)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT ( 189)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA ( 185)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG ( 178)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT ( 177)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT ( 174)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT ( 173)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA ( 171)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG ( 169)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC ( 169)
GATGTAGAGAAGGCAATGATTTTTTTGATGTCGTTTTGGGTGAGAGCACAA ( 168)
GCTCATGGTAGTGGAAGTAGAAGAGCAATTTCTAGGTCAAATAATAGAAAT ( 168)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG ( 165)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT ( 165)
GGGTTATTCTATGGCCAATGCTCTGAAATTTGTGGATCTAACCATAGCTTT ( 165)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT ( 163)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level