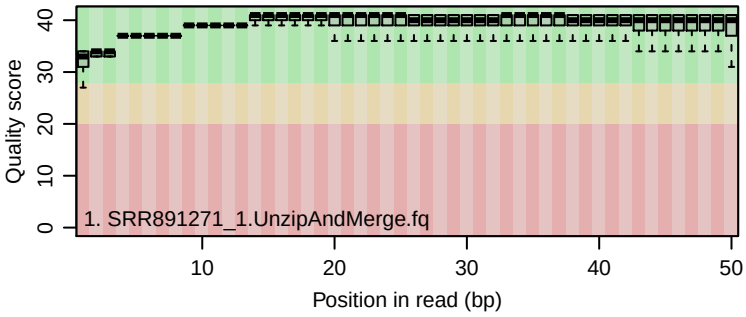
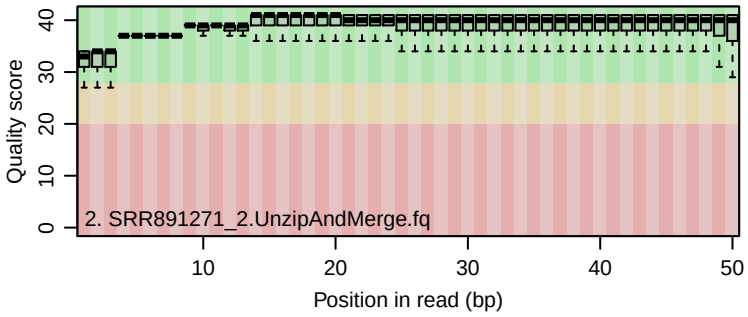
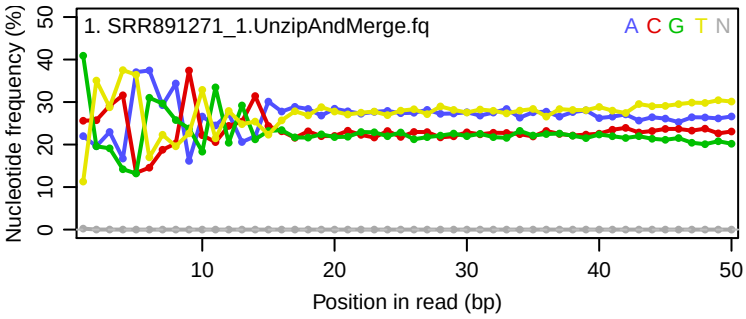
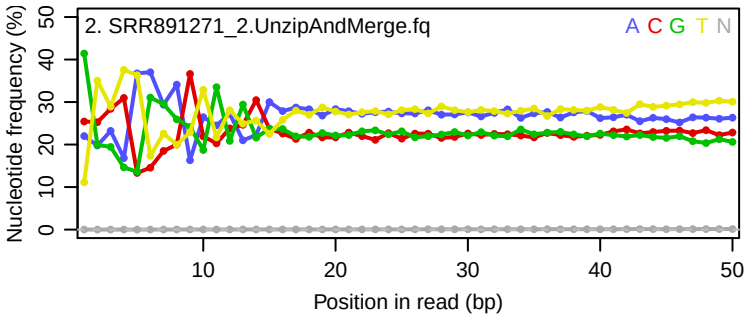
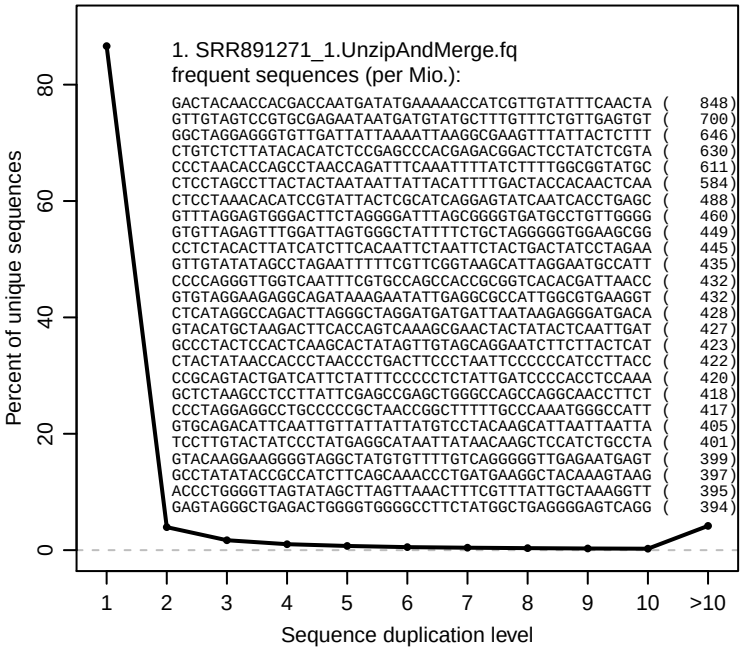
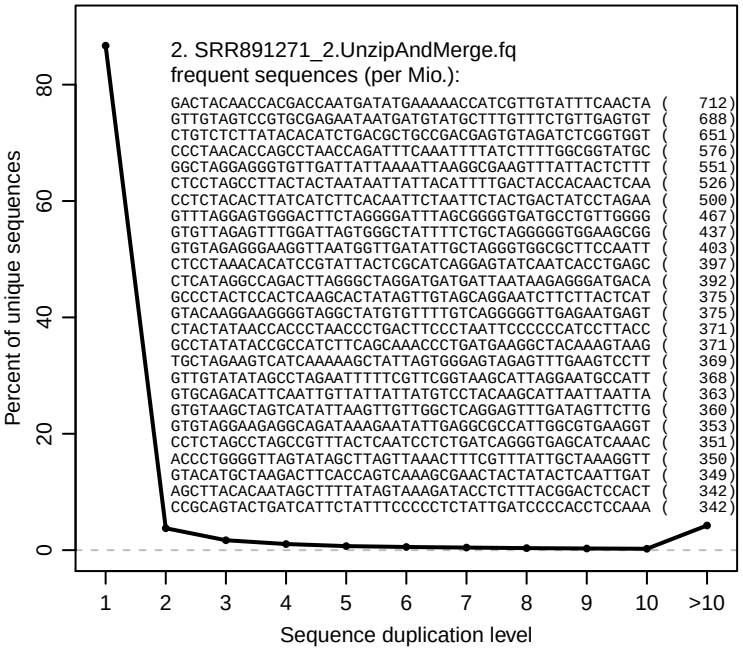

Quality score
0
10
20
30
40
1. SRR891271_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR891271_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR891271_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. SRR891271_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. SRR891271_1.unzipAndMerge.fq
frequent sequences (per Mio.):
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (848)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (700)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (646)
CTGTCTCTTATACACATCTCCGAGCCCACGAGACGGACTCCTATCTCGTA (630)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (611)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (584)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (488)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (460)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (449)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (445)
GTTGTATATAGCCTAGAATTTTTCGTTCGGTAAGCATTAGGAATGCCATT (435)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (432)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (432)
CTCATAGGCCAGACTTAGGGCTAGGATGATGATTAATAAGAGGGATGACA (428)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (427)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (423)
CTACTATAACCACCCTAACCCTGACTTCCCTAATTCCCCCCATCCTTACC (422)
CCGCAGTACTGATCATTCTATTTCCCCCTCTATTGATCCCCACCTCCAAA (420)
GCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCAGGCAACCTTCT (418)
CCCTAGGAGGCCTGCCCCCGCTAACCGGCTTTTTGCCCAAATGGGCCATT (417)
GTGCAGACATTCAATTGTTATTATTATGTCCTACAAGCATTAATTAATTA (405)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (401)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (399)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (397)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (395)
GAGTAGGGCTGAGACTGGGGTGGGGCCTTCTATGGCTGAGGGGAGTCAGG (394)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR891271_2.unzipAndMerge.fq
frequent sequences (per Mio.):
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (712)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (688)
CTGTCTCTTATACACATCTGACGCTGCCGACGAGTGTAGATCTCGGTGGT (651)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (576)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (551)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (526)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (500)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (467)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (437)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (403)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (397)
CTCATAGGCCAGACTTAGGGCTAGGATGATGATTAATAAGAGGGATGACA (392)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (375)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (375)
CTACTATAACCACCCTAACCCTGACTTCCCTAATTCCCCCCATCCTTACC (371)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (371)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (369)
GTTGTATATAGCCTAGAATTTTTCGTTCGGTAAGCATTAGGAATGCCATT (368)
GTGCAGACATTCAATTGTTATTATTATGTCCTACAAGCATTAATTAATTA (363)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (360)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (353)
CCTCTAGCCTAGCCGTTTACTCAATCCTCTGATCAGGGTGAGCATCAAAC (351)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (350)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (349)
AGCTTACACAATAGCTTTTATAGTAAAGATACCTCTTTACGGACTCCACT (342)
CCGCAGTACTGATCATTCTATTTCCCCCTCTATTGATCCCCACCTCCAAA (342)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level