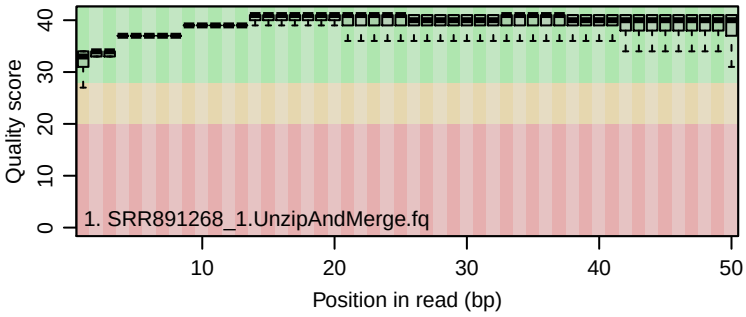
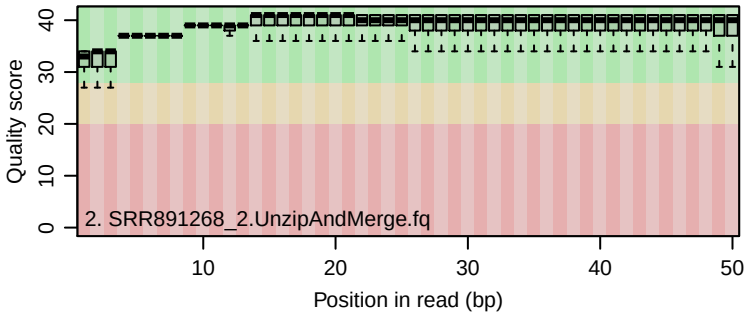
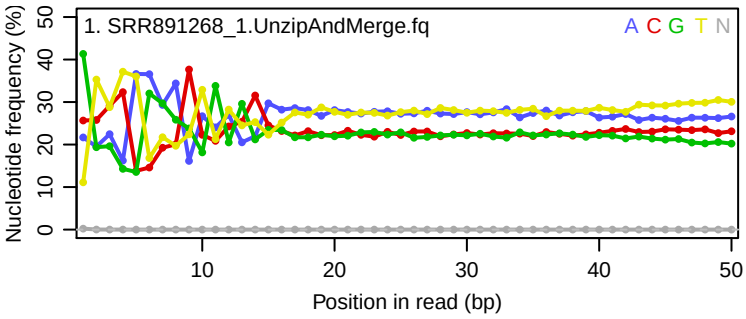
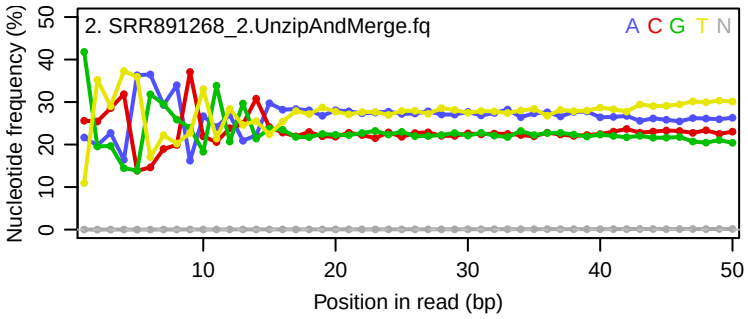
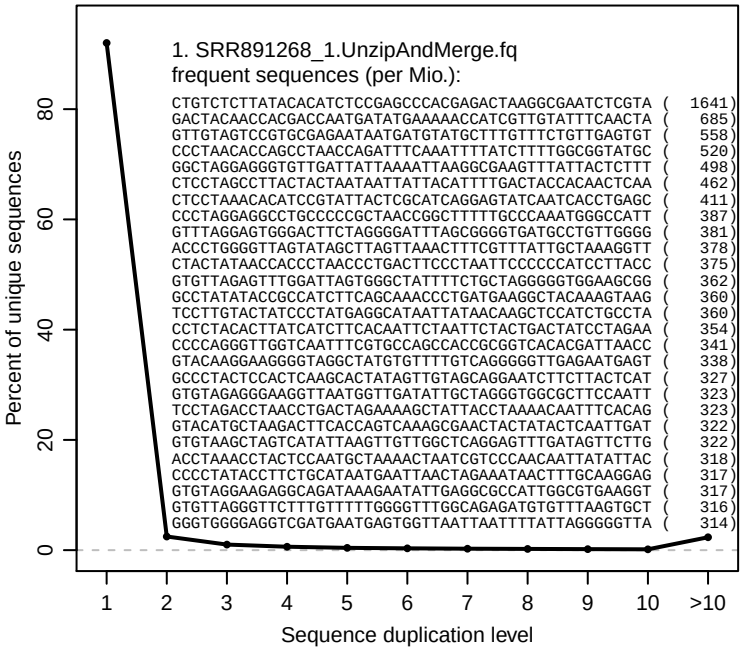

Quality score
0
10
20
30
40
1. SRR891268_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR891268_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR891268_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. SRR891268_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. SRR891268_1.unzipAndMerge.fq
frequent sequences (per Mio.):
CTGTCTCTTATACACATCTCCGAGCCCACGAGACTAAGGCGAATCTCGTA (1641)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (685)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (558)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (520)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (498)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (462)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (411)
CCCTAGGAGGCCTGCCCCCGCTAACCGGCTTTTTGCCCAAATGGGCCATT (387)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (381)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (378)
CTACTATAACCACCCTAACCCTGACTTCCCTAATTCCCCCCATCCTTACC (375)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (362)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (360)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (360)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (354)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (341)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (338)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (327)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (323)
TCCTAGACCTAACCTGACTAGAAAAGCTATTACCTAAAACAATTTCACAG (323)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (322)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (322)
ACCTAAACCTACTCCAATGCTAAAACTAATCGTCCCAACAATTATATTAC (318)
CCCCTATACCTTCTGCATAATGAATTAACTAGAAATAACTTTGCAAGGAG (317)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (317)
GTGTTAGGGTTCTTTGTTTTTGGGGTTTGGCAGAGATGTGTTTAAGTGCT (316)
GGGTGGGGAGGTCGATGAATGAGTGGTTAATTAATTTTATTAGGGGGTTA (314)
Percent of unique sequences
0
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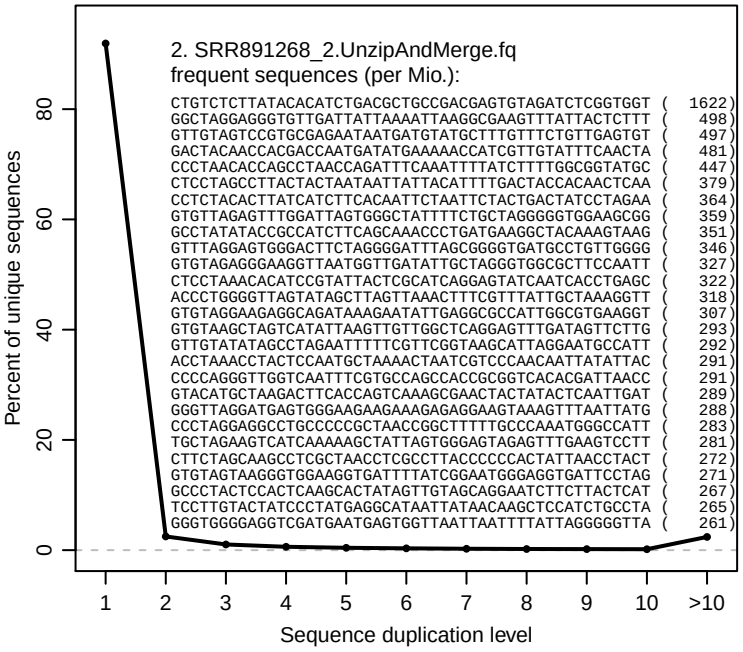
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR891268_2.unzipAndMerge.fq
frequent sequences (per Mio.):
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GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (498)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (497)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (481)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (447)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (379)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (364)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (359)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (351)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (346)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (327)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (322)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (318)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (307)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (293)
GTTGTATATAGCCTAGAATTTTTCGTTCGGTAAGCATTAGGAATGCCATT (292)
ACCTAAACCTACTCCAATGCTAAAACTAATCGTCCCAACAATTATATTAC (291)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (291)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (289)
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CCCTAGGAGGCCTGCCCCCGCTAACCGGCTTTTTGCCCAAATGGGCCATT (283)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (281)
CTTCTAGCAAGCCTCGCTAACCTCGCCTTACCCCCCACTATTAACCTACT (272)
GTGTAGTAAGGGTGGAAGGTGATTTTATCGGAATGGGAGGTGATTCCTAG (271)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (267)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (265)
GGGTGGGGAGGTCGATGAATGAGTGGTTAATTAATTTTATTAGGGGGTTA (261)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level