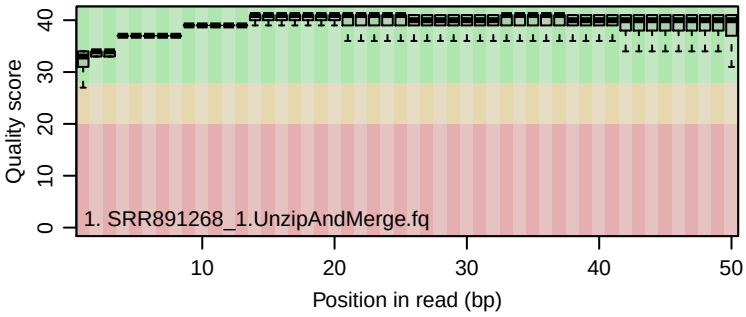
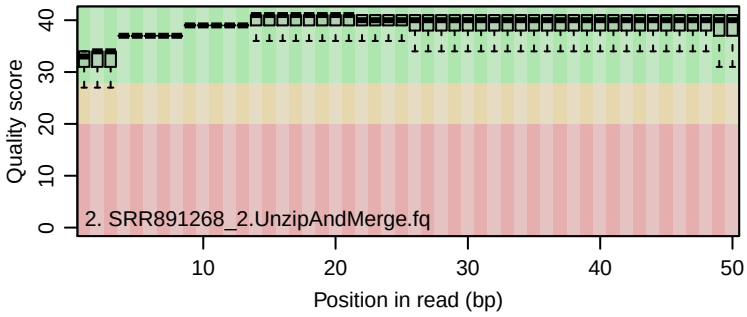
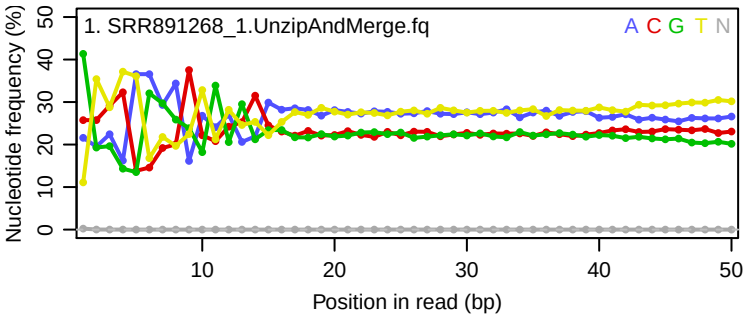
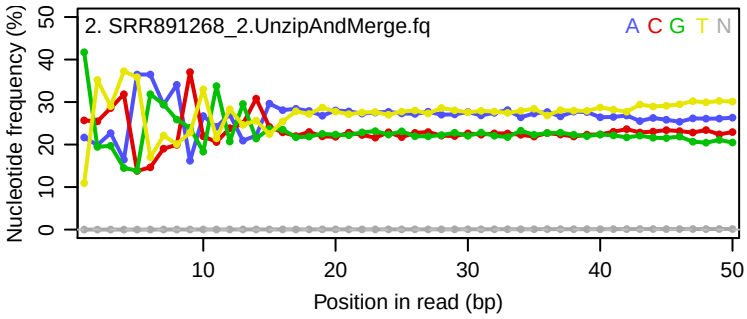
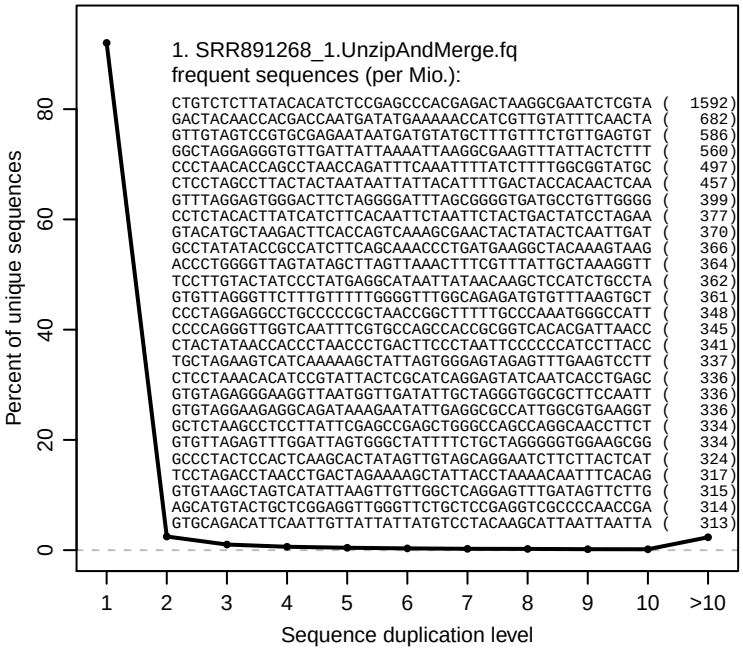
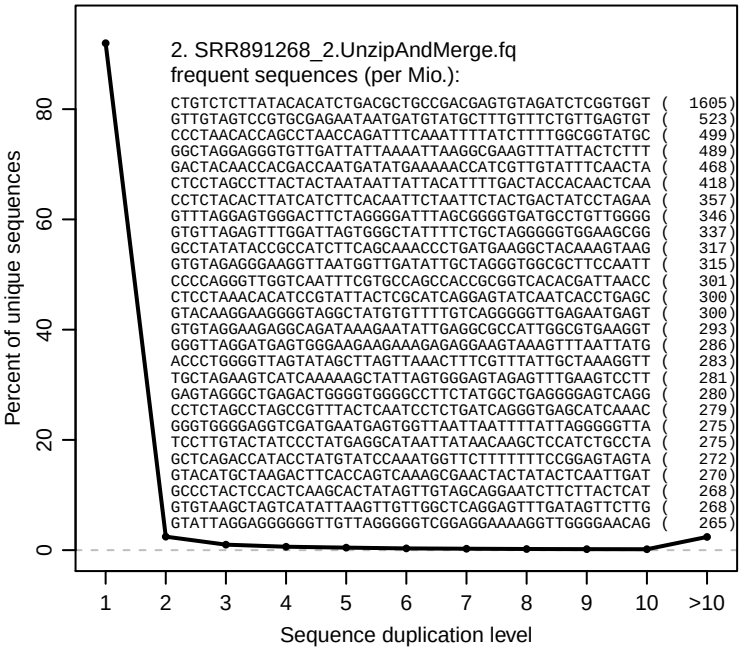

Quality score
0
10
20
30
40
1. SRR891268_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


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 (1592)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (682)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (586)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (560)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (497)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (457)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (399)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (377)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (370)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (366)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (364)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (362)
GTGTTAGGGTTCTTTGTTTTTGGGGTTTGGCAGAGATGTGTTTAAGTGCT (361)
CCCTAGGAGGCCTGCCCCCGCTAACCGGCTTTTTGCCCAAATGGGCCATT (348)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (345)
CTACTATAACCACCCTAACCCTGACTTCCCTAATTCCCCCCATCCTTACC (341)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (337)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (336)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (336)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (336)
GCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCAGGCAACCTTCT (334)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (334)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (324)
TCCTAGACCTAACCTGACTAGAAAAGCTATTACCTAAAACAATTTCACAG (317)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (315)
AGCATGTACTGCTCGGAGGTTGGGTTCTGCTCCGAGGTCGCCCCAACCGA (314)
GTGCAGACATTCAATTGTTATTATTATGTCCTACAAGCATTAATTAATTA (313)
Percent of unique sequences
0
20
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.):
CTGTCTCTTATACACATCTGACGCTGCCGACGAGTGTAGATCTCGGTGGT (1605)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (523)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (499)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (489)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (468)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (418)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (357)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (346)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (337)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (317)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (315)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (301)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (300)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (300)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (293)
GGGTTAGGATGAGTGGGAAGAAGAAAGAGAGGAAGTAAAGTTTAATTATG (286)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (283)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (281)
GAGTAGGGCTGAGACTGGGGTGGGGCCTTCTATGGCTGAGGGGAGTCAGG (280)
CCTCTAGCCTAGCCGTTTACTCAATCCTCTGATCAGGGTGAGCATCAAAC (279)
GGGTGGGGAGGTCGATGAATGAGTGGTTAATTAATTTTATTAGGGGGTTA (275)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (275)
GCTCAGACCATACCTATGTATCCAAATGGTTCTTTTTTTCCGGAGTAGTA (272)
GTACATGCTAAGACTTCACCAGTCAAAGCGAACTACTATACTCAATTGAT (270)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (268)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (268)
GTATTAGGAGGGGGGTTGTTAGGGGGTCGGAGGAAAAGGTTGGGGAACAG (265)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level