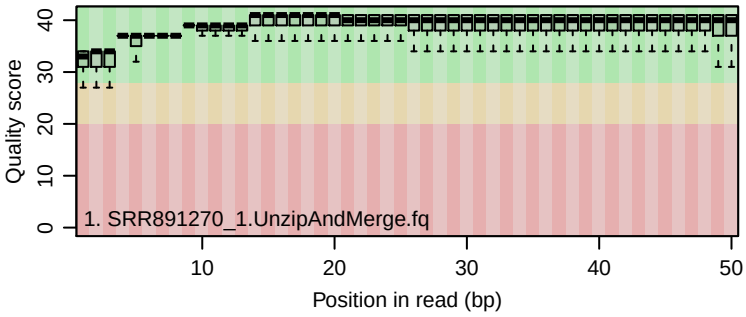
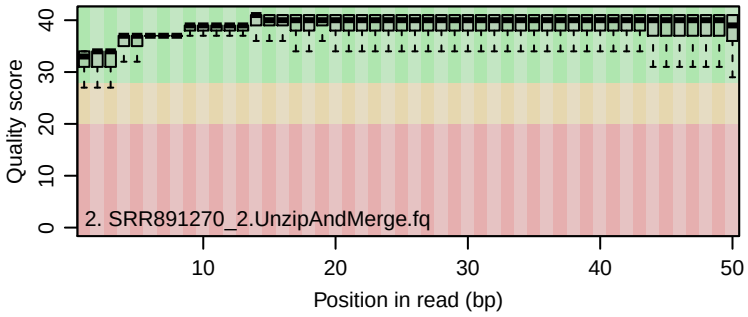
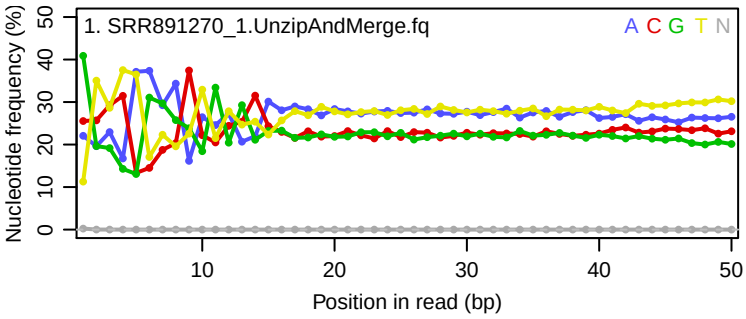
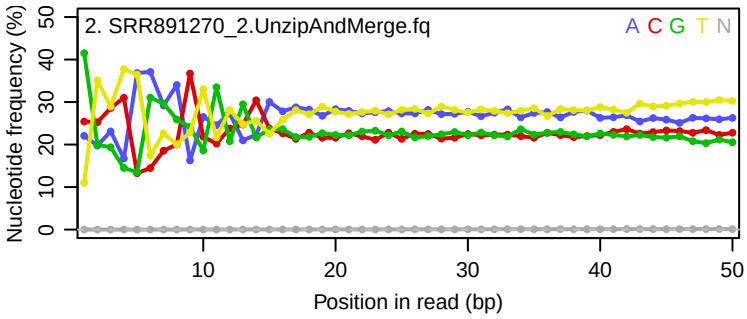
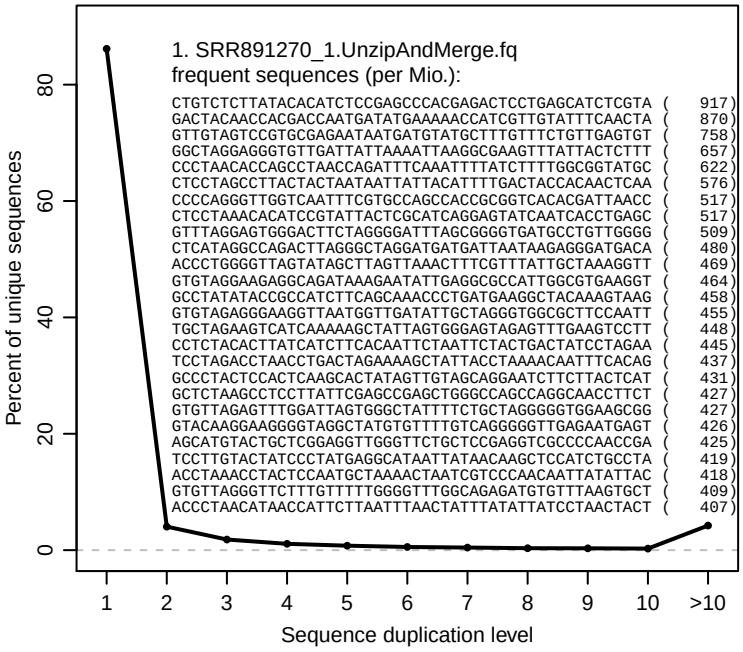
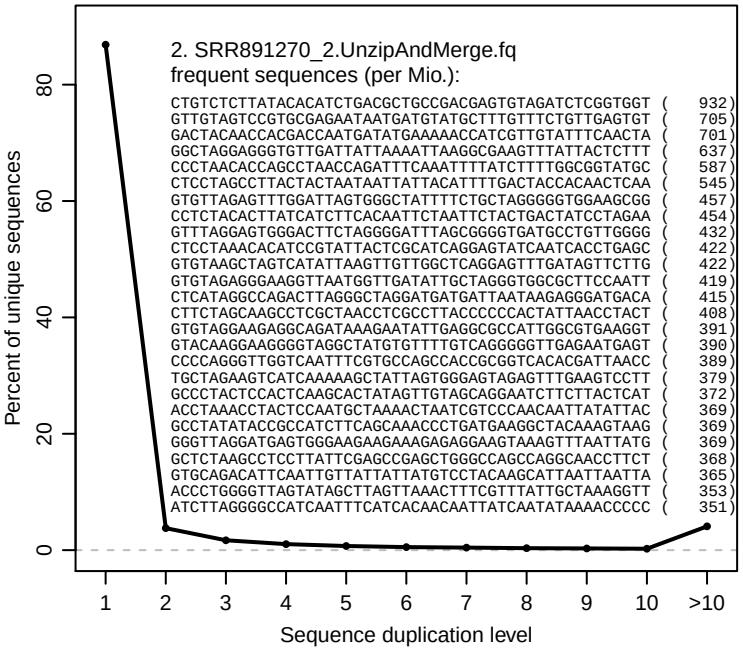

Quality score
0
10
20
30
40
1. SRR891270_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR891270_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR891270_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. SRR891270_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. SRR891270_1.UnzipAndMerge.fq
frequent sequences (per Mio.):
CTGTCTCTTATACACATCTCCGAGCCCACGAGACTCCTGAGCATCTCGTA (917)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (870)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (758)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (657)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (622)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (576)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (517)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (517)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (509)
CTCATAGGCCAGACTTAGGGCTAGGATGATGATTAATAAGAGGGATGACA (480)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (469)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (464)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (458)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (455)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (448)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (445)
TCCTAGACCTAACCTGACTAGAAAAGCTATTACCTAAAACAATTTCACAG (437)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (431)
GCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCAGGCAACCTTCT (427)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (427)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (426)
AGCATGTACTGCTCGGAGGTTGGGTTCTGCTCCGAGGTCGCCCCAACCGA (425)
TCCTTGTACTATCCCTATGAGGCATAATTATAACAAGCTCCATCTGCCTA (419)
ACCTAAACCTACTCCAATGCTAAAACTAATCGTCCCAACAATTATATTAC (418)
GTGTTAGGGTTCTTTGTTTTTGGGGTTTGGCAGAGATGTGTTTAAGTGCT (409)
ACCCTAACATAACCATTCTTAATTTAACTATTTATATTATCCTAACTACT (407)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR891270_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
CTGTCTCTTATACACATCTGACGCTGCCGACGAGTGTAGATCTCGGTGGT (932)
GTTGTAGTCCGTGCGAGAATAATGATGTATGCTTTGTTTCTGTTGAGTGT (705)
GACTACAACCACGACCAATGATATGAAAAACCATCGTTGTATTTCAACTA (701)
GGCTAGGAGGGTGTTGATTATTAAAATTAAGGCGAAGTTTATTACTCTTT (637)
CCCTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGC (587)
CTCCTAGCCTTACTACTAATAATTATTACATTTTGACTACCACAACTCAA (545)
GTGTTAGAGTTTGGATTAGTGGGCTATTTTCTGCTAGGGGGTGGAAGCGG (457)
CCTCTACACTTATCATCTTCACAATTCTAATTCTACTGACTATCCTAGAA (454)
GTTTAGGAGTGGGACTTCTAGGGGATTTAGCGGGGTGATGCCTGTTGGGG (432)
CTCCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGC (422)
GTGTAAGCTAGTCATATTAAGTTGTTGGCTCAGGAGTTTGATAGTTCTTG (422)
GTGTAGAGGGAAGGTTAATGGTTGATATTGCTAGGGTGGCGCTTCCAATT (419)
CTCATAGGCCAGACTTAGGGCTAGGATGATGATTAATAAGAGGGATGACA (415)
CTTCTAGCAAGCCTCGCTAACCTCGCCTTACCCCCCCACTATTAACCTACT (408)
GTGTAGGAAGAGGCAGATAAAGAATATTGAGGCGCCATTGGCGTGAAGGT (391)
GTACAAGGAAGGGGTAGGCTATGTGTTTTGTCAGGGGGTTGAGAATGAGT (390)
CCCCAGGGTTGGTCAATTTCGTGCCAGCCACCGCGGTCACACGATTAACC (389)
TGCTAGAAGTCATCAAAAAGCTATTAGTGGGAGTAGAGTTTGAAGTCCTT (379)
GCCCTACTCCACTCAAGCACTATAGTTGTAGCAGGAATCTTCTTACTCAT (372)
ACCTAAACCTACTCCAATGCTAAAACTAATCGTCCCAACAATTATATTAC (369)
GCCTATATACCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAG (369)
GGGTTAGGATGAGTGGGAAGAAGAAAGAGAGGAAGTAAAGTTTAATTATG (369)
GCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCAGGCAACCTTCT (368)
GTGCAGACATTCAATTGTTATTATTATGTCCTACAAGCATTAATTAATTA (365)
ACCCTGGGGTTAGTATAGCTTAGTTAAACTTTCGTTTATTGCTAAAGGTT (353)
ATCTTAGGGGCCATCAATTTCATCACAACAATTATCAATATAAAACCCCC (351)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level