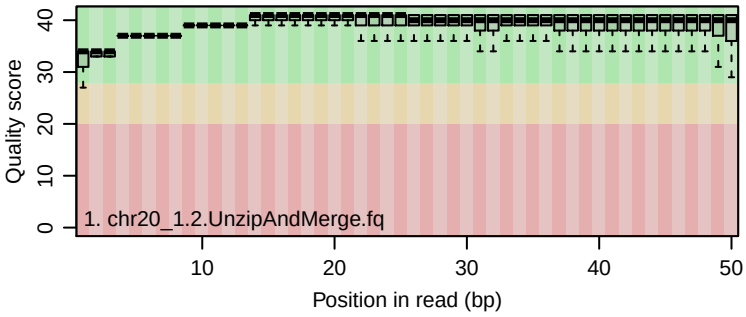
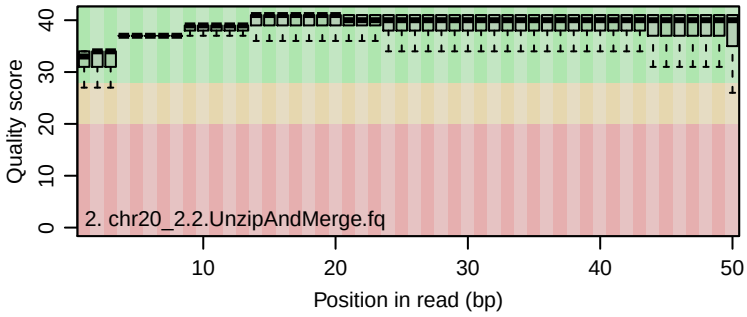
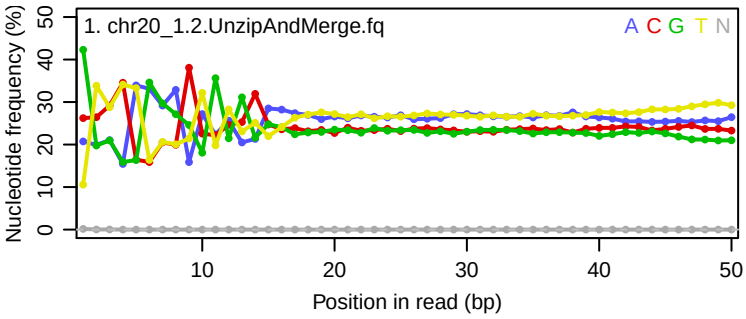
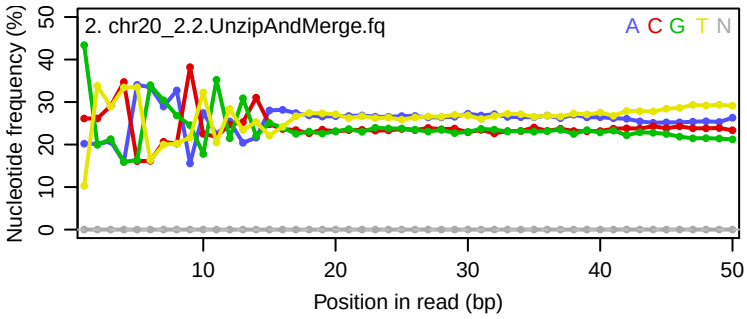
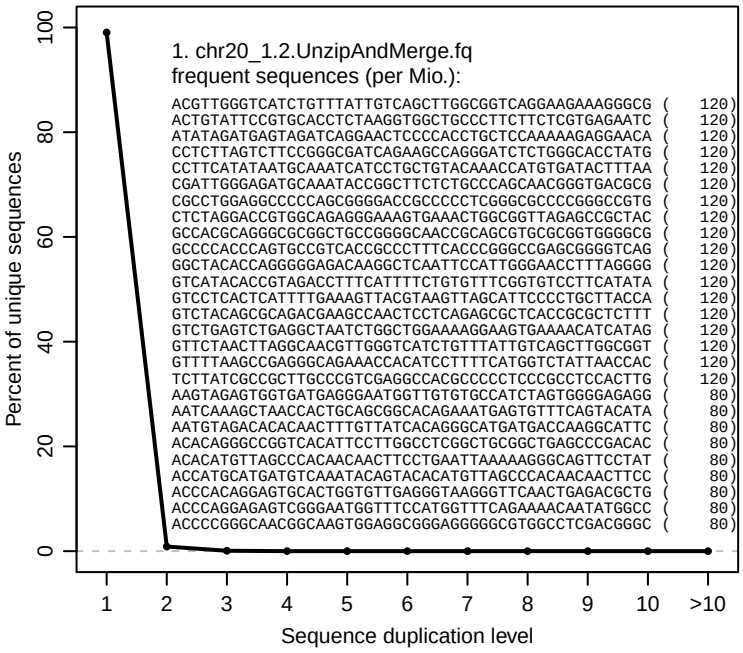
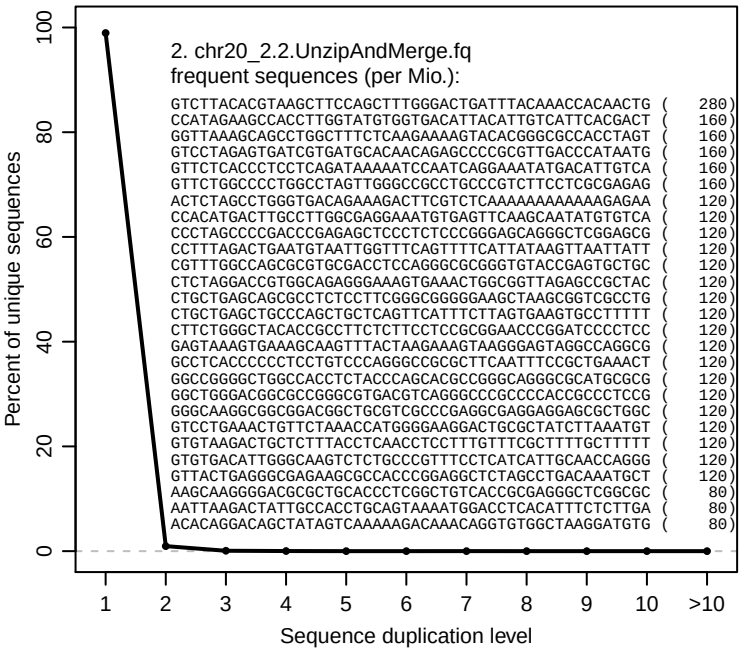

Quality score
0
10
20
30
40
1. chr20_1.2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. chr20_2.2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. chr20_1.2.UnzipAndMerge.fq
A C G T N
Nucleotide frequency (%)
0
10
20
30
40
50
10
20
30
40
50
Position in read (bp)


2. chr20_2.2.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. chr20_1.2.UnzipAndMerge.fq
frequent sequences (per Mio.):
ACGTTGGGTCATCTGTTTATTGTCAGCTTGGCGGTCAGGAAGAAAGGGCG (120)
ACTGTATTCCGTGCACCTCTAAGGTGGCTGCCCTTCTTCTCGTGAGAATC (120)
ATATAGATGAGTAGATCAGGAACTCCCCACCTGCTCCAAAAAGAGGAACA (120)
CCTCTTAGTCTTCCGGGCGATCAGAAGCCAGGGATCTCTGGGCACCTATG (120)
CCTTCATATAATGCAAATCATCCTGCTGTACAAACCATGTGATACTTTAA (120)
CGATTGGGAGATGCAAATACCGGCTTCTCTGCCCAGCAACGGGTGACGCG (120)
CGCCTGGAGGCCCCCAGCGGGGACCGCCCCCTCGGGCGCCCCGGGCCGTG (120)
CTCTAGGACCGTGGCAGAGGGAAAGTGAAACTGGCGGTTAGAGCCGCTAC (120)
GCCACGCAGGGCGCGGCTGCCGGGGCAACCGCAGCGTGCGCGGTGGGGCG (120)
GCCCCACCCAGTGCCGTCACCGCCCTTTCACCCGGGCCGAGCGGGGTCAG (120)
GGCTACACCAGGGGGAGACAAGGCTCAATTCCATTGGGAACCTTTAGGGG (120)
GTCATACACCGTAGACCTTTCATTTTCTGTGTTTCGGTGTCCTTCATATA (120)
GTCCTCACTCATTTTGAAAGTTACGTAAGTTAGCATTCCCCTGCTTACCA (120)
GTCTACAGCGCAGACGAAGCCAACTCCTCAGAGCGCTCACCGCGCTCTTT (120)
GTCTGAGTCTGAGGCTAATCTGGCTGGAAAAGGAAGTGAAAACATCATAG (120)
GTTCTAACTTAGGCAACGTTGGGTCATCTGTTTATTGTCAGCTTGGCGGT (120)
GTTTTAAGCCGAGGGCAGAAACCACATCCTTTTCATGGTCTATTAACCAC (120)
TCTTATCGCCGCTTGCCCGTCGAGGCCACGCCCCCTCCCGCCTCCACTTG (120)
AAGTAGAGTGGTGATGAGGGAATGGTTGTGTGCCATCTAGTGGGGAGAGG (80)
AATCAAAGCTAACCACTGCAGCGGCACAGAAATGAGTGTTTCAGTACATA (80)
AATGTAGACACACAACTTTGTTATCACAGGGCATGATGACCAAGGCATTC (80)
ACACAGGGCCGGTCACATTCCTTGGCCTCGGCTGCGGCTGAGCCCGACAC (80)
ACACATGTTAGCCCACAACAACTTCCTGAATTAAAAAGGGCAGTTCCTAT (80)
ACCATGCATGATGTCAAATACAGTACACATGTTAGCCCACAACAACTTCC (80)
ACCCACAGGAGTGCACTGGTGTTGAGGGTAAGGGTTCAACTGAGACGCTG (80)
ACCCAGGAGAGTCGGGAATGGTTTCCATGGTTTCAGAAAACAATATGGCC (80)
ACCCCGGGCAACGGCAAGTGGAGGCGGGAGGGGGCGTGGCCTCGACGGGC (80)
Percent of unique sequences
0
20
40
60
80
100
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. chr20_2.2.UnzipAndMerge.fq
frequent sequences (per Mio.):
GTCTTACACGTAAGCTTCCAGCTTTGGGACTGATTTACAAACCACAACTG (280)
CCATAGAAGCCACCTTGGTATGTGGTGACATTACATTGTCATTCACGACT (160)
GGTTAAAGCAGCCTGGCTTTCTCAAGAAAAGTACACGGGCGCCACCTAGT (160)
GTCCTAGAGTGATCGTGATGCACAACAGAGCCCCGCGTTGACCCATAATG (160)
GTTCTCACCCTCCTCAGATAAAAATCCAATCAGGAAATATGACATTGTCA (160)
GTTCTGGCCCCTGGCCTAGTTGGGCCGCCTGCCCGTCTTCCTCGCGAGAG (160)
ACTCTAGCCTGGGTGACAGAAAGACTTCGTCTCAAAAAAAAAAAAAGAGAA (120)
CCACATGACTTGCCTTGGCGAGGAAATGTGAGTTCAAGCAATATGTGTCA (120)
CCCTAGCCCCGACCCGAGAGCTCCCTCTCCCGGGAGCAGGGCTCGGAGCG (120)
CCTTTAGACTGAATGTAATTGGTTTCAGTTTTCATTATAAGTTAATTATT (120)
CGTTTGGCCAGCGCGTGCGACCTCCAGGGCGCGGGTGTACCGAGTGCTGC (120)
CTCTAGGACCGTGGCAGAGGGAAAGTGAAACTGGCGGTTAGAGCCGCTAC (120)
CTGCTGAGCAGCGCCTCTCCTTCGGGCGGGGGAAGCTAAGCGGTCGCCTG (120)
CTGCTGAGCTGCCCAGCTGCTCAGTTCATTTCTTAGTGAAGTGCCTTTTT (120)
CTTCTGGGCTACACCGCCTTCTCTTCCTCCGCGGAACCCGGATCCCCTCC (120)
GAGTAAAGTGAAAGCAAGTTTACTAAGAAAGTAAGGGAGTAGGCCAGGCG (120)
GCCTCACCCCCCTCCTGTCCCAGGGCCGCGCTTCAATTTCCGCTGAAACT (120)
GGCCGGGGCTGGCCACCTCTACCCAGCACGCCGGGCAGGGCGCATGCGCG (120)
GGCTGGGACGGCGCCGGGCGTGACGTCAGGGCCCGCCCCACCGCCCTCCG (120)
GGGCAAGGCGGCGGACGGCTGCGTCGCCCGAGGCGAGGAGGAGCGCTGGC (120)
GTCCTGAAACTGTTCTAAACCATGGGGAAGGACTGCGCTATCTTAAATGT (120)
GTGTAAGACTGCTCTTTACCTCAACCTCCTTTGTTTCGCTTTTGCTTTTT (120)
GTGTGACATTGGGCAAGTCTCTGCCCGTTTCCTCATCATTGCAACCAGGG (120)
GTTACTGAGGGCGAGAAGCGCCACCCGGAGGCTCTAGCCTGACAAATGCT (120)
AAGCAAGGGGACGCGCTGCACCCTCGGCTGTCACCGCGAGGGCTCGGCGC (80)
AATTAAGACTATTGCCACCTGCAGTAAAATGGACCTCACATTTCTCTTGA (80)
ACACAGGACAGCTATAGTCAAAAAGACAAACAGGTGTGGCTAAGGATGTG (80)
Percent of unique sequences
0
20
40
60
80
100
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level