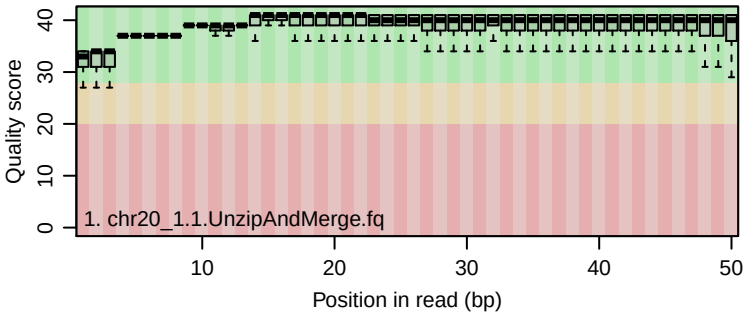
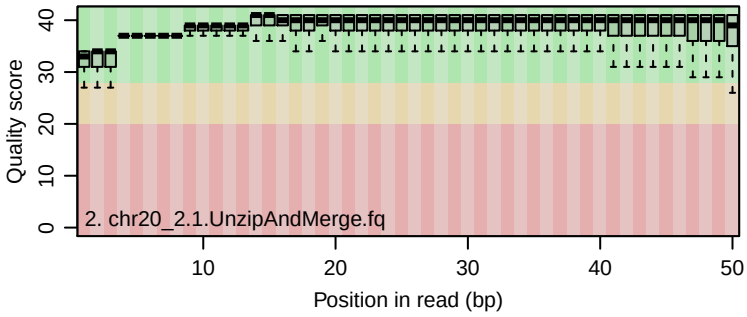

Quality score
0
10
20
30
40
1. chr20_1.1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
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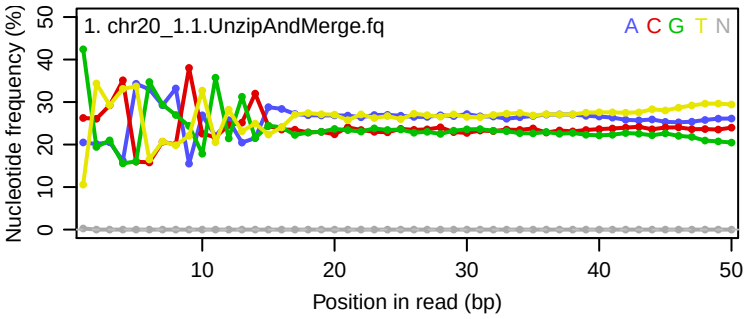
Position in read (bp)


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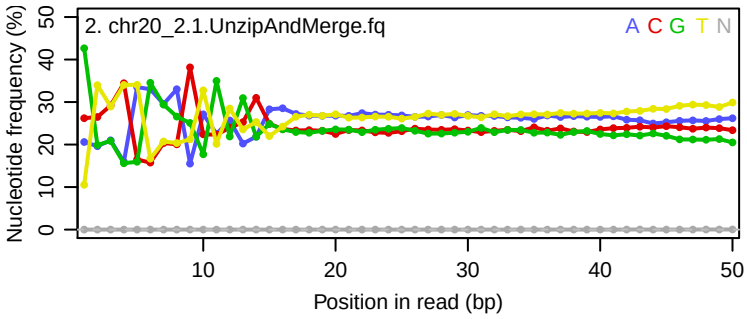
40
50
Position in read (bp)


2. chr20_2.1.UnzipAndMerge.fq
A C G T N
Nucleotide frequency (%)
0
10
20
30
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50
10
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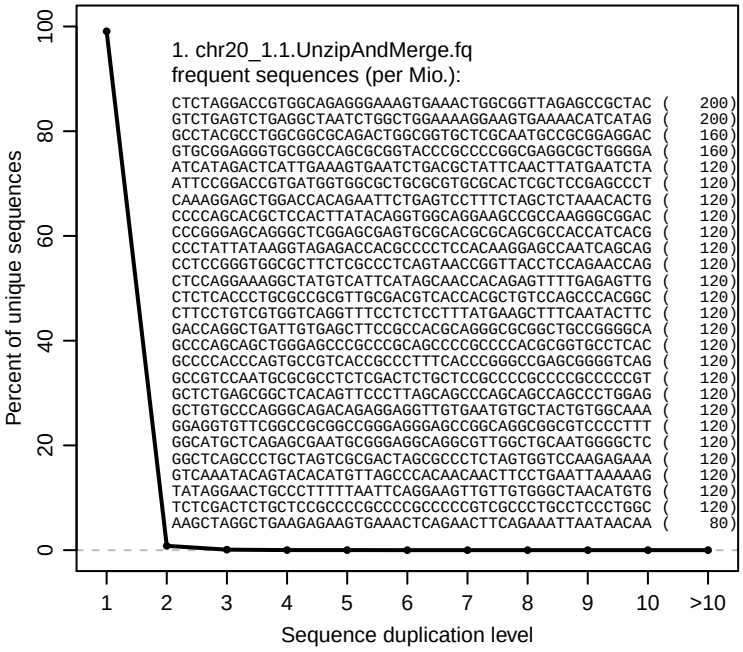
Position in read (bp)


1. chr20_1.1.UnzipAndMerge.fq
frequent sequences (per Mio.):
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GTCTGAGTCTGAGGCTAATCTGGCTGGAAAAGGAAGTGAAAACATCATAG (200)
GCCTACGCCTGGCGGCGCAGACTGGCGGTGCTCGCAATGCCGCGGAGGAC (160)
GTGCGGAGGGTGCGGCCAGCGCGGTACCCGCCCCGGCGAGGCGCTGGGGA (160)
ATCATAGACTCATTGAAAGTGAATCTGACGCTATTCAACTTATGAATCTA (120)
ATTCCGGACCGTGATGGTGGCGCTGCGCGTGCGCACTCGCTCCGAGCCCT (120)
CAAAGGAGCTGGACCACAGAATTCTGAGTCCTTTCTAGCTCTAAACACTG (120)
CCCCAGCACGCTCCACTTATACAGGTGGCAGGAAGCCGCCAAGGGCGGAC (120)
CCCGGGAGCAGGGCTCGGAGCGAGTGCGCACGCGCAGCGCCACCATCACG (120)
CCTCCGGGTGGCGCTTCTCGCCCTCAGTAACCGGTTACCTCCAGAACCAG (120)
CTCCAGGAAAGGCTATGTCATTCATAGCAACCACAGAGTTTTGAGAGTTG (120)
CTCTCACCCTGCGCCGCGTTGCGACGTCACCACGCTGTCCAGCCCACGGC (120)
CTTCCTGTCGTGGTCAGGTTTCCTCTCCTTTATGAAGCTTTCAATACTTC (120)
GACCAGGCTGATTGTGAGCTTCCGCCACGCAGGGCGCGGCTGCCGGGGCA (120)
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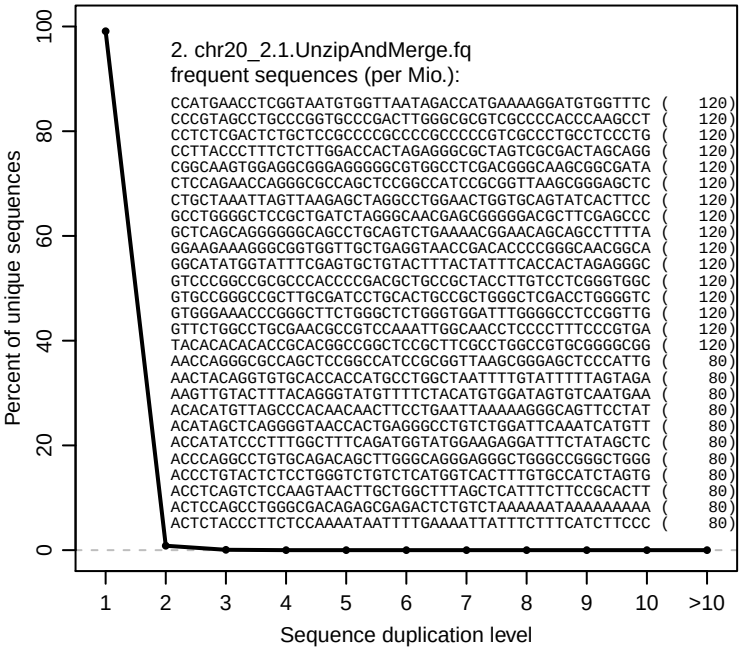
GCTGTGCCCAGGGCAGACAGAGGAGGTTGTGAATGTGCTACTGTGGCAAA (120)
GGAGGTGTTCGGCCGCGGCCGGGAGGGAGCCGGCAGGCGGCGTCCCCTTT (120)
GGCATGCTCAGAGCGAATGCGGGAGGCAGGCGTTGGCTGCAATGGGGCTC (120)
GGCTCAGCCCTGCTAGTCGCGACTAGCGCCCTCTAGTGGTCCAAGAGAAA (120)
GTCAAATACAGTACACATGTTAGCCCACAACAACTTCCTGAATTAAAAAG (120)
TATAGGAACTGCCCTTTTTAATTCAGGAAGTTGTTGTGGGCTAACATGTG (120)
TCTCGACTCTGCTCCGCCCCGCCCCGCCCCCGTCGCCCTGCCTCCCTGGC (120)
AAGCTAGGCTGAAGAGAAGTGAAACTCAGAACTTCAGAAATTAATAACAA (80)
Percent of unique sequences
Sequence duplication level


2. chr20_2.1.UnzipAndMerge.fq
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CCTTACCCTTTCTCTTGGACCACTAGAGGGCGCTAGTCGCGACTAGCAGG (120)
CGGCAAGTGGAGGCGGGAGGGGGCGTGGCCTCGACGGGCAAGCGGCGATA (120)
CTCCAGAACCAGGGCGCCAGCTCCGGCCATCCGCGGTTAAGCGGGAGCTC (120)
CTGCTAAATTAGTTAAGAGCTAGGCCTGGAACTGGTGCAGTATCACTTCC (120)
GCCTGGGGCTCCGCTGATCTAGGGCAACGAGCGGGGGACGCTTCGAGCCC (120)
GCTCAGCAGGGGGGCAGCCTGCAGTCTGAAAACGGAACAGCAGCCTTTTA (120)
GGAAGAAAGGGCGGTGGTTGCTGAGGTAACCGACACCCCGGGCAACGGCA (120)
GGCATATGGTATTTCGAGTGCTGTACTTTACTATTTCACCACTAGAGGGC (120)
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GTGCCGGGCCGCTTGCGATCCTGCACTGCCGCTGGGCTCGACCTGGGGTC (120)
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GTTCTGGCCTGCGAACGCCGTCCAAATTGGCAACCTCCCCTTTCCCGTGA (120)
TACACACACACCGCACGGCCGGCTCCGCTTCGCCTGGCCGTGCGGGGCGG (120)
AACCAGGGCGCCAGCTCCGGCCATCCGCGGTTAAGCGGGAGCTCCCATTG (80)
AACTACAGGTGTGCACCACCATGCCTGGCTAATTTTGTATTTTTAGTAGA (80)
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ACTCTACCCTTCTCCAAAATAATTTTGAAAATTATTTCTTTCATCTTCCC (80)
Percent of unique sequences
Sequence duplication level