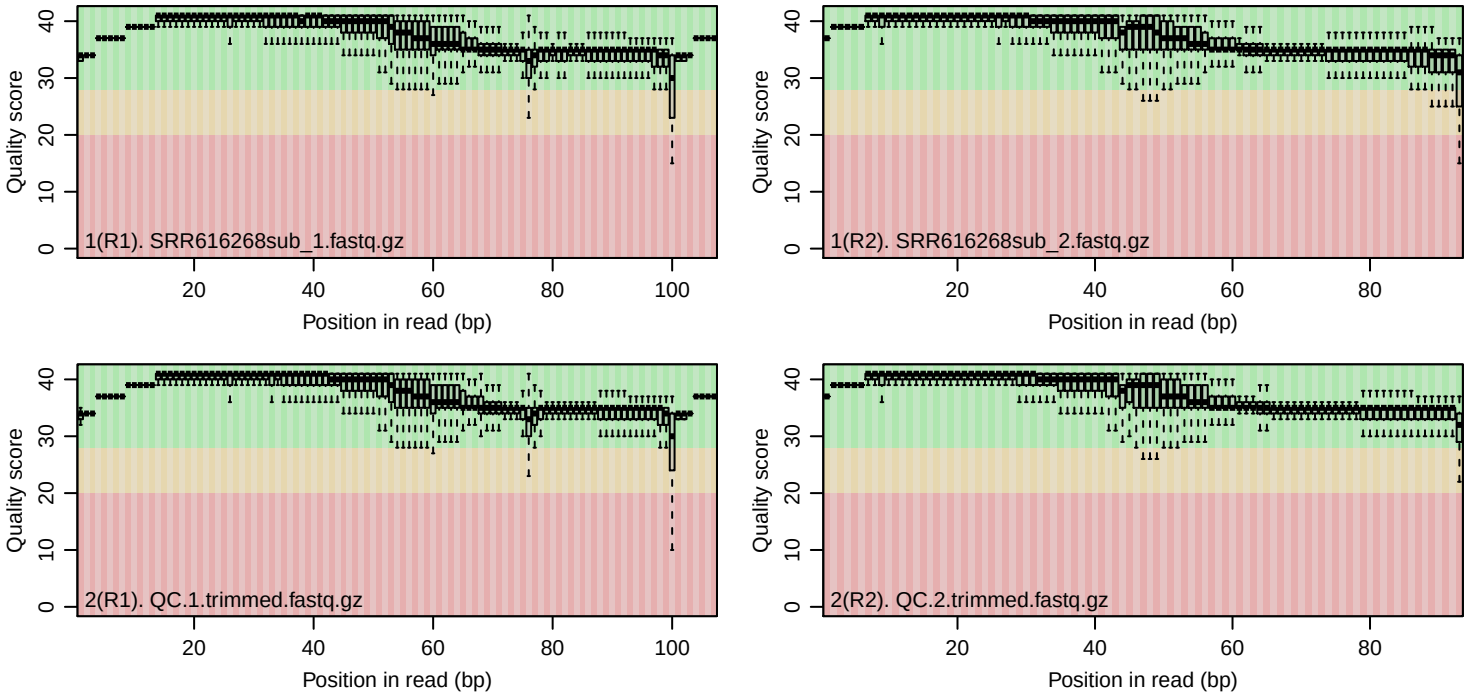
Quality score
Position in read (bp)
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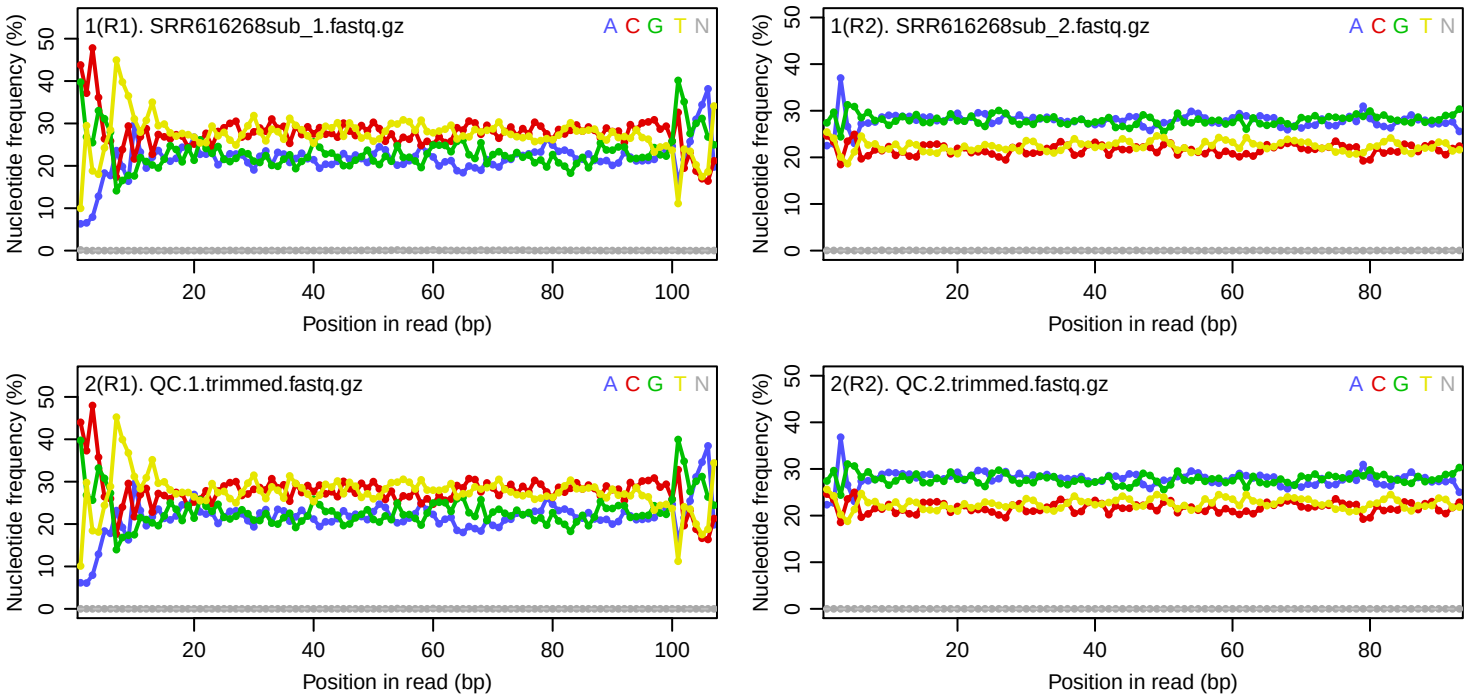
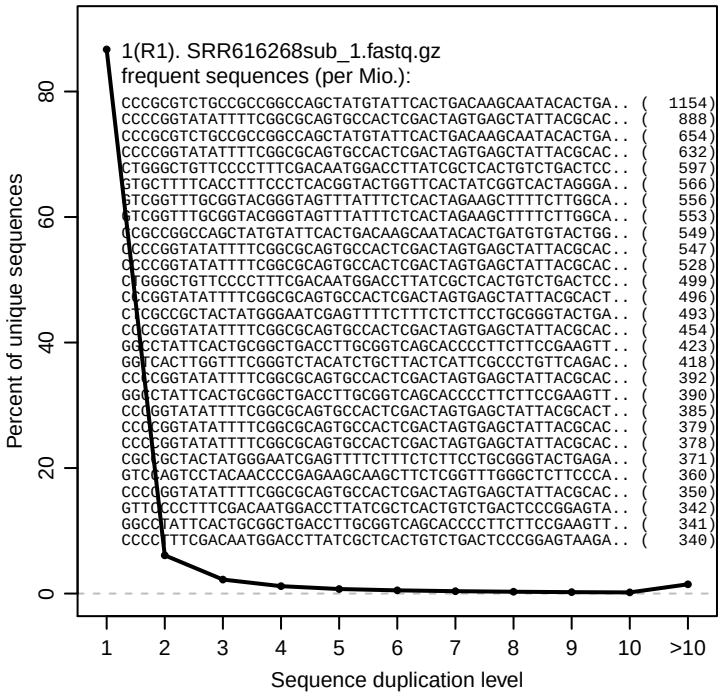
1(R2). SRR616268sub_2.fastq.gz
2(R1). QC.1.trimmed.fastq.gz
2(R2). QC.2.trimmed.fastq.gz


1(R1). SRR616268sub_1.fastq.gz
A C G T N
Nucleotide frequency (%)
Position in read (bp)
1(R2). SRR616268sub_2.fastq.gz
A C G T N
Nucleotide frequency (%)
Position in read (bp)
2(R1). QC.1.trimmed.fastq.gz
A C G T N
Nucleotide frequency (%)
Position in read (bp)
2(R2). QC.2.trimmed.fastq.gz
A C G T N
Nucleotide frequency (%)
Position in read (bp)


1(R1). SRR616268sub_1.fastq.gz
frequent sequences (per Mio.):
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CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (888)
CCCGCGTCTGCCGCCGGCCAGCTATGTATTCACTGACAAGCAATACACTGA.. (654)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (632)
CTGGGCTGTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCC.. (597)
GTGCTTTTCACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGGGA.. (566)
GTCGGTTTGCGGTACGGGTAGTTTATTTCTCACTAGAAGCTTTTCTTGGCA.. (556)
GTCGGTTTGCGGTACGGGTAGTTTATTTCTCACTAGAAGCTTTTCTTGGCA.. (553)
CCGCCGGCCAGCTATGTATTCACTGACAAGCAATACACTGATGTGTACTGG.. (549)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (547)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (528)
CTGGGCTGTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCC.. (499)
CCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCACT.. (496)
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CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (454)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (423)
GGTCACTTGGTTTCGGGTCTACATCTGCTTACTCATTCGCCCTGTTCAGAC.. (418)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (392)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (390)
CCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCACT.. (385)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (379)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (378)
CGCCGCTACTATGGGAATCGAGTTTTCTTTCTCTTCCTGCGGGTACTGAGA.. (371)
GTCCAGTCCTACAACCCCGAGAAGCAAGCTTCTCGGTTTGGGCTCTTCCCA.. (360)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCACT.. (350)
GTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCCCGGAGTA.. (342)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (341)
CCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCCCGGAGTAAGA.. (340)
Percent of unique sequences
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60
80
1
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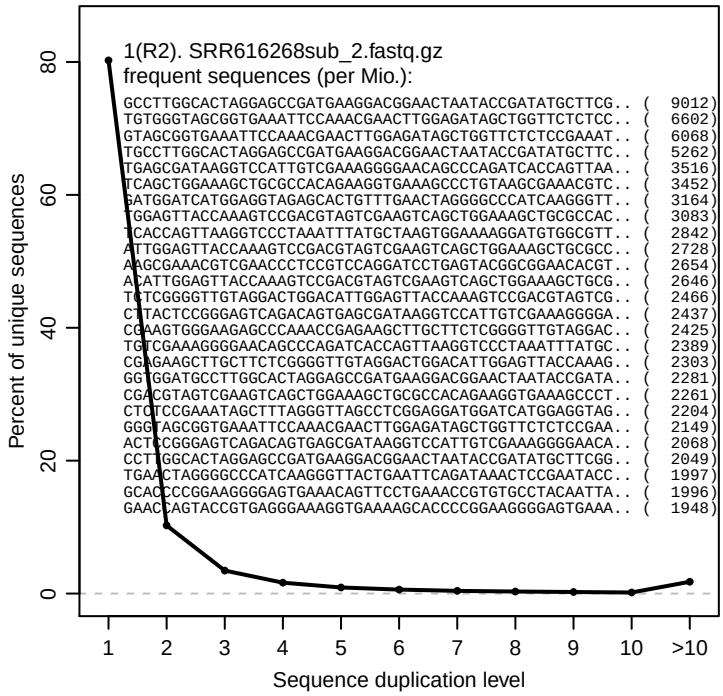
6
7
8
9
10
>10
Sequence duplication level


1(R2). SRR616268sub_2.fastq.gz
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TGCCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATATGCTTC.. (5262)
TGAGCGATAAGGTCCATTGTCGAAAGGGGAACAGCCCAGATCACCAGTTAA.. (3516)
TCAGCTGGAAAGCTGCGCCACAGAAGGTGAAAGCCCTGTAAGCGAAACGTC.. (3452)
GATGGATCATGGAGGTAGAGCACTGTTTGAACTAGGGGCCCATCAAGGGTT.. (3164)
TGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCCAC.. (3083)
TCACCAGTTAAGGTCCCTAAATTTATGCTAAGTGGAAAAGGATGTGGCGTT.. (2842)
ATTGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCC.. (2728)
AAGCGAAACGTCGAACCCTCCGTCCAGGATCCTGAGTACGGCGGAACACGT.. (2654)
ACATTGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCG.. (2646)
TCTCGGGGTTGTAGGACTGGACATTGGAGTTACCAAAGTCCGACGTAGTCG.. (2466)
CTTACTCCGGGAGTCAGACAGTGAGCGATAAGGTCCATTGTCGAAAGGGGA.. (2437)
CGAAGTGGGAAGAGCCCAAACCGAGAAGCTTGCTTCTCGGGGTTGTAGGAC.. (2425)
TGTCGAAAGGGGAACAGCCCAGATCACCAGTTAAGGTCCCTAAATTTATGC.. (2389)
CGAGAAGCTTGCTTCTCGGGGTTGTAGGACTGGACATTGGAGTTACCAAAG.. (2303)
GGTGGATGCCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATA.. (2281)
CGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCCACAGAAGGTGAAAGCCCT.. (2261)
CTCTCCGAAATAGCTTTAGGGTTAGCCTCGGAGGATGGATCATGGAGGTAG.. (2204)
GGGTAGCGGTGAAATTCCAAACGAACTTGGAGATAGCTGGTTCTCTCCGAA.. (2149)
ACTCCGGGAGTCAGACAGTGAGCGATAAGGTCCATTGTCGAAAGGGGAACA.. (2068)
CCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATATGCTTCGG.. (2049)
TGAACTAGGGGCCCATCAAGGGTTACTGAATTCAGATAAACTCCGAATACC.. (1997)
GCACCCCGGAAGGGGAGTGAAACAGTTCCTGAAACCGTGTGCCTACAATTA.. (1996)
GAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCGGAAGGGGAGTGAAA.. (1948)
Percent of unique sequences
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40
60
80
1
2
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4
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6
7
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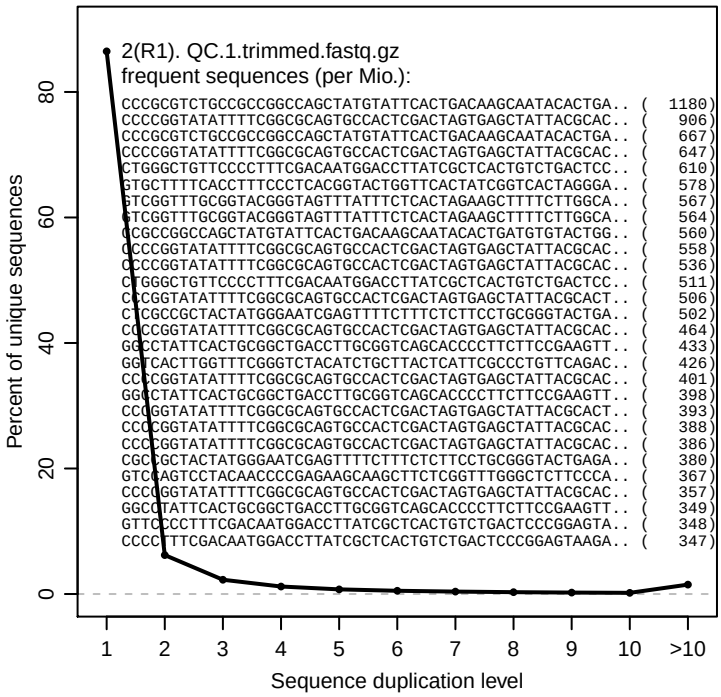
10
>10
Sequence duplication level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CCCGCGTCTGCCGCCGGCCAGCTATGTATTCACTGACAAGCAATACACTGA.. (667)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (647)
CTGGGCTGTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCC.. (610)
GTGCTTTTCACCTTTCCCTCACGGTACTGGTTCACTATCGGTCACTAGGGA.. (578)
GTCGGTTTGCGGTACGGGTAGTTTATTTCTCACTAGAAGCTTTTCTTGGCA.. (567)
GTCGGTTTGCGGTACGGGTAGTTTATTTCTCACTAGAAGCTTTTCTTGGCA.. (564)
CCGCCGGCCAGCTATGTATTCACTGACAAGCAATACACTGATGTGTACTGG.. (560)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (558)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (536)
CTGGGCTGTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCC.. (511)
CCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCACT.. (506)
CTCGCCGCTACTATGGGAATCGAGTTTTCTTTCTCTTCCTGCGGGTACTGA.. (502)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (464)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (433)
GGTCACTTGGTTTCGGGTCTACATCTGCTTACTCATTCGCCCTGTTCAGAC.. (426)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (401)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (398)
CCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCACT.. (393)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (388)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (386)
CGCCGCTACTATGGGAATCGAGTTTTCTTTCTCTTCCTGCGGGTACTGAGA.. (380)
GTCCAGTCCTACAACCCCGAGAAGCAAGCTTCTCGGTTTGGGCTCTTCCCA.. (367)
CCCCGGTATATTTTCGGCGCAGTGCCACTCGACTAGTGAGCTATTACGCAC.. (357)
GGCCTATTCACTGCGGCTGACCTTGCGGTCAGCACCCCTTCTTCCGAAGTT.. (349)
GTTCCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCCCGGAGTA.. (348)
CCCCTTTCGACAATGGACCTTATCGCTCACTGTCTGACTCCCGGAGTAAGA.. (347)
Percent of unique sequences
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60
80
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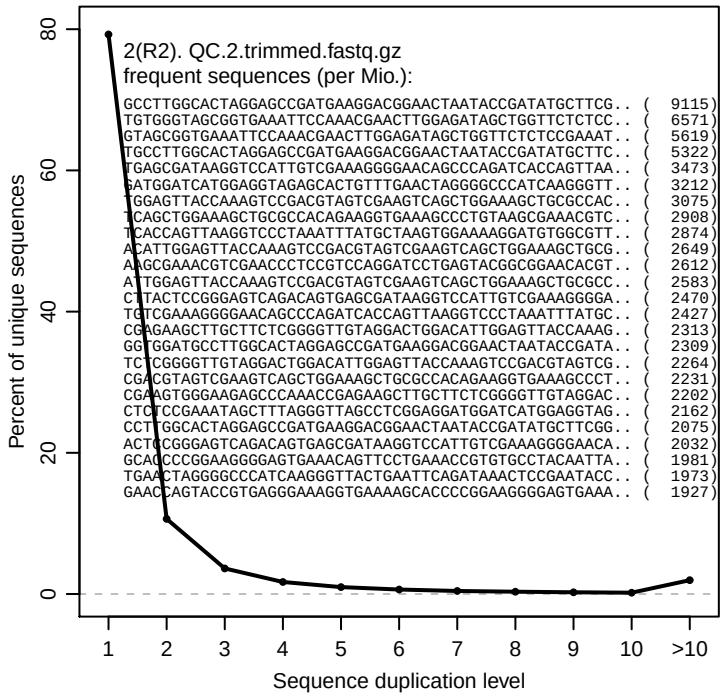
10
>10
Sequence duplication level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frequent sequences (per Mio.):
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TGCCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATATGCTTC.. (5322)
TGAGCGATAAGGTCCATTGTCGAAAGGGGAACAGCCCAGATCACCAGTTAA.. (3473)
GATGGATCATGGAGGTAGAGCACTGTTTGAACTAGGGGCCCATCAAGGGTT.. (3212)
TGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCCAC.. (3075)
TCAGCTGGAAAGCTGCGCCACAGAAGGTGAAAGCCCTGTAAGCGAAACGTC.. (2908)
TCACCAGTTAAGGTCCCTAAATTTATGCTAAGTGGAAAAGGATGTGGCGTT.. (2874)
ACATTGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCG.. (2649)
AAGCGAAACGTCGAACCCTCCGTCCAGGATCCTGAGTACGGCGGAACACGT.. (2612)
ATTGGAGTTACCAAAGTCCGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCC.. (2583)
CTTACTCCGGGAGTCAGACAGTGAGCGATAAGGTCCATTGTCGAAAGGGGA.. (2470)
TGTCGAAAGGGGAACAGCCCAGATCACCAGTTAAGGTCCCTAAATTTATGC.. (2427)
CGAGAAGCTTGCTTCTCGGGGTTGTAGGACTGGACATTGGAGTTACCAAAG.. (2313)
GGTGGATGCCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATA.. (2309)
TCTCGGGGTTGTAGGACTGGACATTGGAGTTACCAAAGTCCGACGTAGTCG.. (2264)
CGACGTAGTCGAAGTCAGCTGGAAAGCTGCGCCACAGAAGGTGAAAGCCCT.. (2231)
CGAAGTGGGAAGAGCCCAAACCGAGAAGCTTGCTTCTCGGGGTTGTAGGAC.. (2202)
CTCTCCGAAATAGCTTTAGGGTTAGCCTCGGAGGATGGATCATGGAGGTAG.. (2162)
CCTTGGCACTAGGAGCCGATGAAGGACGGAACTAATACCGATATGCTTCGG.. (2075)
ACTCCGGGAGTCAGACAGTGAGCGATAAGGTCCATTGTCGAAAGGGGAACA.. (2032)
GCACCCCGGAAGGGGAGTGAAACAGTTCCTGAAACCGTGTGCCTACAATTA.. (1981)
TGAACTAGGGGCCCATCAAGGGTTACTGAATTCAGATAAACTCCGAATACC.. (1973)
GAACCAGTACCGTGAGGGAAAGGTGAAAAGCACCCCGGAAGGGGAGTGAAA.. (1927)
Percent of unique sequences
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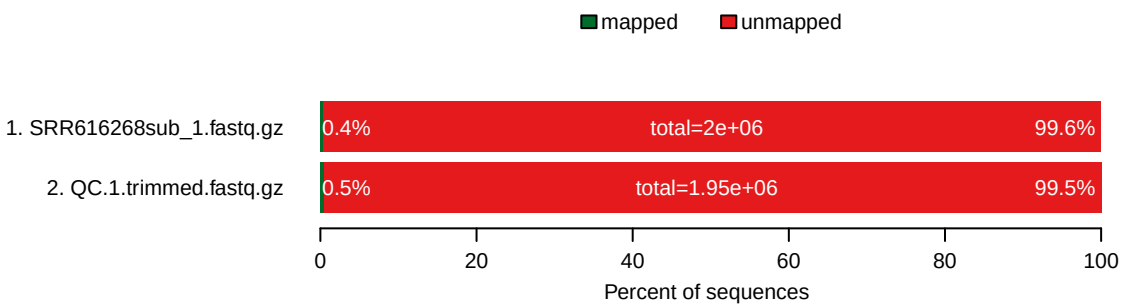
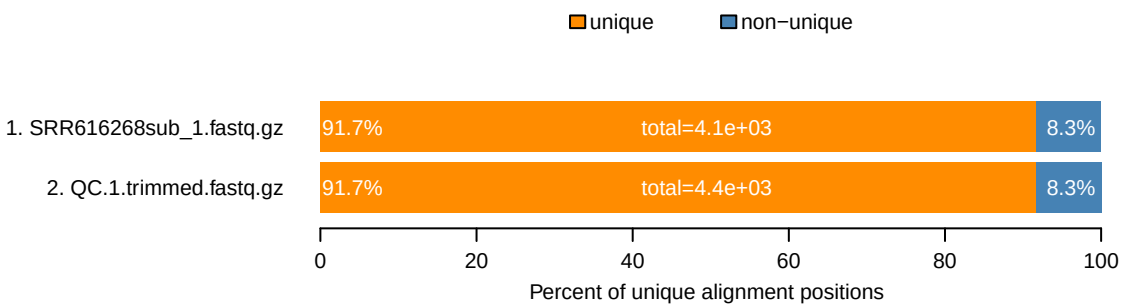
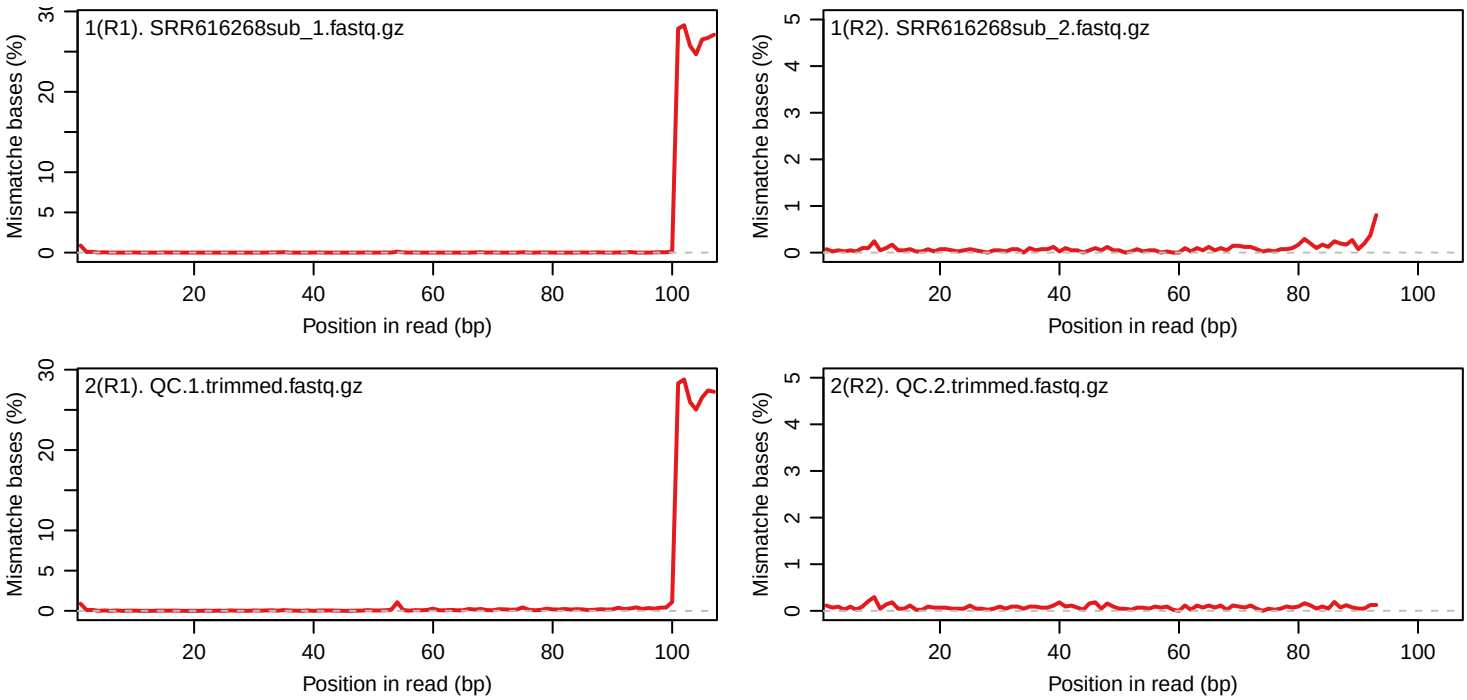
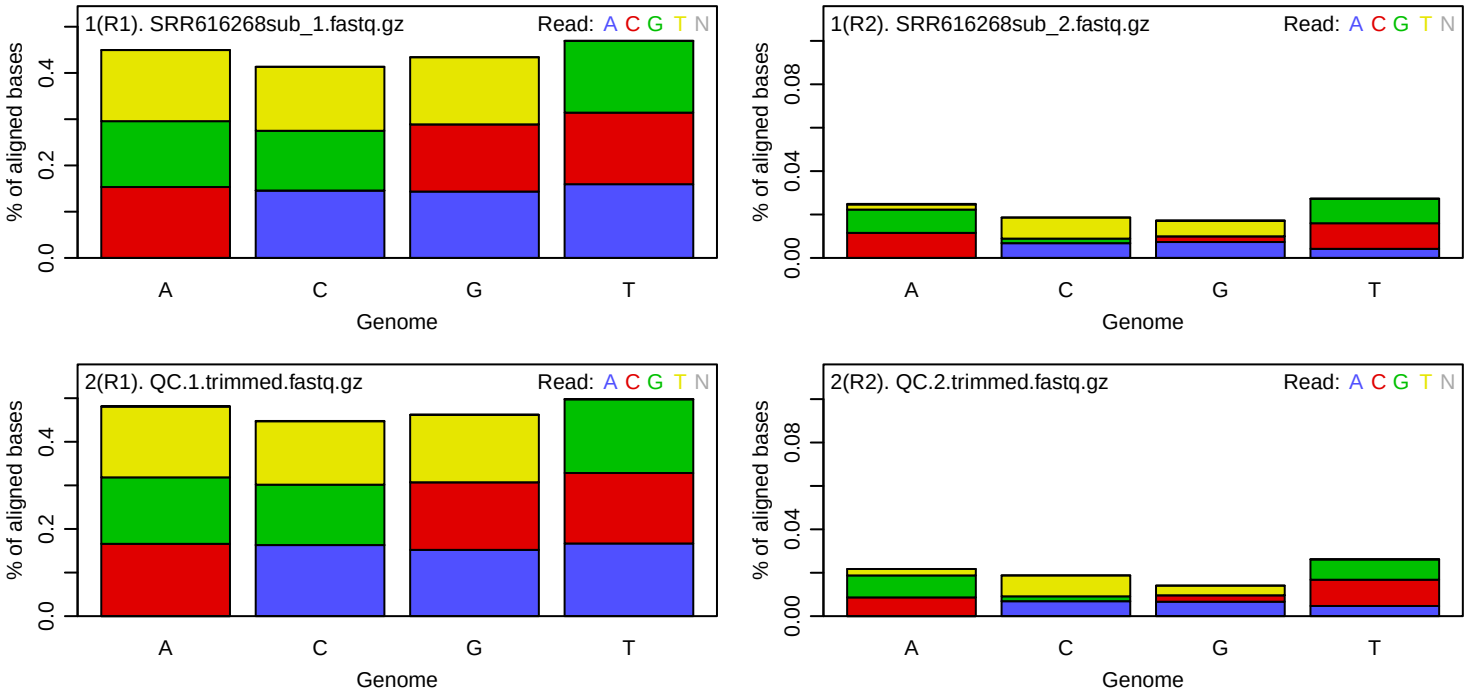
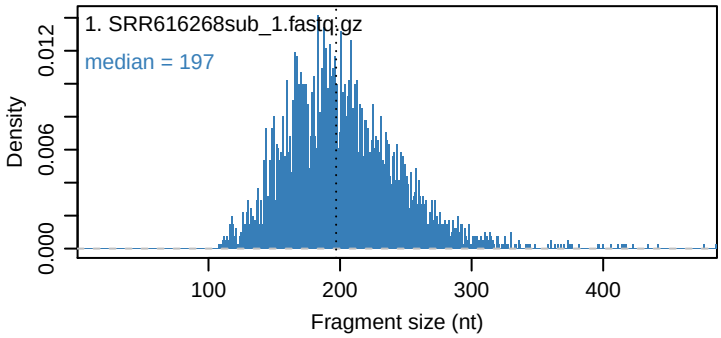
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


mapped
unmapped
1. SRR616268sub_1.fastq.gz
0.4%
total=2e+06
99.6%
2. QC.1.trimmed.fastq.gz
0.5%
total=1.95e+06
99.5%
0
20
40
60
80
100
Percent of sequences


unique
non−unique
1. SRR616268sub_1.fastq.gz
91.7%
total=4.1e+03
8.3%
2. QC.1.trimmed.fastq.gz
91.7%
total=4.4e+03
8.3%
0
20
40
60
80
100
Percent of unique alignment positions


1(R1). SRR616268sub_1.fastq.gz
Mismatche bases (%)
Position in read (bp)
1(R2). SRR616268sub_2.fastq.gz
Mismatche bases (%)
Position in read (bp)
2(R1). QC.1.trimmed.fastq.gz
Mismatche bases (%)
Position in read (bp)
2(R2). QC.2.trimmed.fastq.gz
Mismatche bases (%)
Position in read (bp)


1(R1). SRR616268sub_1.fastq.gz
Read: A C G T N
% of aligned bases
0.0
0.2
0.4
A
C
G
T
Genome
1(R2). SRR616268sub_2.fastq.gz
Read: A C G T N
% of aligned bases
0.00
0.04
0.08
A
C
G
T
Genome
2(R1). QC.1.trimmed.fastq.gz
Read: A C G T N
% of aligned bases
0.0
0.2
0.4
A
C
G
T
Genome
2(R2). QC.2.trimmed.fastq.gz
Read: A C G T N
% of aligned bases
0.00
0.04
0.08
A
C
G
T
Genome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Density
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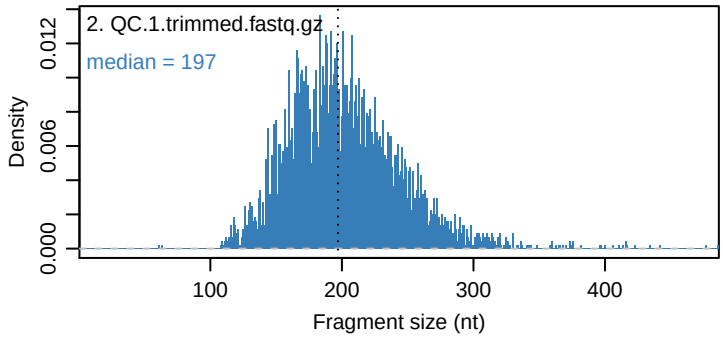
0.006
0.012
100
200
300
400
Fragment size (nt)


2. QC.1.trimmed.fastq.gz
median = 197
Density
0.000
0.006
0.012
100
200
300
400
Fragment size (nt)