Report

	SRR1191991_fw_80_complete
# contigs (>= 0 bp)	71
# contigs (>= 1000 bp)	43
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	270199
Total length (>= 1000 bp)	249684
Total length (>= 5000 bp)	208527
Total length (>= 10000 bp)	141059
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	71
Largest contig	14979
Total length	270199
Reference length	30114
N50	10392
N75	5018
L50	11
L75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.782
Duplication ratio	10.839
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4849.77
# indels per 100 kbp	20.06
Largest alignment	14978
Total aligned length	270133
NA50	10391
NA75	5017
LA50	11
LA75	21

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

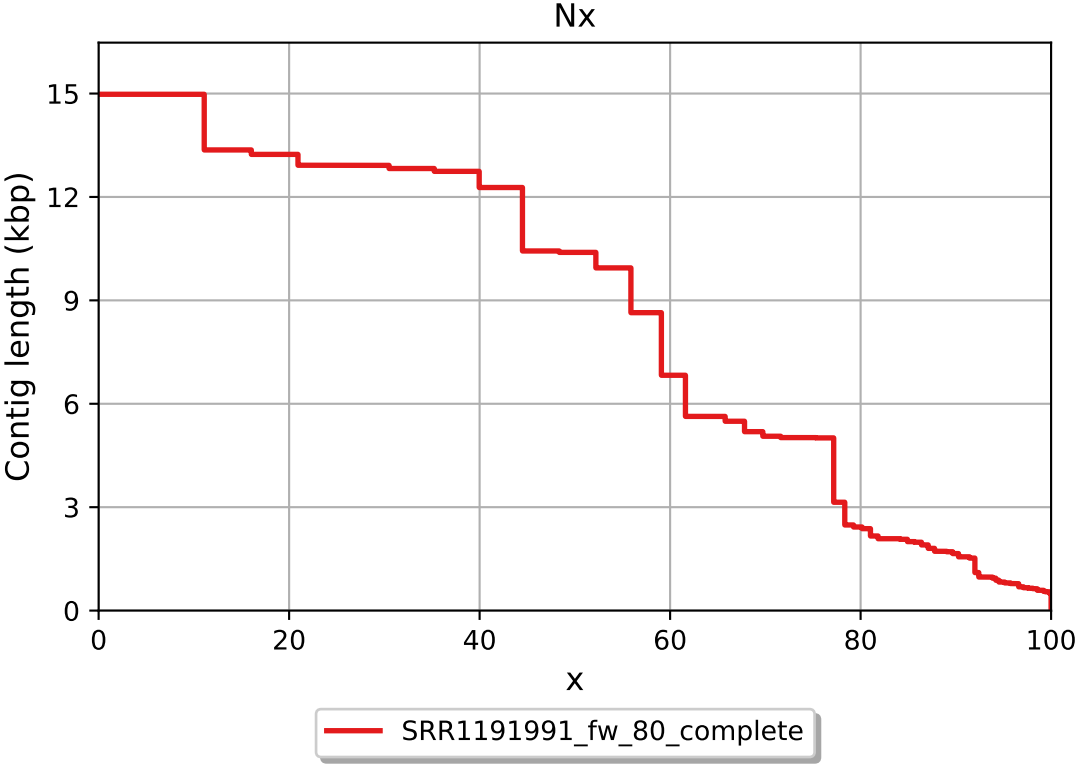
	SRR1191991_fw_80_complete
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1209
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	14

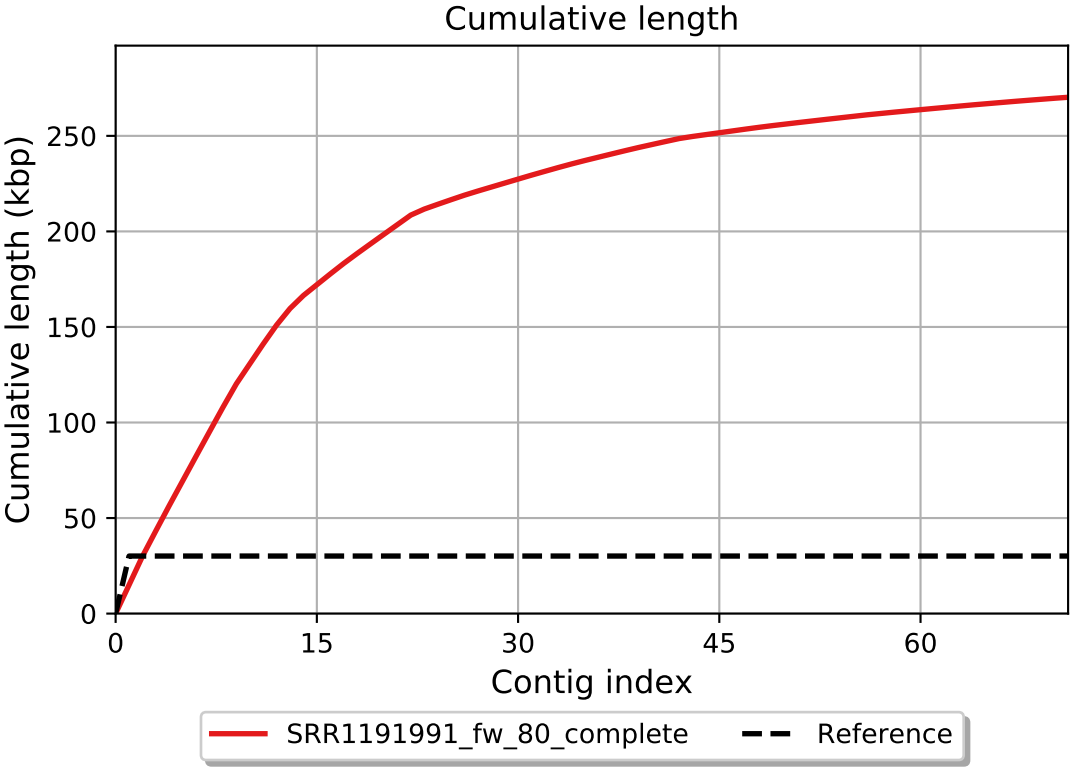
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

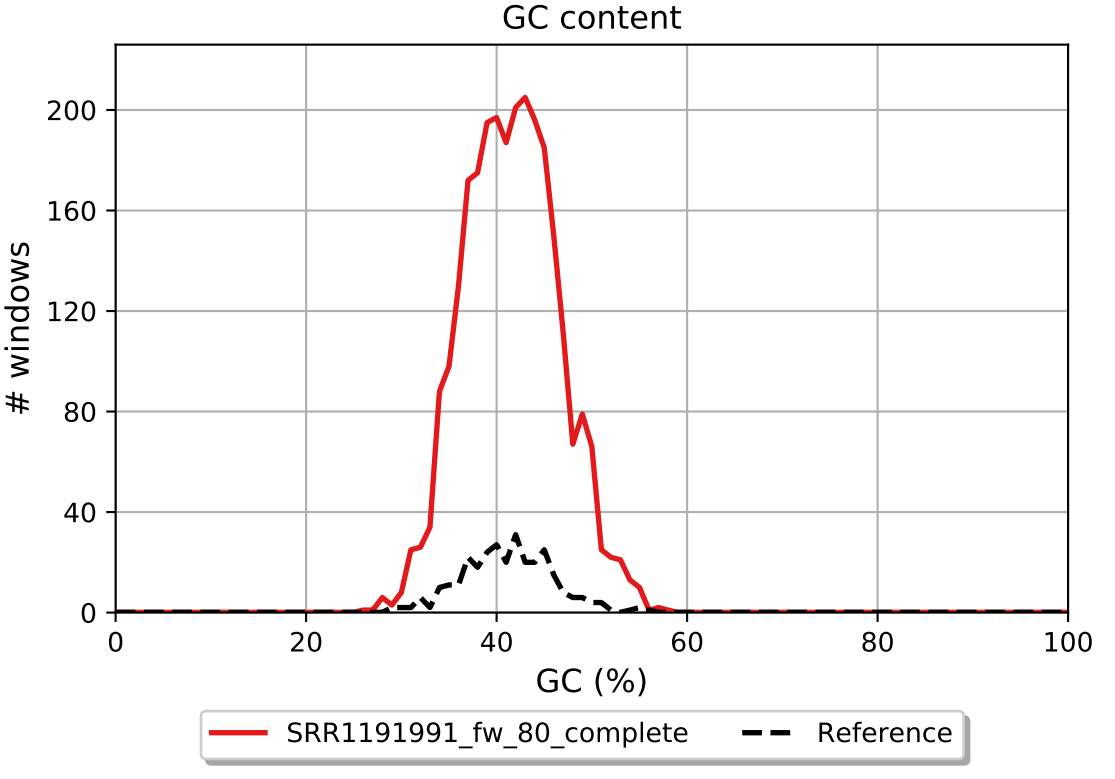
Unaligned report

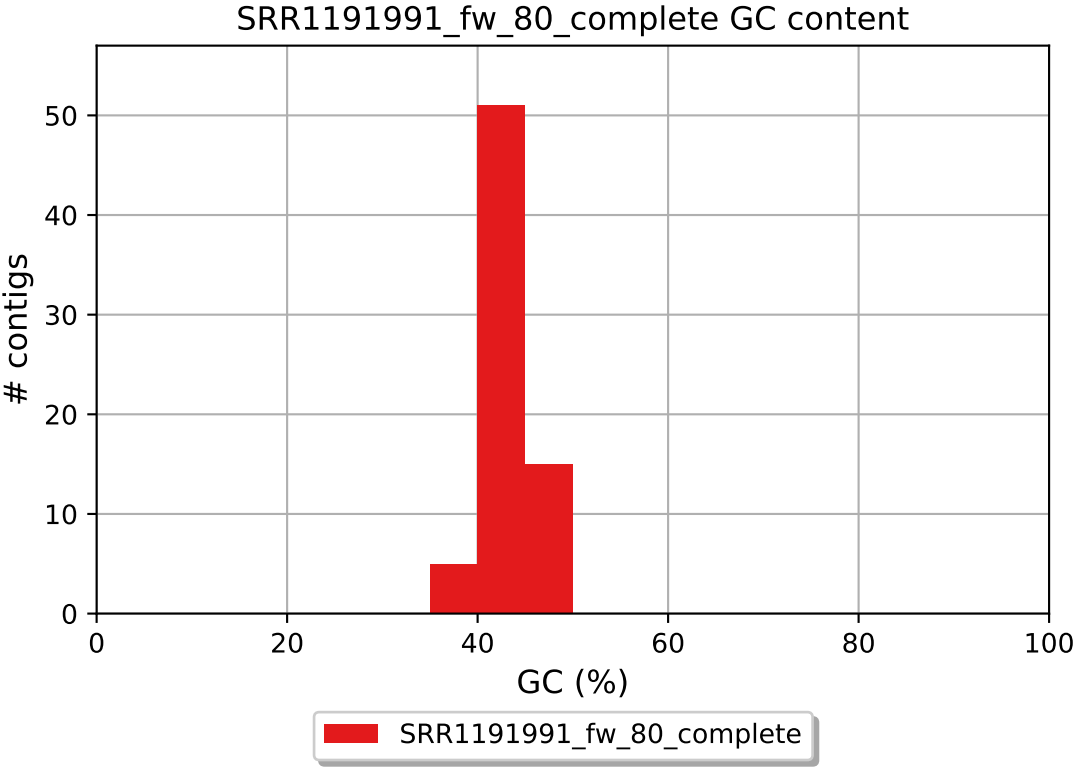
	SRR1191991_fw_80_complete
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

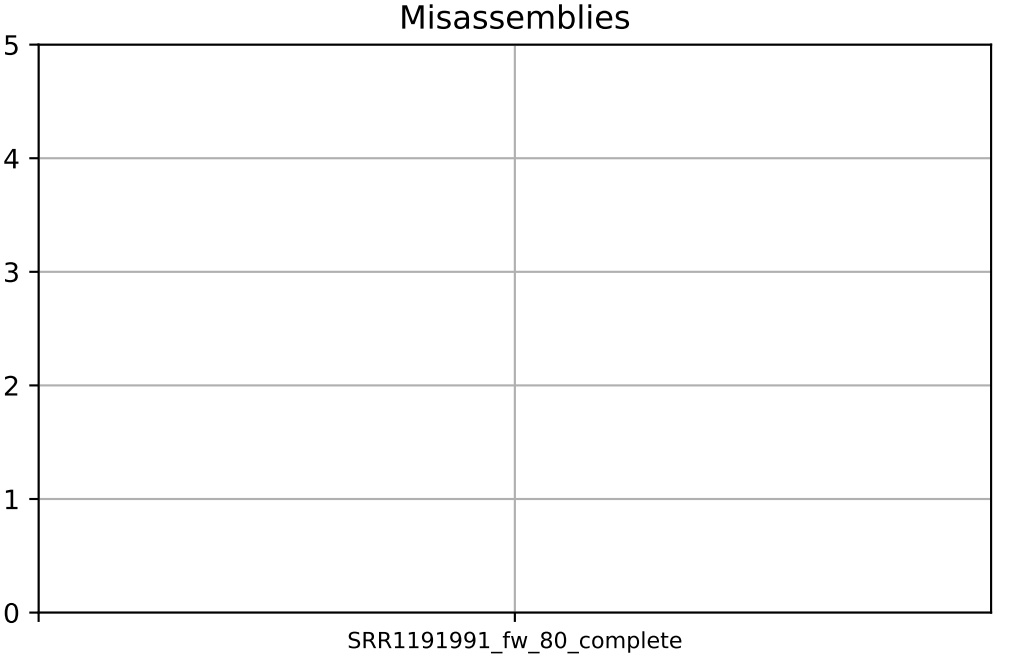
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

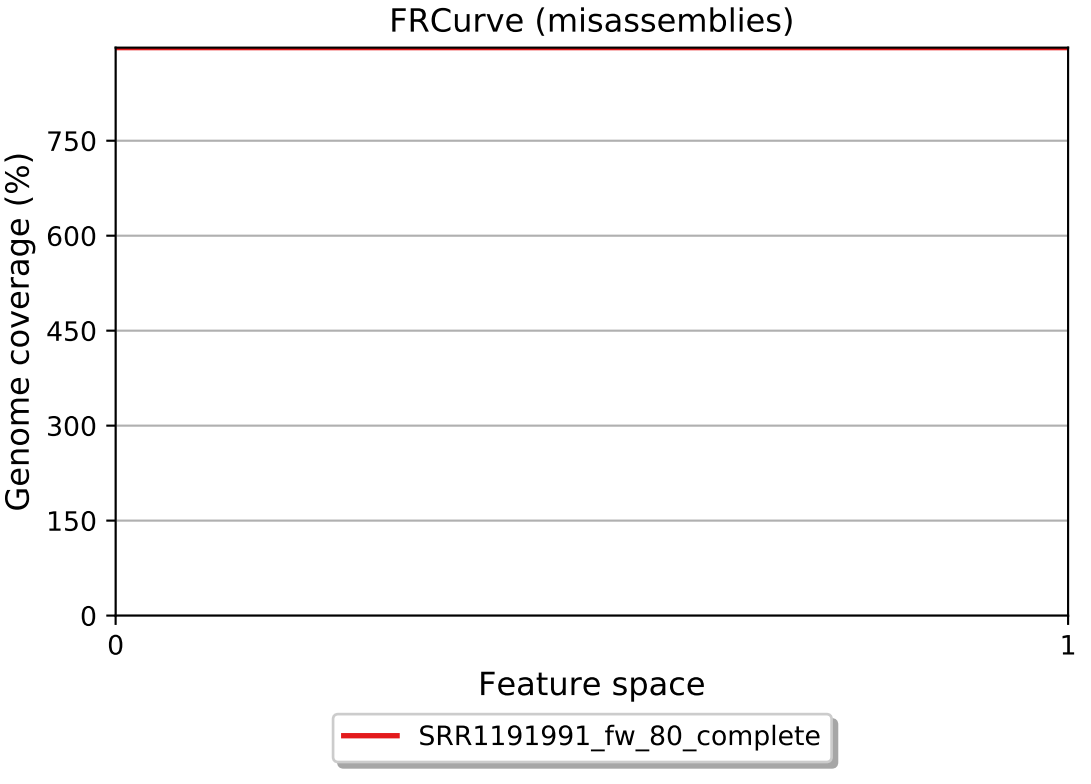

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
SRR1191991_fw_80_complete

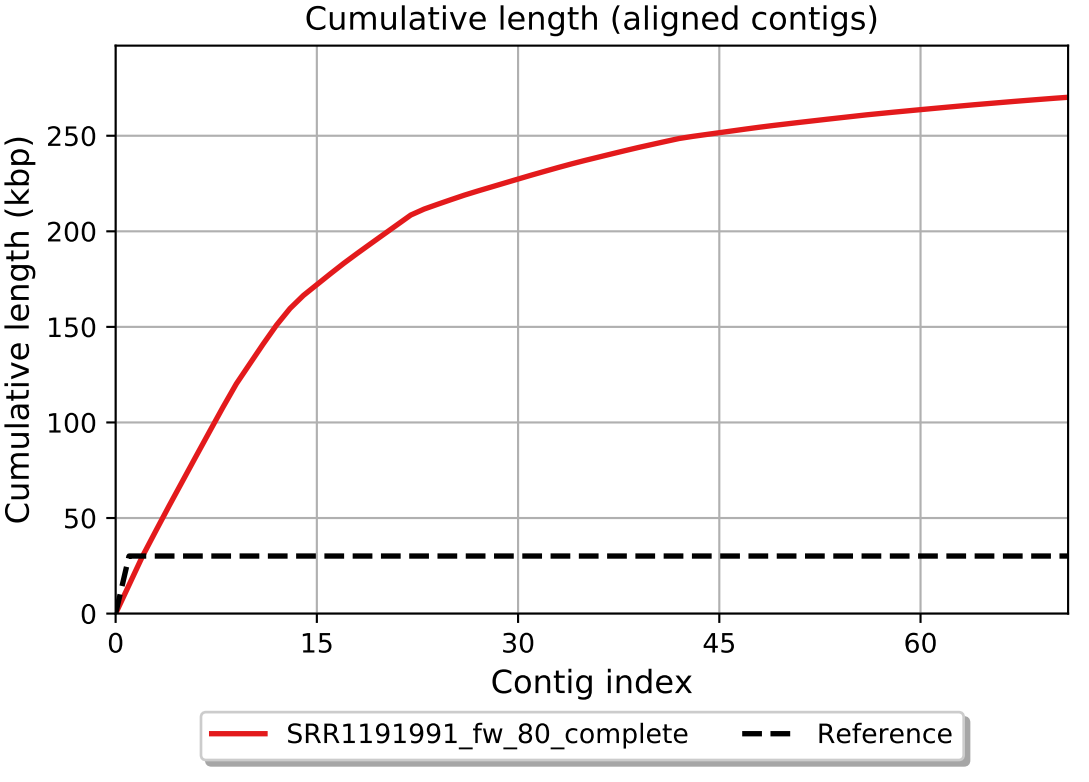

Cumulative length
Cumulative length (kbp)
250
200
150
100
50
0
0
15
30
45
60
Contig index
SRR1191991_fw_80_complete
Reference

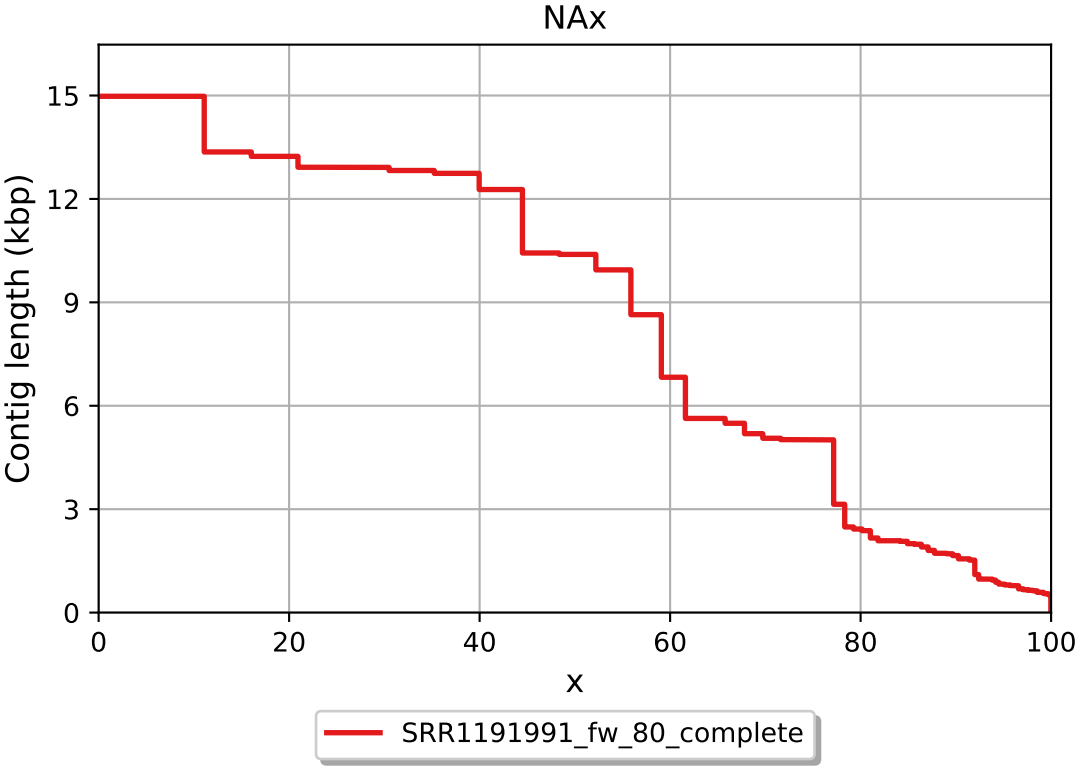

GC content
windows
200
160
120
80
40
0
0
20
40
60
80
100
GC (%)
SRR1191991_fw_80_complete
Reference


SRR1191991_fw_80_complete GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
SRR1191991_fw_80_complete


Misassemblies
5
4
3
2
1
0
SRR1191991_fw_80_complete


FRCurve (misassemblies)
Genome coverage (%)
750
600
450
300
150
0
0
1
Feature space
SRR1191991_fw_80_complete


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
50
100
150
200
250
0
15
30
45
60
Contig index
SRR1191991_fw_80_complete
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
SRR1191991_fw_80_complete