Report

	SRR.asm.bp.p_ctg
# contigs (>= 0 bp)	49
# contigs (>= 1000 bp)	49
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	12730920
Total length (>= 1000 bp)	12730920
Total length (>= 5000 bp)	12730920
Total length (>= 10000 bp)	12730920
Total length (>= 25000 bp)	12243602
Total length (>= 50000 bp)	12121907
# contigs	49
Largest contig	1506376
Total length	12730920
Reference length	12157105
GC (%)	38.44
Reference GC (%)	38.15
N50	809047
NG50	809047
N90	350316
NG90	441569
auN	820915.5
auNG	859662.7
L50	6
LG50	6
L90	15
LG90	14
# misassemblies	119
# misassembled contigs	41
Misassembled contigs length	12606913
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 17 part
Unaligned length	112206
Genome fraction (%)	97.420
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	205.78
# indels per 100 kbp	27.64
Largest alignment	843303
Total aligned length	12608885
NA50	273893
NGA50	284119
NA90	73482
NGA90	109892
auNA	357642.4
auNGA	374523.1
LA50	13
LGA50	12
LA90	46
LGA90	40

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

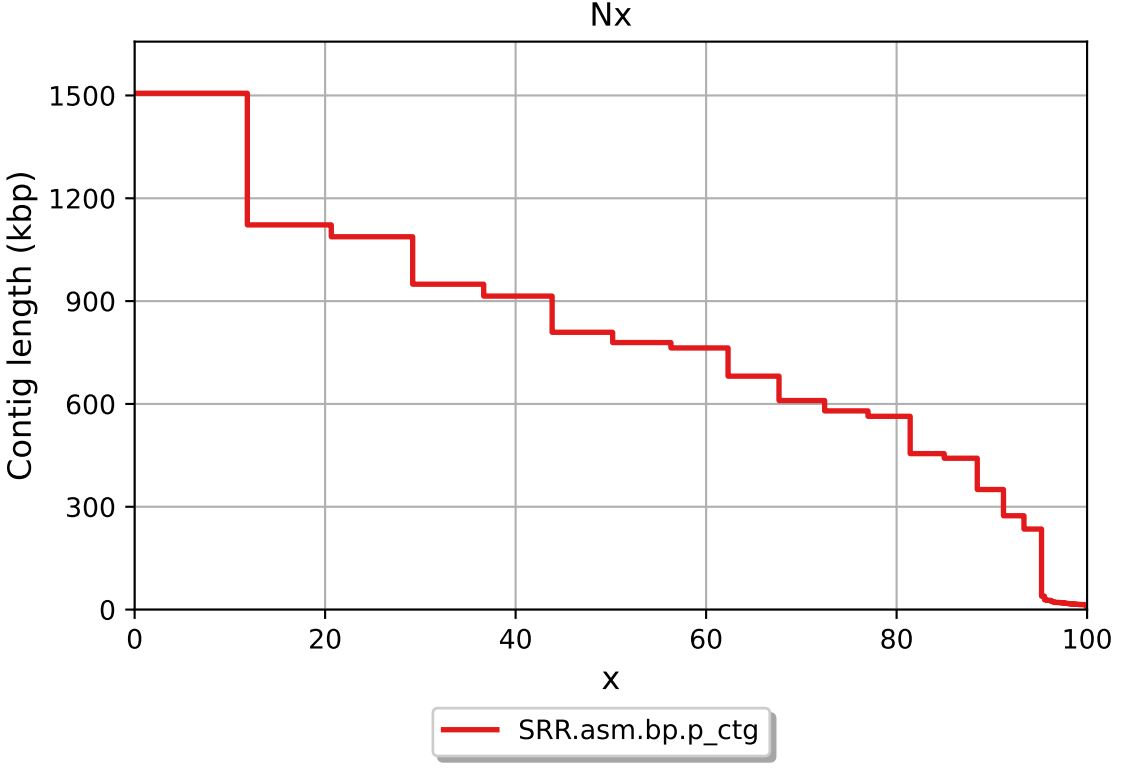
	SRR.asm.bp.p_ctg
# misassemblies	119
# contig misassemblies	119
# c. relocations	61
# c. translocations	58
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	41
Misassembled contigs length	12606913
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	25947
# indels	3485
# indels (<= 5 bp)	3002
# indels (> 5 bp)	483
Indels length	17599

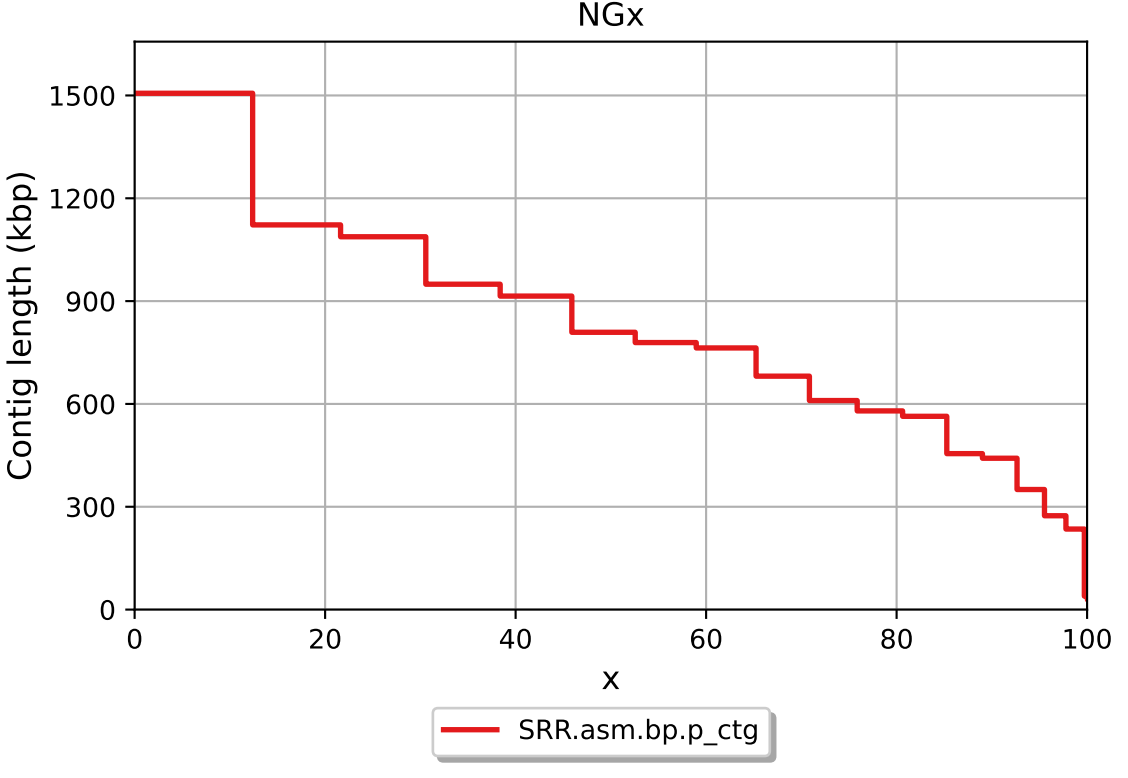
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

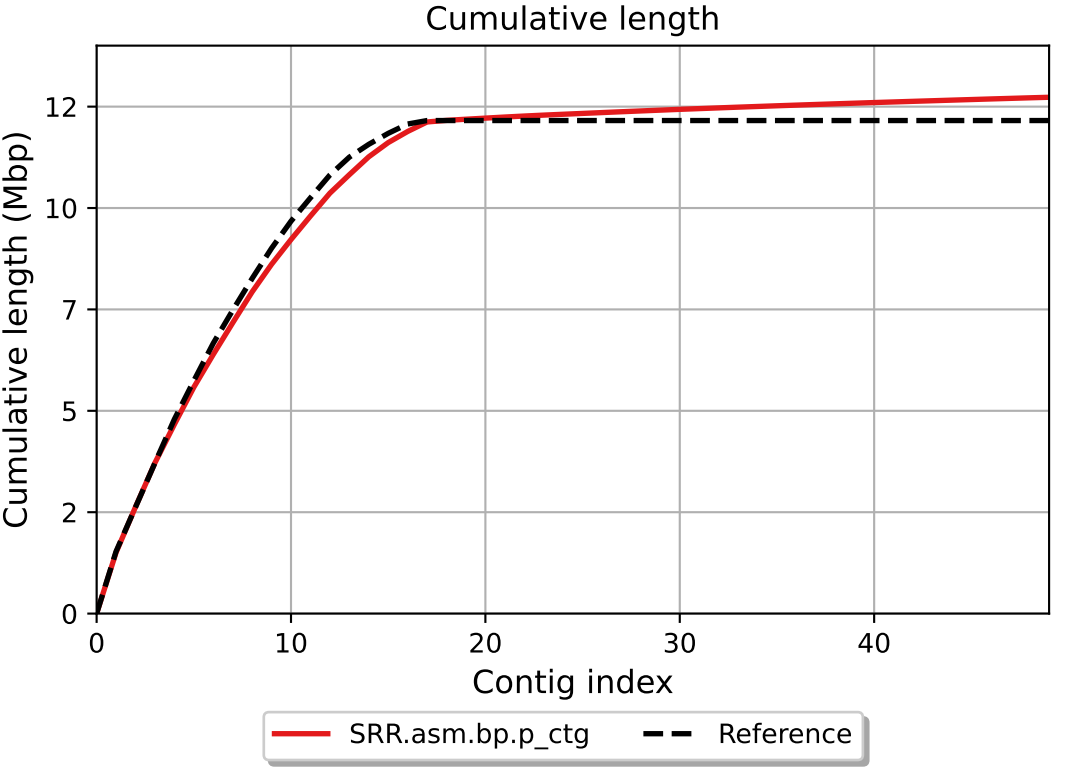
Unaligned report

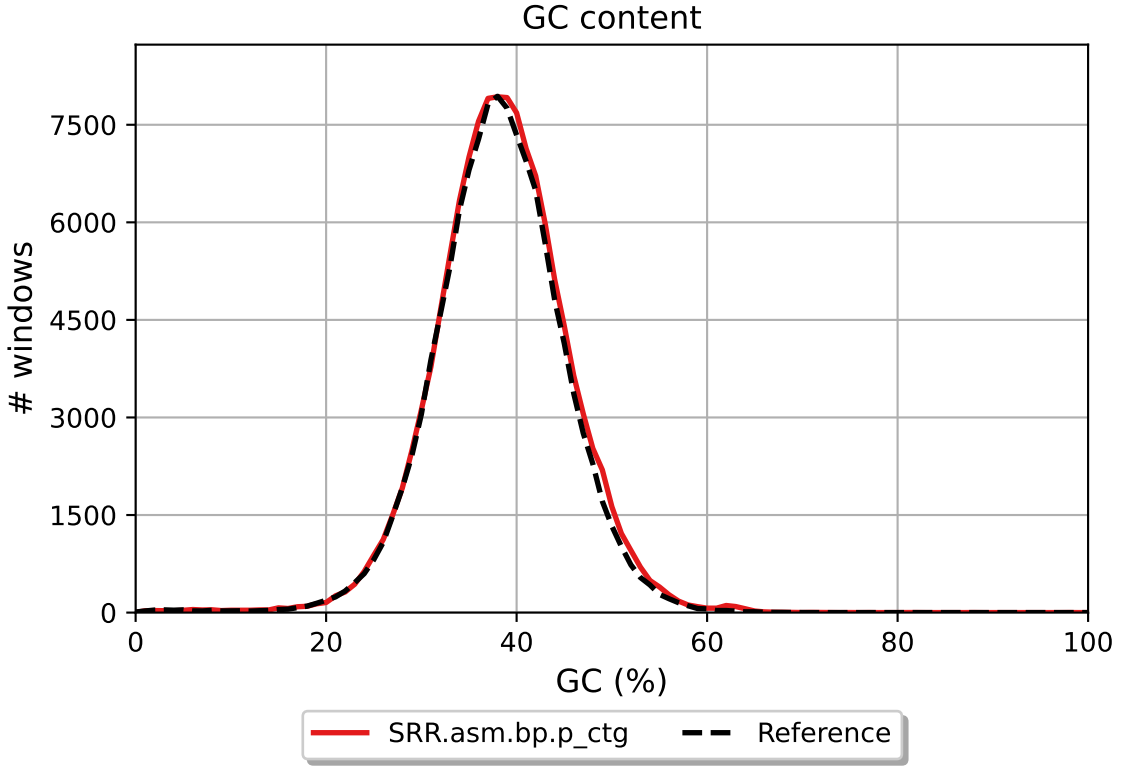
	SRR.asm.bp.p_ctg
# fully unaligned contigs	1
Fully unaligned length	16066
# partially unaligned contigs	17
Partially unaligned length	96140
# N's	0

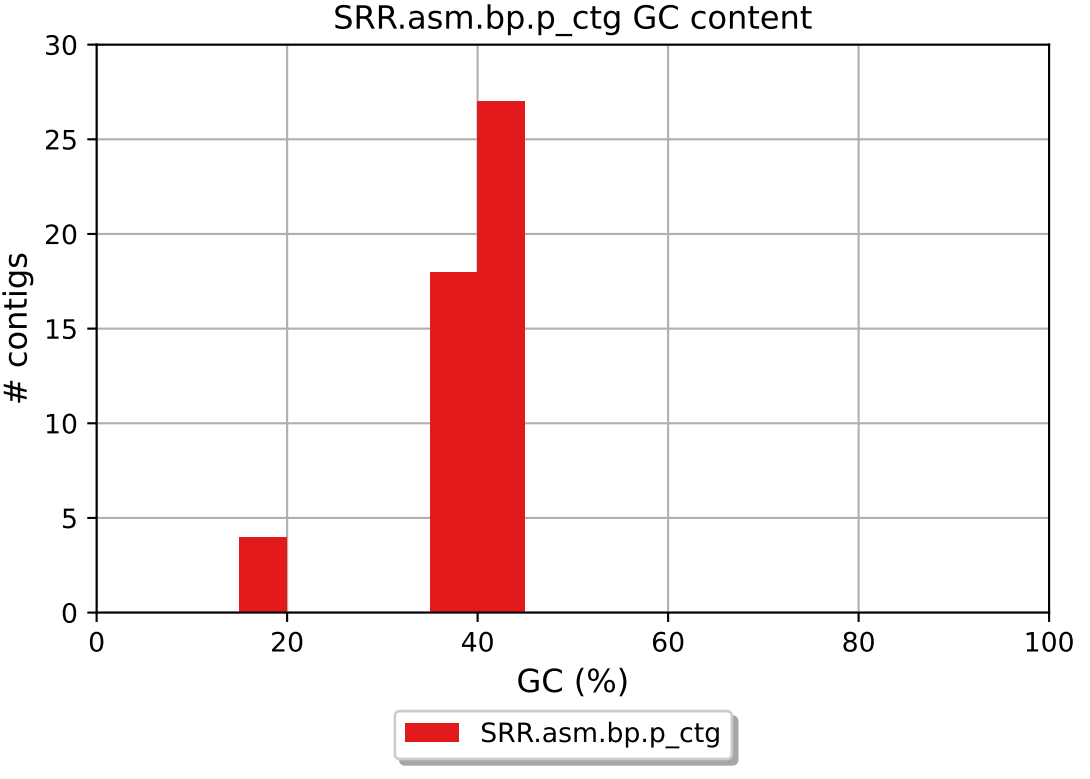
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

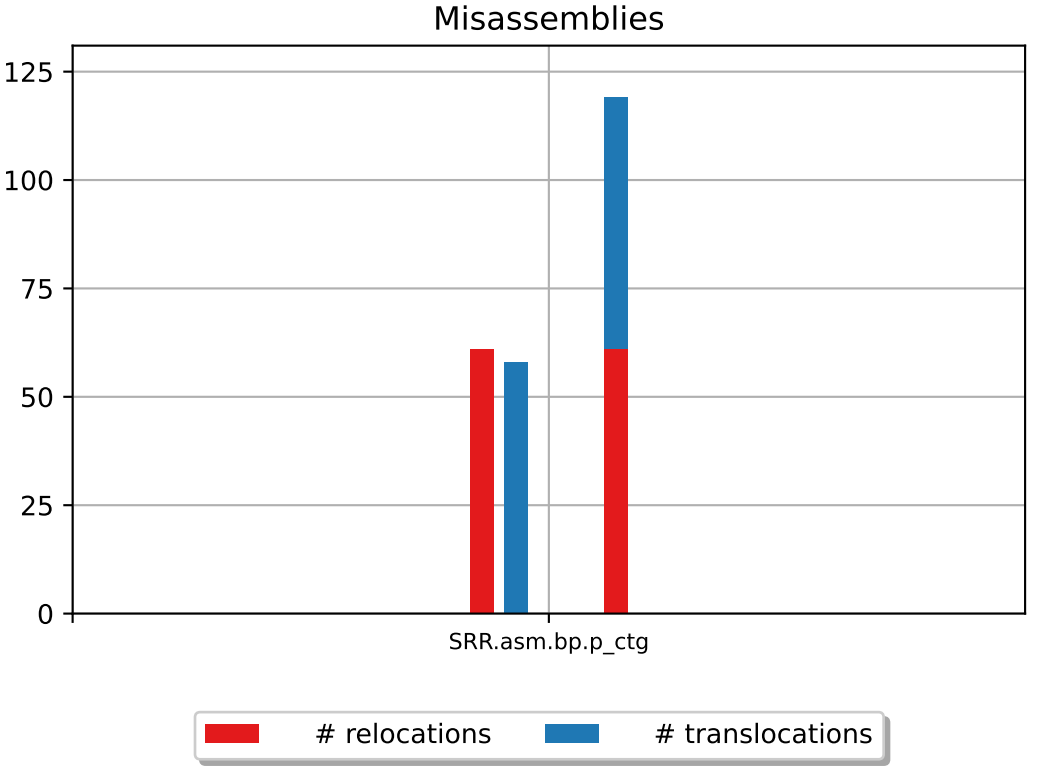

Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
SRR.asm.bp.p_ctg

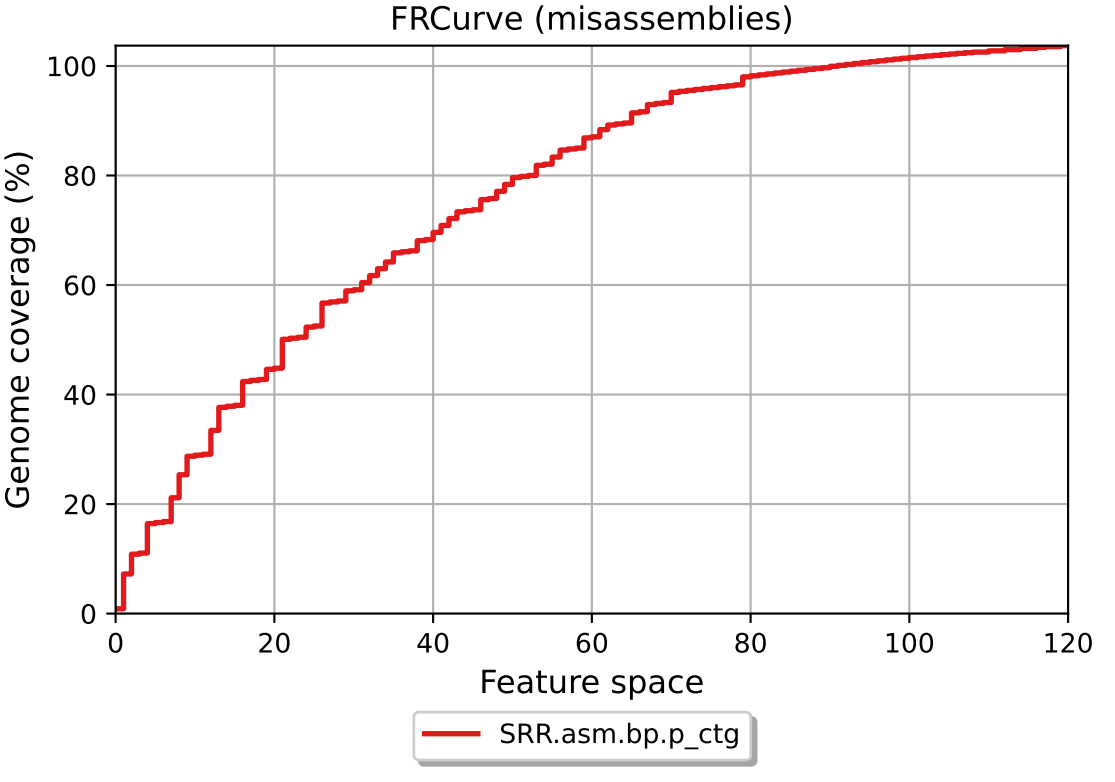

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
SRR.asm.bp.p_ctg

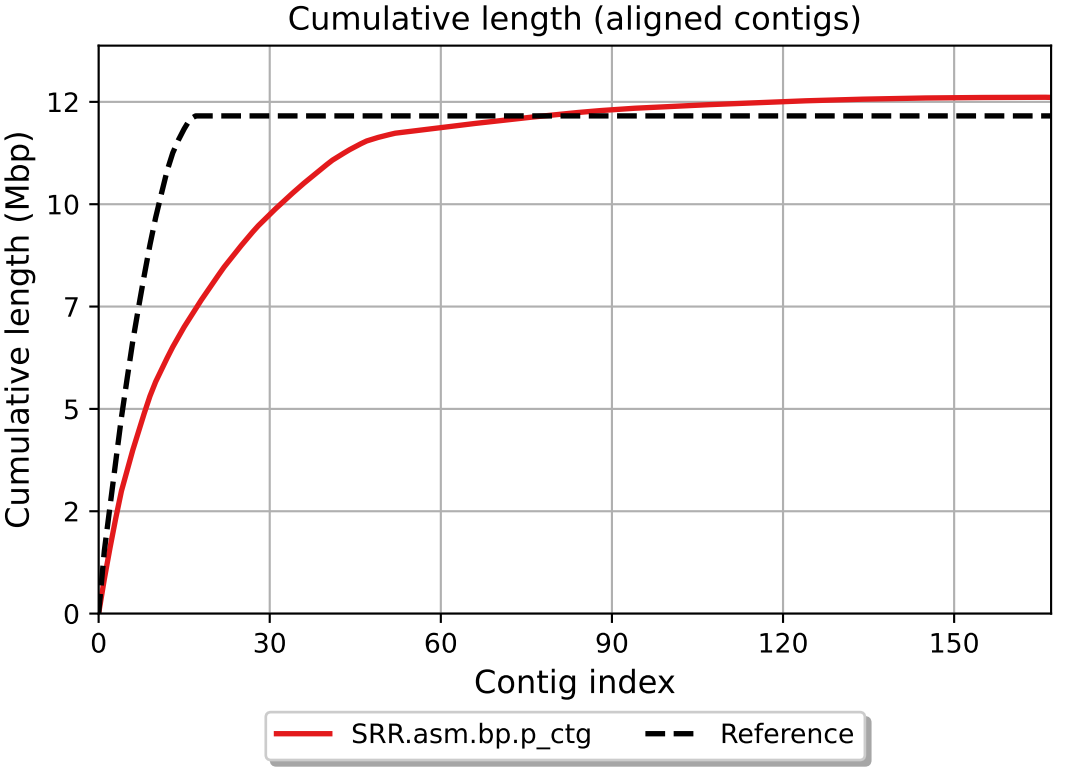

Cumulative length
Cumulative length (Mbp)
0
2
5
7
10
12
0
10
20
30
40
Contig index
SRR.asm.bp.p_ctg
Reference

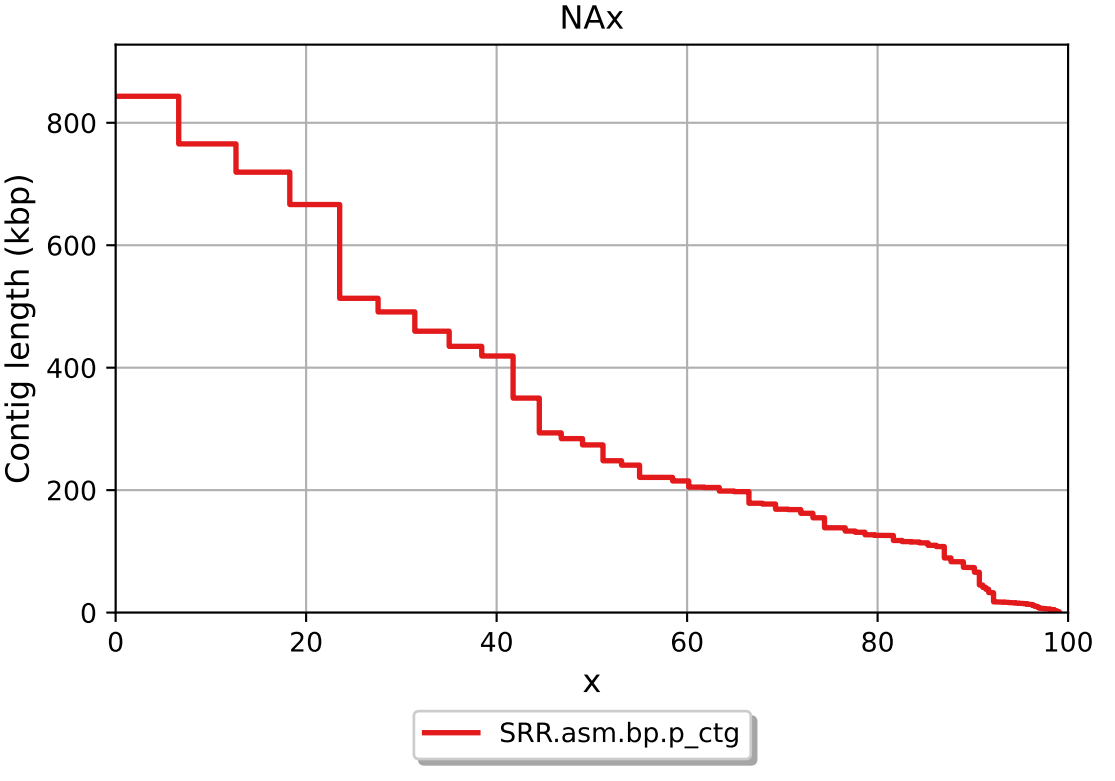

GC content
7500
6000
4500
3000
1500
0
windows
0
20
40
60
80
100
GC (%)
SRR.asm.bp.p_ctg
Reference

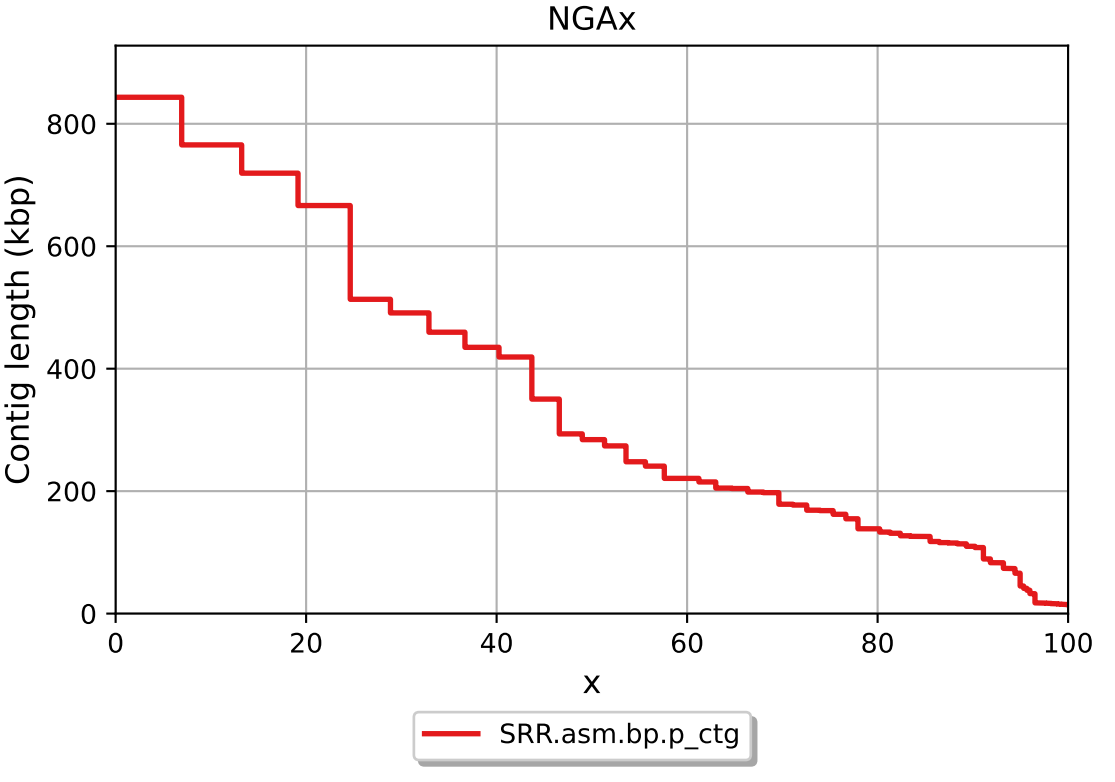

SRR.asm.bp.p_ctg GC content
contigs
GC (%)
0
5
10
15
20
25
30
0
20
40
60
80
100
SRR.asm.bp.p_ctg


Misassemblies
125
100
75
50
25
0
SRR.asm.bp.p_ctg
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
0
20
40
60
80
100
0
20
40
60
80
100
120
Feature space
SRR.asm.bp.p_ctg


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
5
7
10
12
0
30
60
90
120
150
Contig index
SRR.asm.bp.p_ctg
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
SRR.asm.bp.p_ctg


NGAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
SRR.asm.bp.p_ctg