Report

	contigs
# contigs (>= 0 bp)	197
# contigs (>= 1000 bp)	116
# contigs (>= 5000 bp)	85
# contigs (>= 10000 bp)	71
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4573456
Total length (>= 1000 bp)	4553700
Total length (>= 5000 bp)	4485632
Total length (>= 10000 bp)	4383570
Total length (>= 25000 bp)	4086828
Total length (>= 50000 bp)	3325416
# contigs	128
Largest contig	327173
Total length	4561737
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	95119
NG50	88116
N75	44523
NG75	43853
L50	17
LG50	18
L75	35
LG75	36
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	199773
# local misassemblies	7
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.191
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.81
# indels per 100 kbp	0.29
Largest alignment	327173
NA50	88101
NGA50	88101
NA75	44523
NGA75	43059
LA50	18
LGA50	18
LA75	35
LGA75	37

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

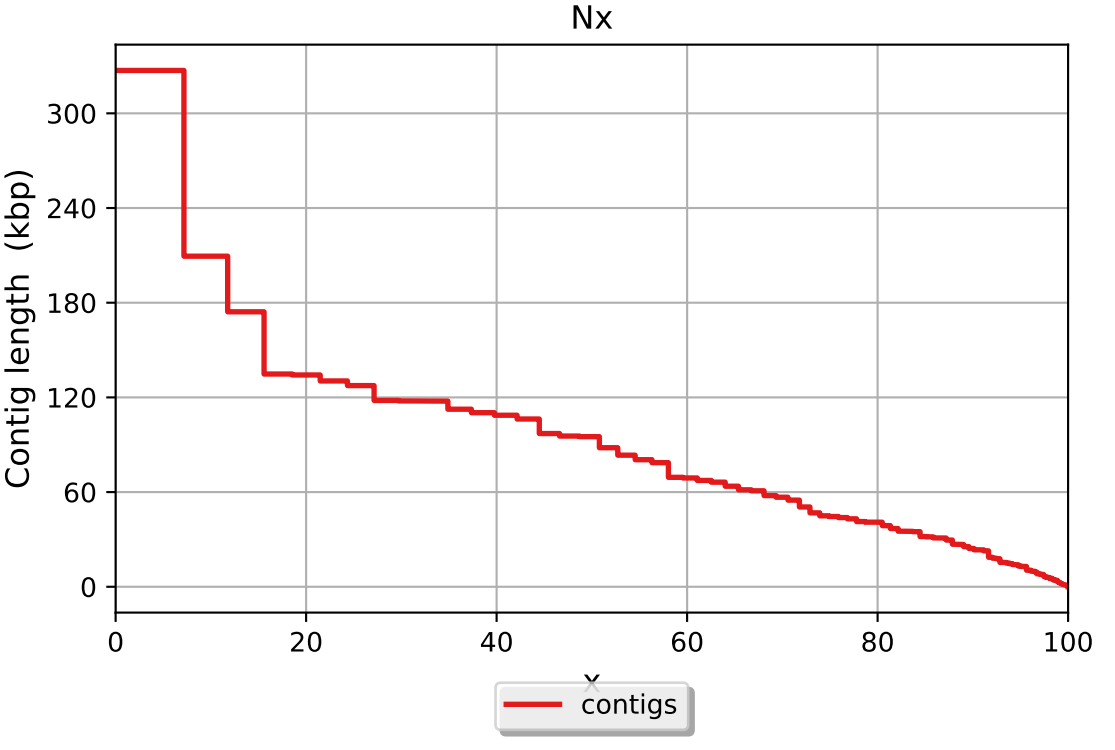
	contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	199773
# local misassemblies	7
# mismatches	675
# indels	13
# short indels	11
# long indels	2
Indels length	94

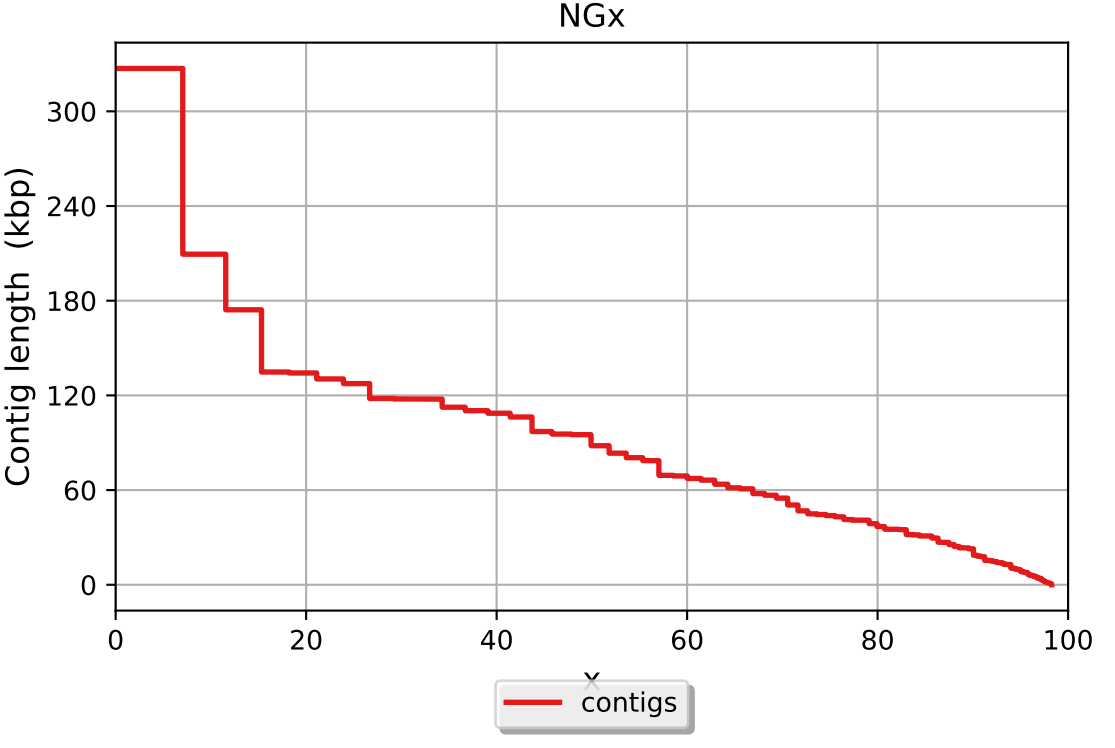
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

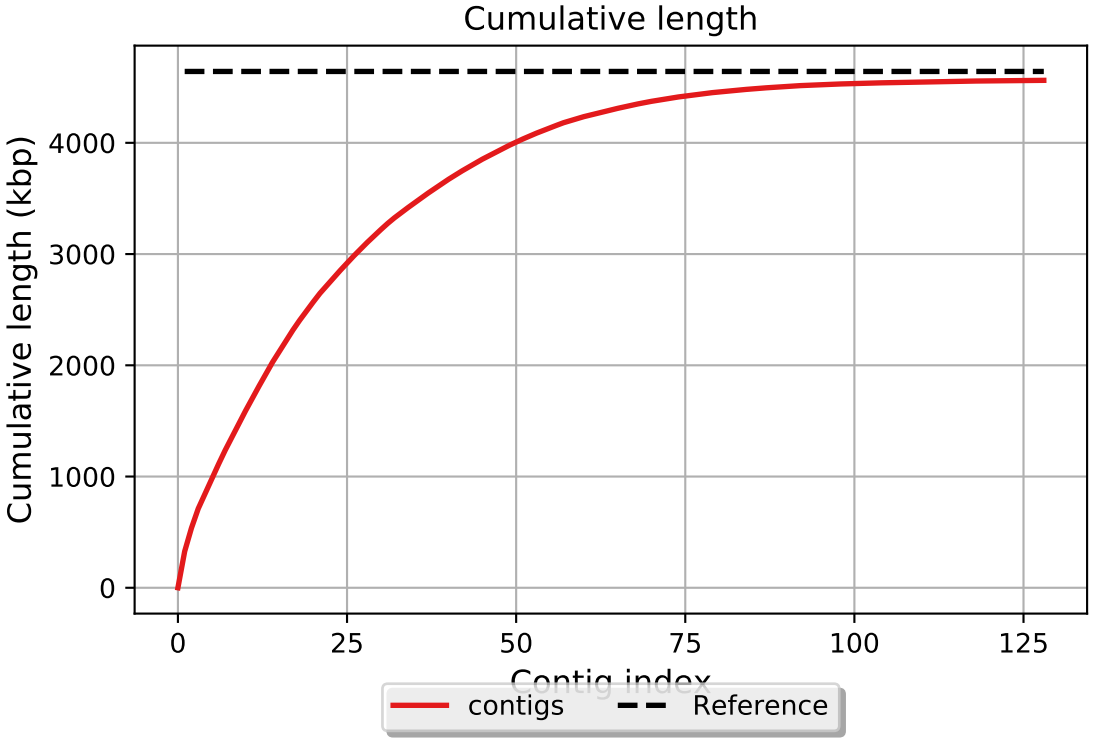
Unaligned report

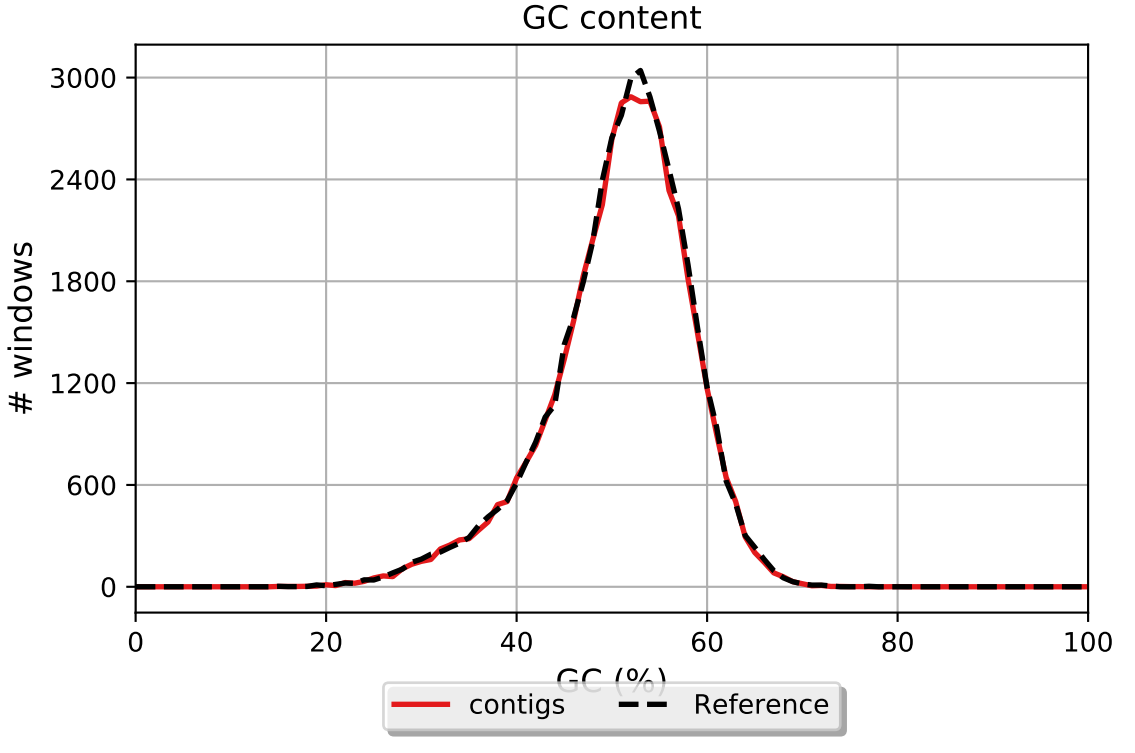
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

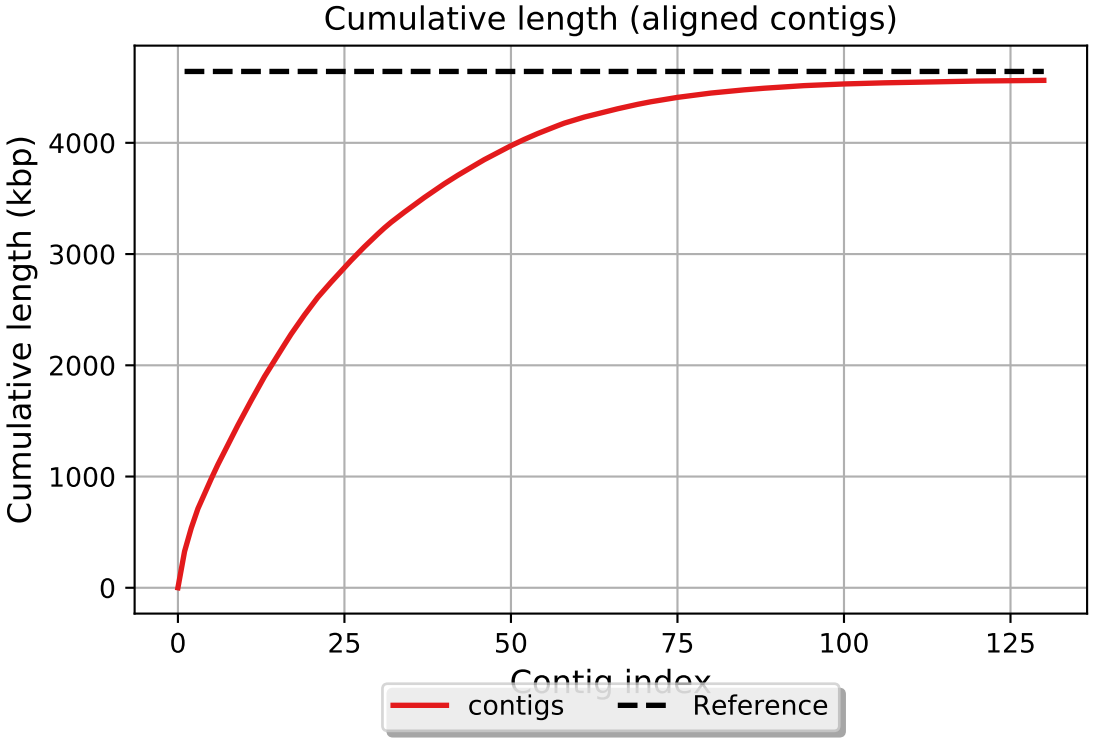

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

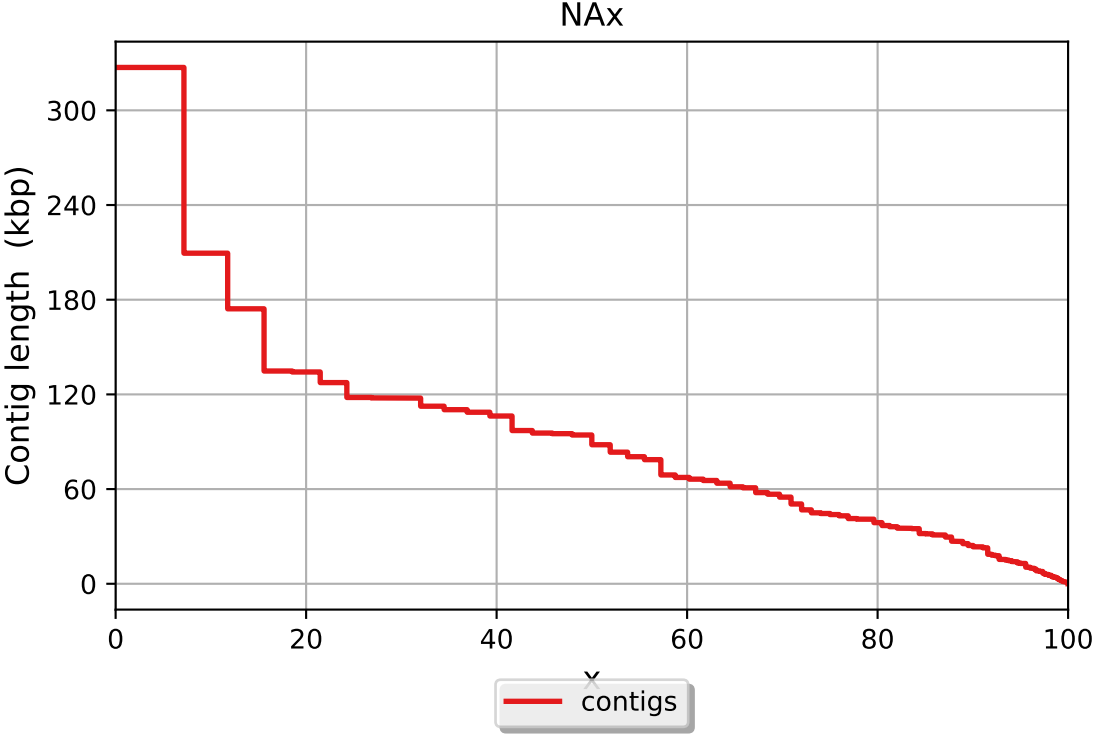

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

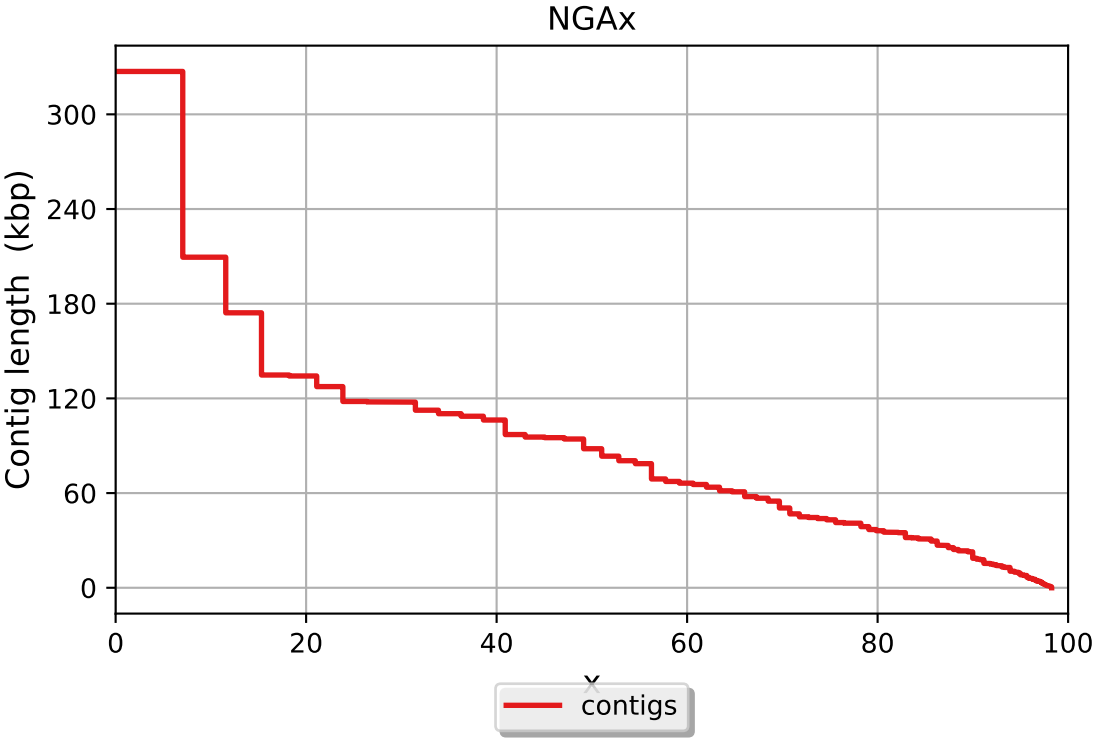

Cumulative length
Cumulative length (kbp)
4000
3000
2000
1000
0
0
25
50
75
100
125
Contig index
contigs
Reference


GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
contigs
Reference

Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3000
2000
1000
0
0
25
50
75
100
125
Contig index
contigs
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs