Report

	contigs
# contigs (>= 0 bp)	1439
# contigs (>= 1000 bp)	96
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	29
Total length (>= 0 bp)	4891409
Total length (>= 1000 bp)	4553143
Total length (>= 5000 bp)	4491736
Total length (>= 10000 bp)	4433828
Total length (>= 25000 bp)	4258232
Total length (>= 50000 bp)	3534534
# contigs	114
Largest contig	311471
Total length	4564544
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	112386
NG50	112386
N75	56614
NG75	54902
L50	14
LG50	14
L75	28
LG75	29
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	45103
# local misassemblies	1
# unaligned contigs	1 + 0 part
Unaligned length	572
Genome fraction (%)	98.185
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.01
# indels per 100 kbp	0.39
Largest alignment	311471
NA50	112386
NGA50	112386
NA75	56614
NGA75	54902
LA50	14
LGA50	14
LA75	28
LGA75	29

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

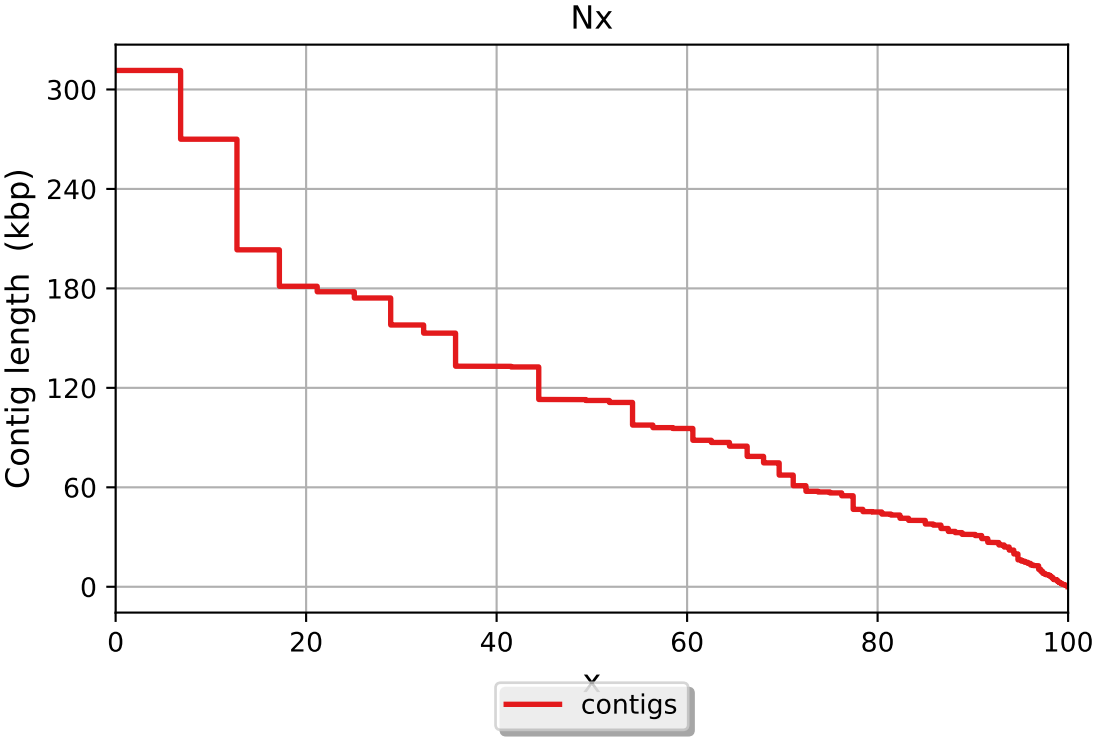
	contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	45103
# local misassemblies	1
# mismatches	456
# indels	18
# short indels	18
# long indels	0
Indels length	22

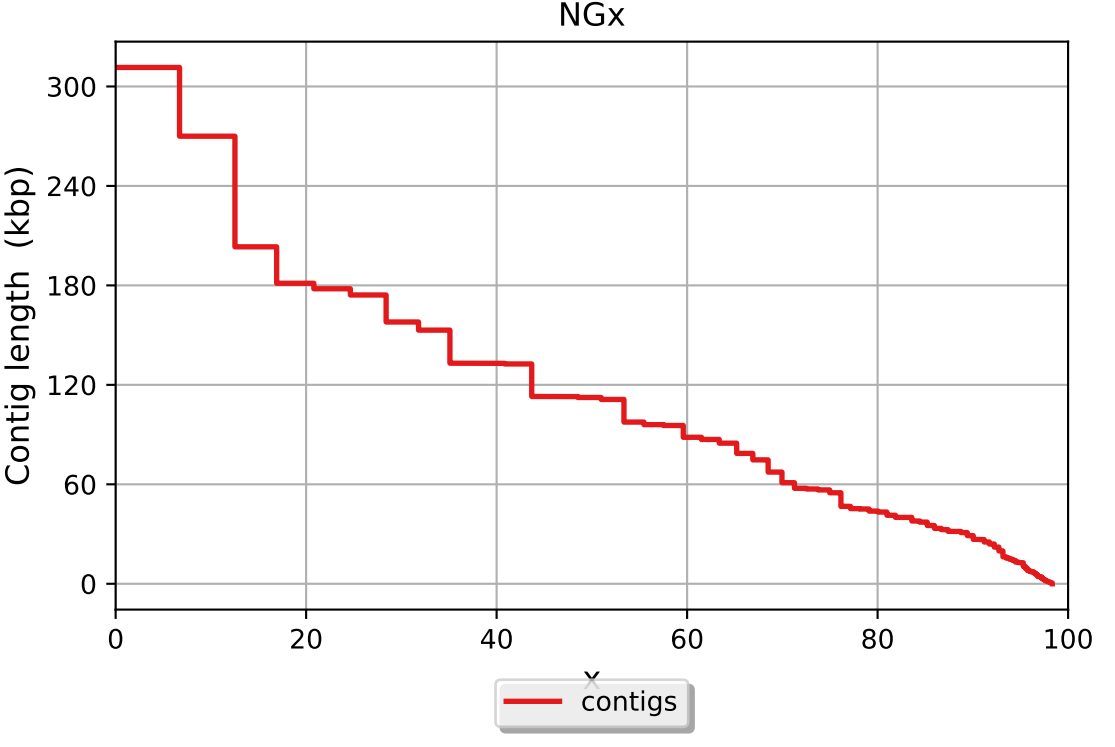
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

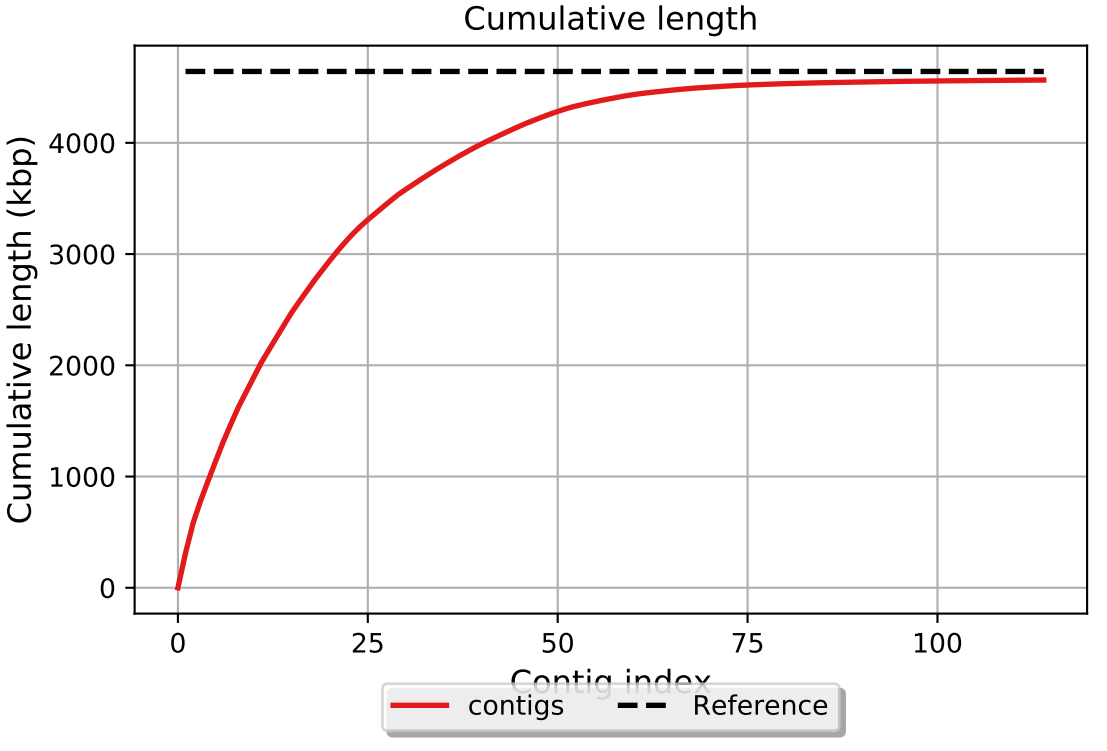
Unaligned report

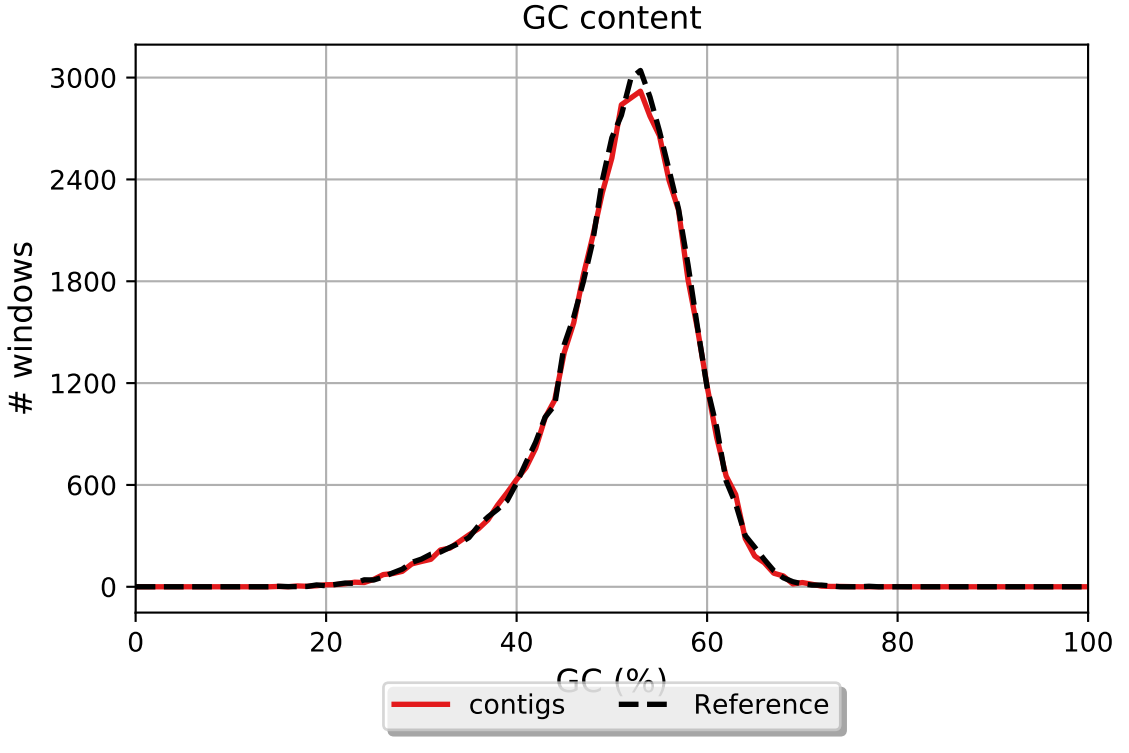
	contigs
# fully unaligned contigs	1
Fully unaligned length	572
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

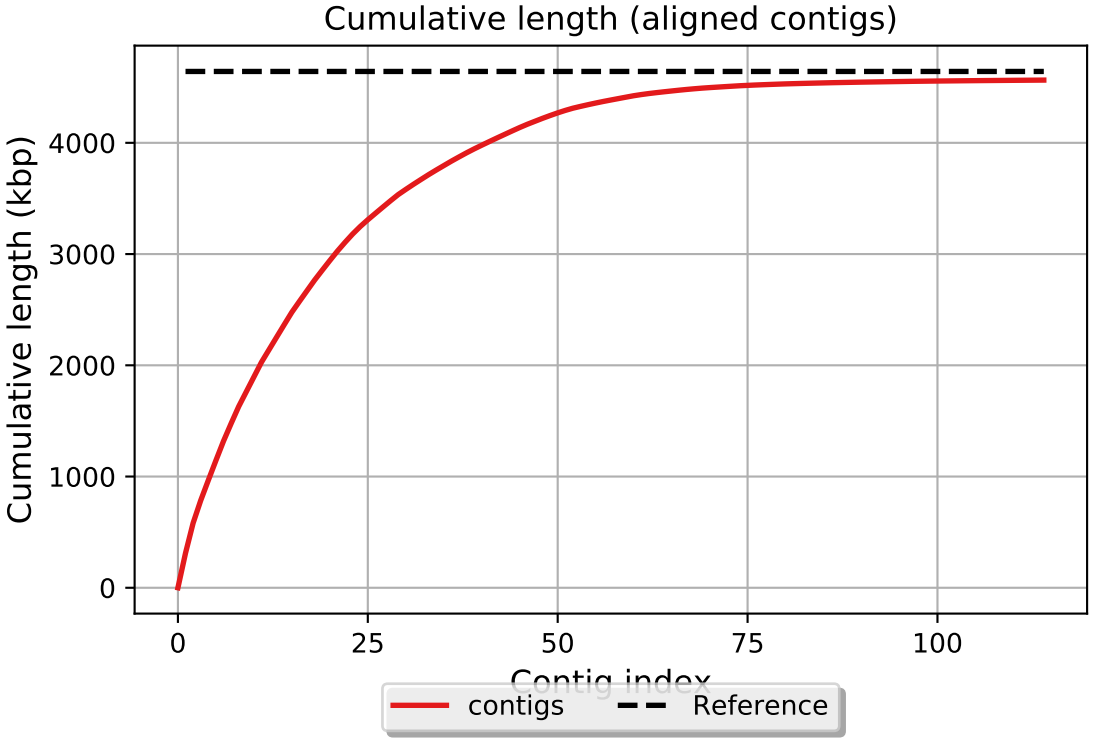

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

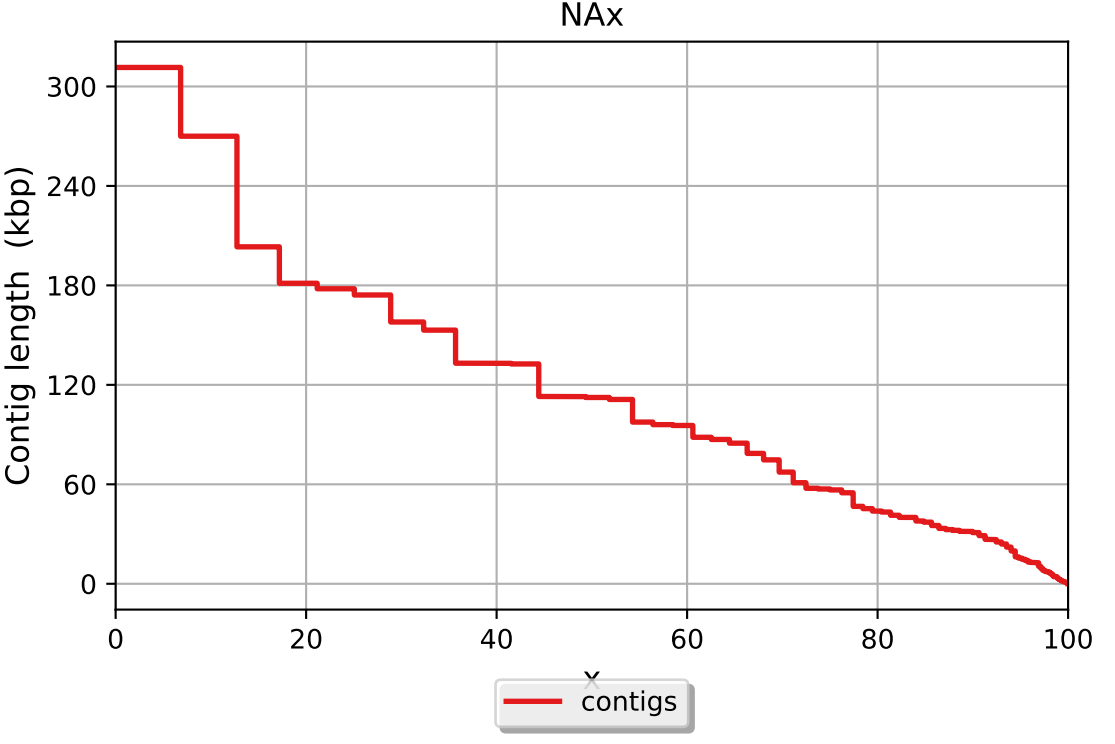

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

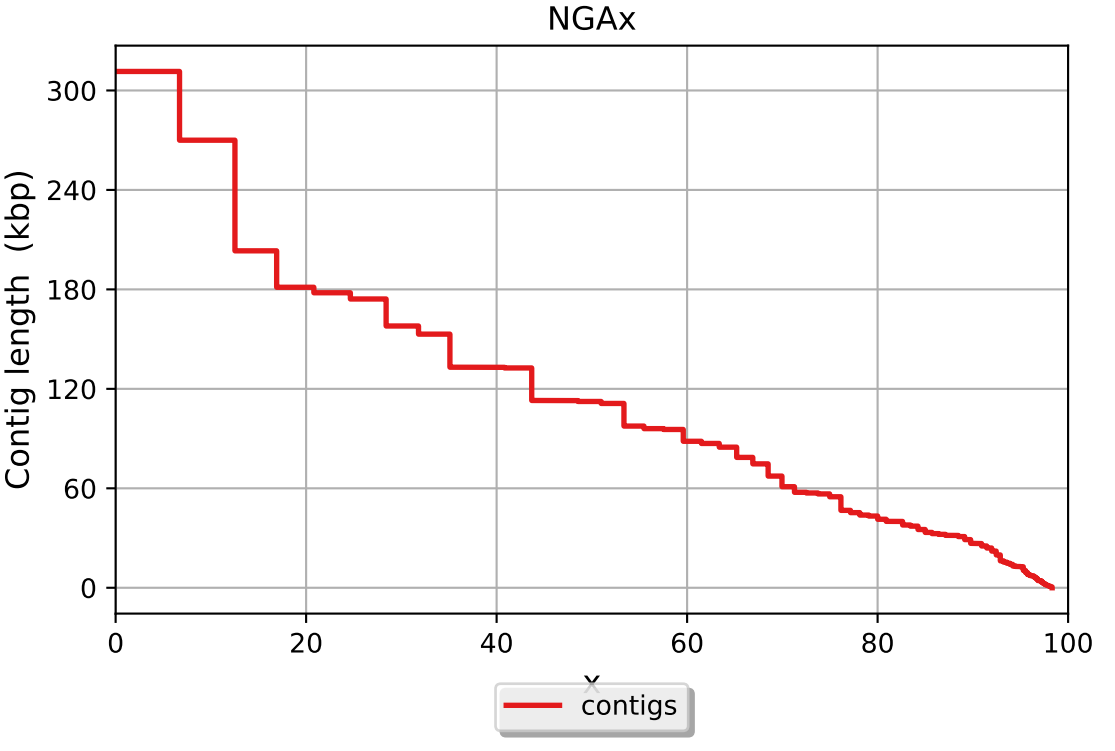

Cumulative length
Cumulative length (kbp)
4000
3000
2000
1000
0
0
25
50
75
100
Contig index
contigs
Reference


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

Misassemblies
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0.00
contigs
relocations


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