Report

	contigs
# contigs (>= 0 bp)	160
# contigs (>= 1000 bp)	90
# contigs (>= 5000 bp)	68
# contigs (>= 10000 bp)	59
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4571928
Total length (>= 1000 bp)	4553020
Total length (>= 5000 bp)	4507349
Total length (>= 10000 bp)	4441484
Total length (>= 25000 bp)	4338502
Total length (>= 50000 bp)	3601681
# contigs	97
Largest contig	327173
Total length	4558108
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	112835
NG50	112514
N75	57306
NG75	56658
L50	14
LG50	15
L75	29
LG75	30
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	6
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.166
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.62
# indels per 100 kbp	0.07
Largest alignment	327173
NA50	112835
NGA50	112514
NA75	57306
NGA75	56658
LA50	14
LGA50	15
LA75	29
LGA75	30

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

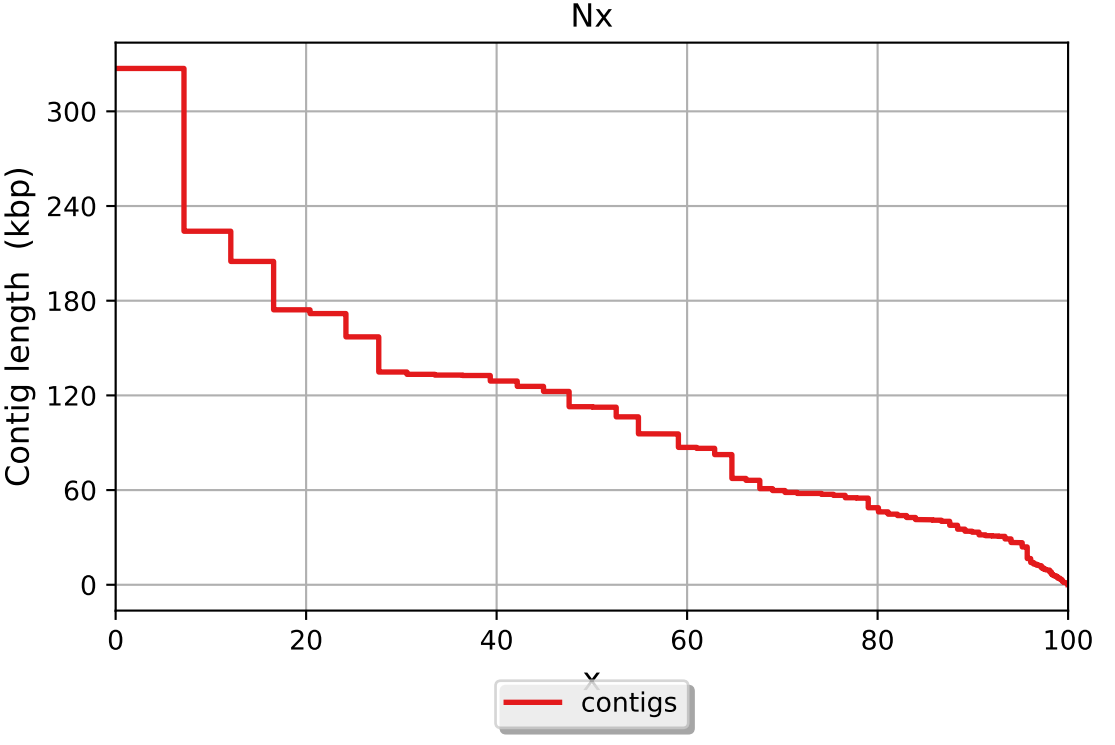
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	6
# mismatches	256
# indels	3
# short indels	3
# long indels	0
Indels length	3

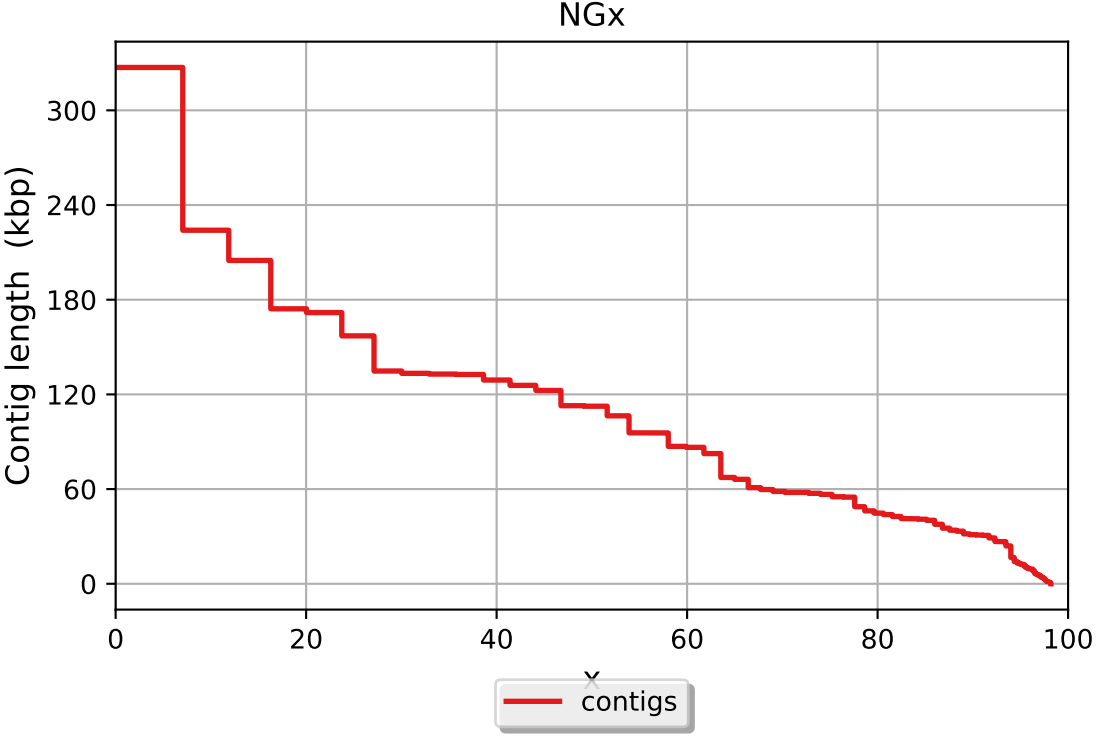
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

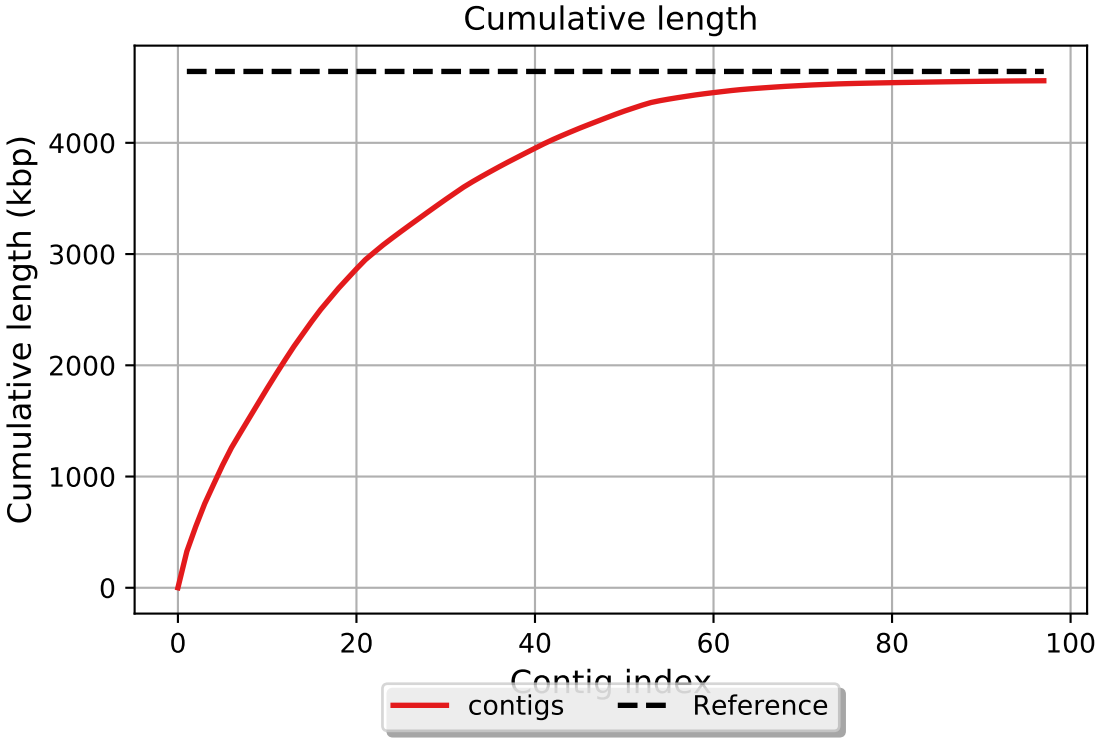
Unaligned report

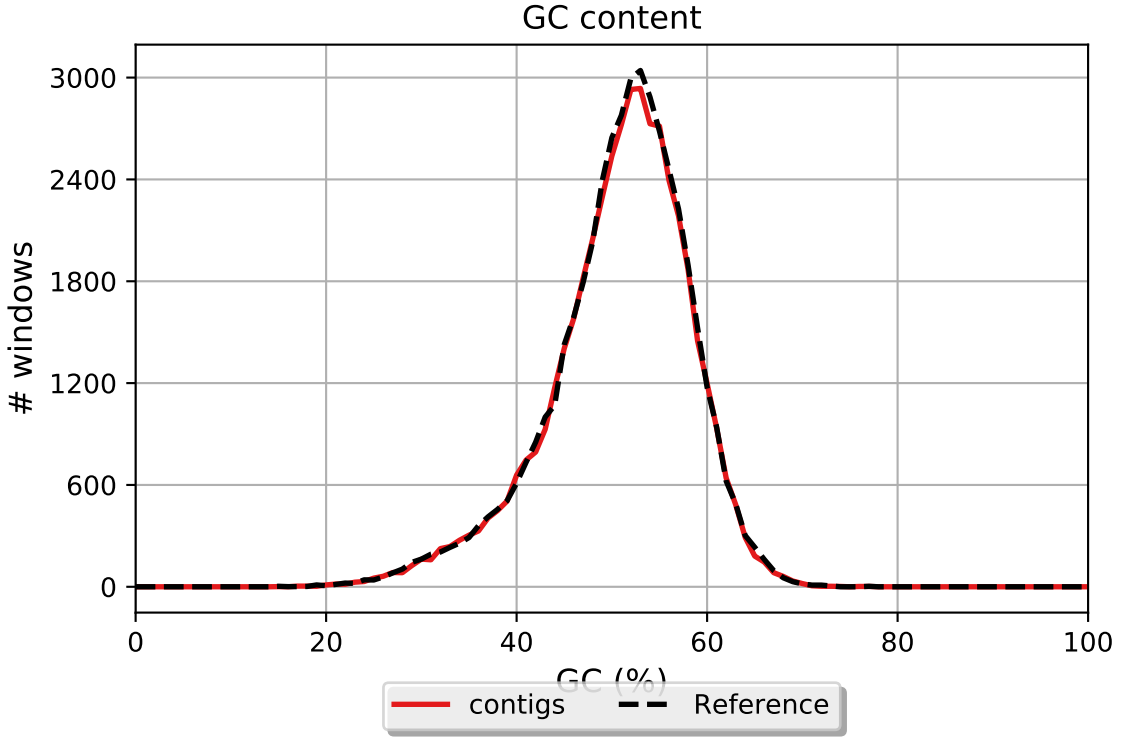
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

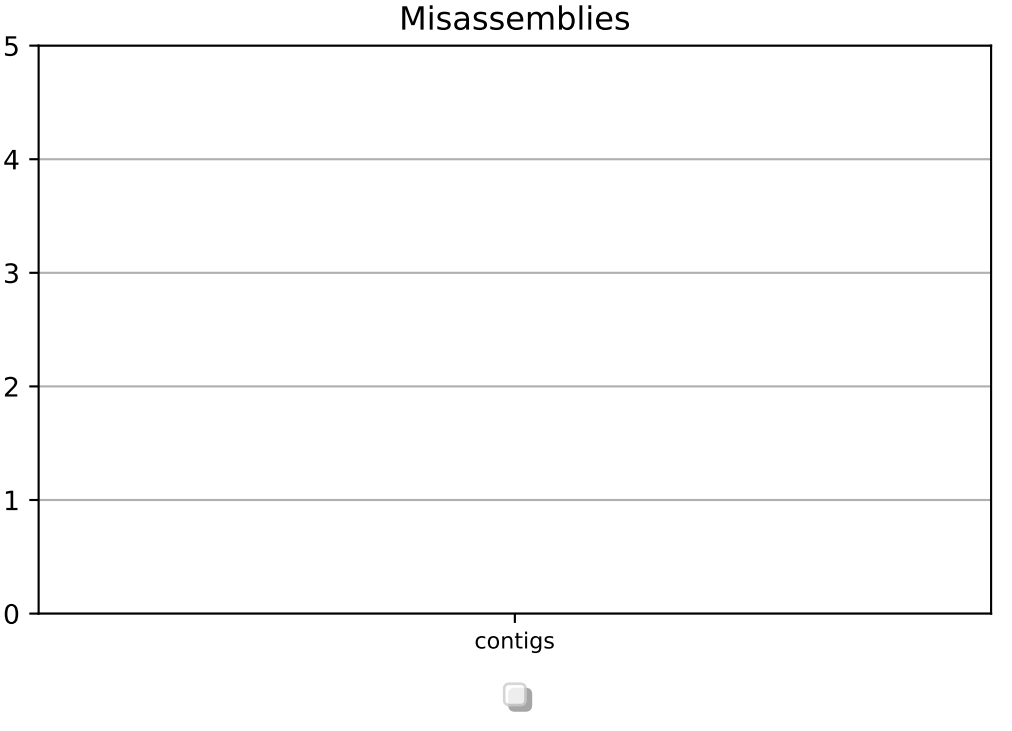
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

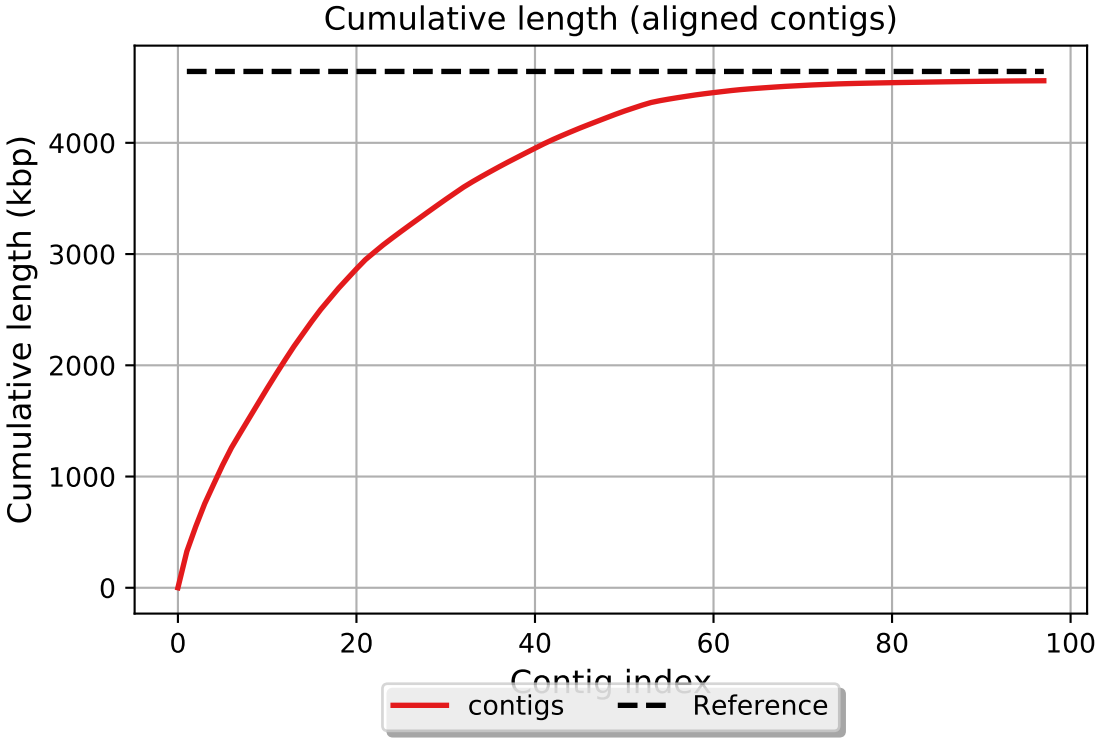

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

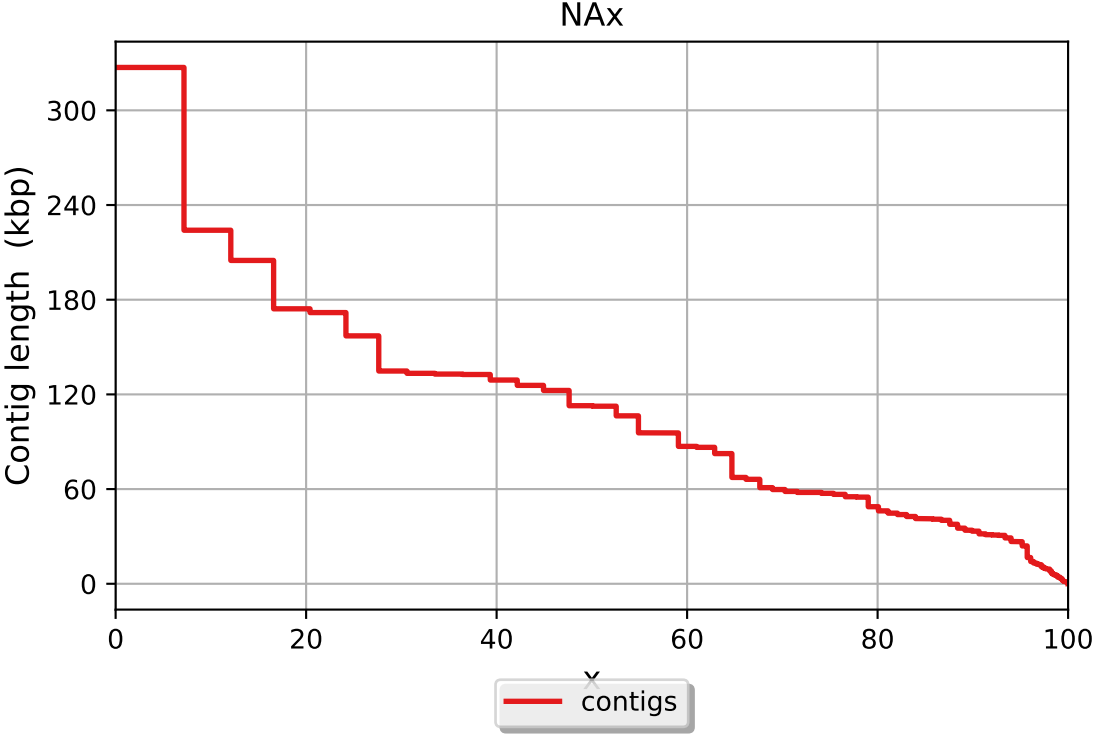

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

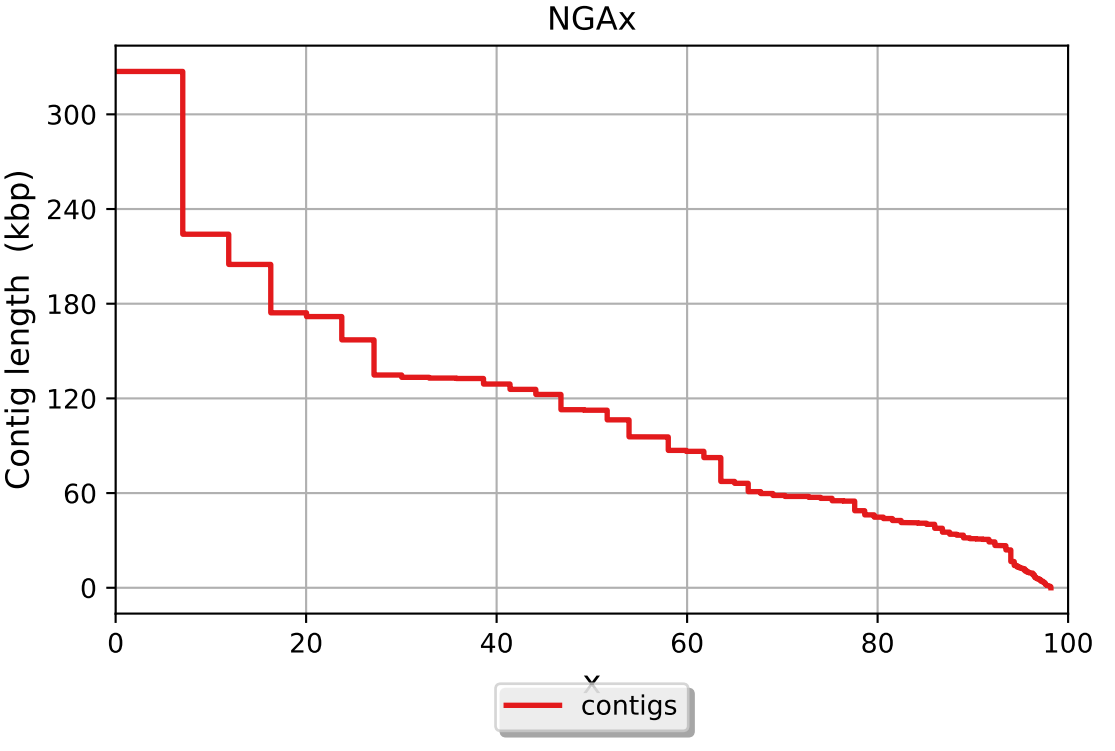

Cumulative length
Cumulative length (kbp)
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
contigs
Reference


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


Misassemblies
5
4
3
2
1
0
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
4000
3000
2000
1000
0
0
20
40
60
80
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