Report

	contigs
# contigs (>= 0 bp)	666
# contigs (>= 1000 bp)	116
# contigs (>= 5000 bp)	86
# contigs (>= 10000 bp)	76
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	31
Total length (>= 0 bp)	4657925
Total length (>= 1000 bp)	4542796
Total length (>= 5000 bp)	4475649
Total length (>= 10000 bp)	4401086
Total length (>= 25000 bp)	4105198
Total length (>= 50000 bp)	3157711
# contigs	130
Largest contig	269813
Total length	4552571
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	88369
NG50	87415
N75	42572
NG75	41323
L50	18
LG50	19
L75	37
LG75	39
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.018
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.67
# indels per 100 kbp	0.42
Largest alignment	269813
NA50	88369
NGA50	87415
NA75	42572
NGA75	41323
LA50	18
LGA50	19
LA75	37
LGA75	39

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

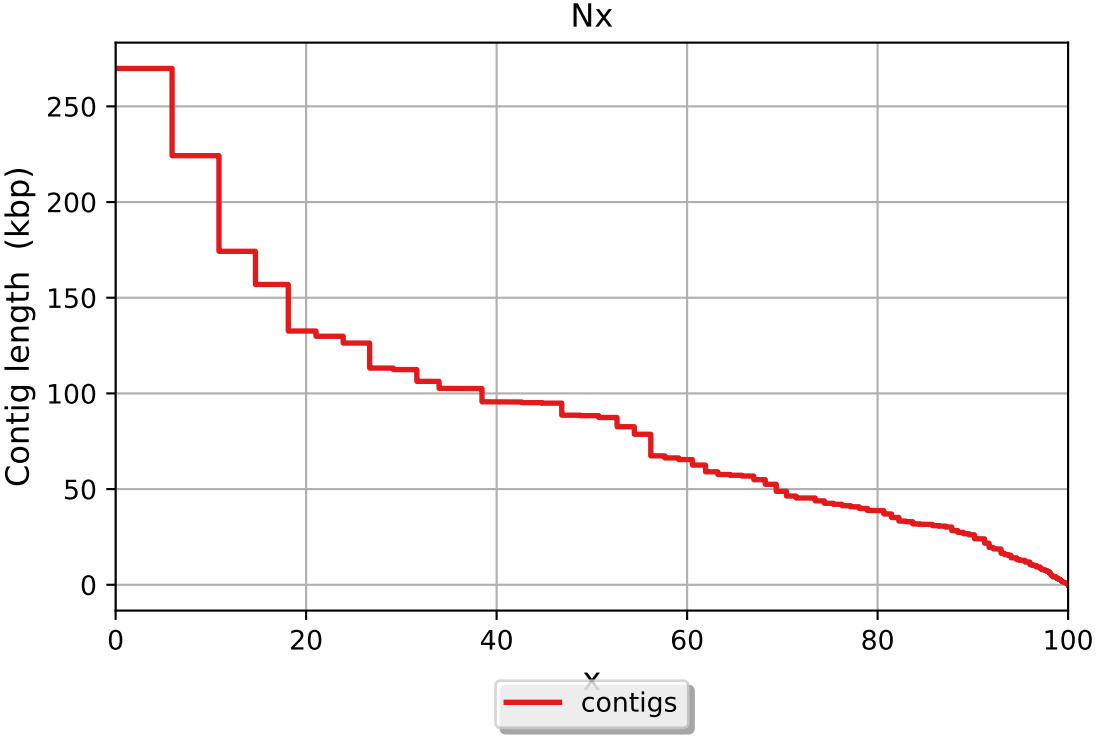
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	440
# indels	19
# short indels	19
# long indels	0
Indels length	27

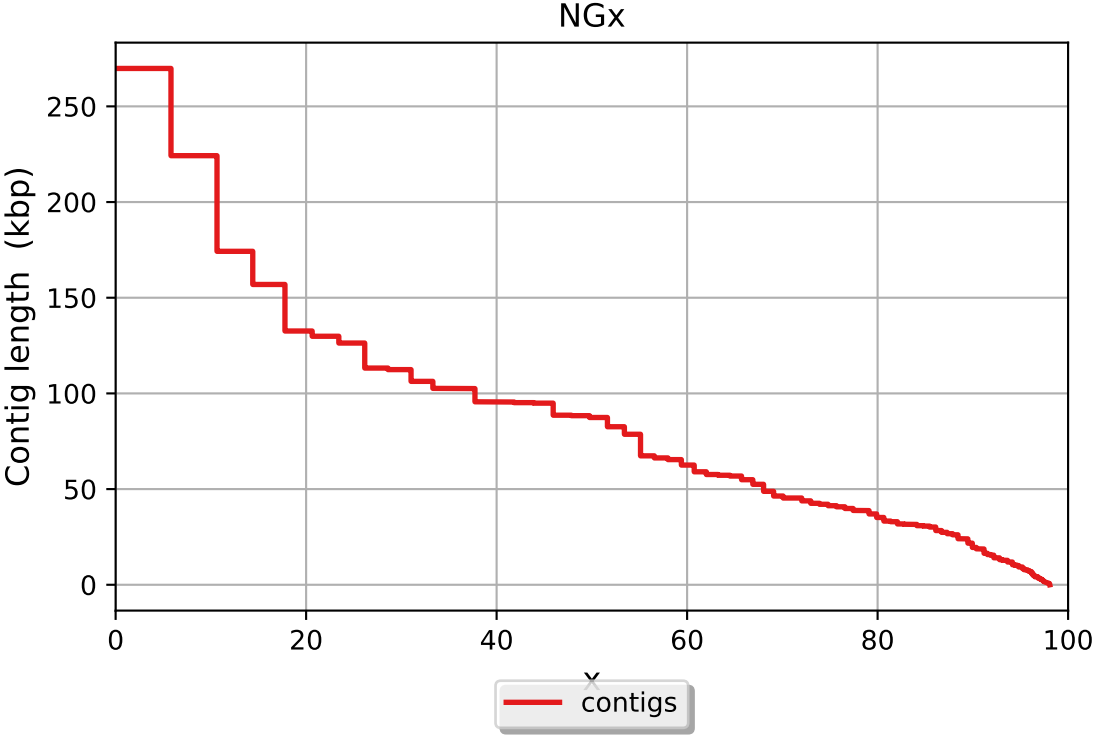
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

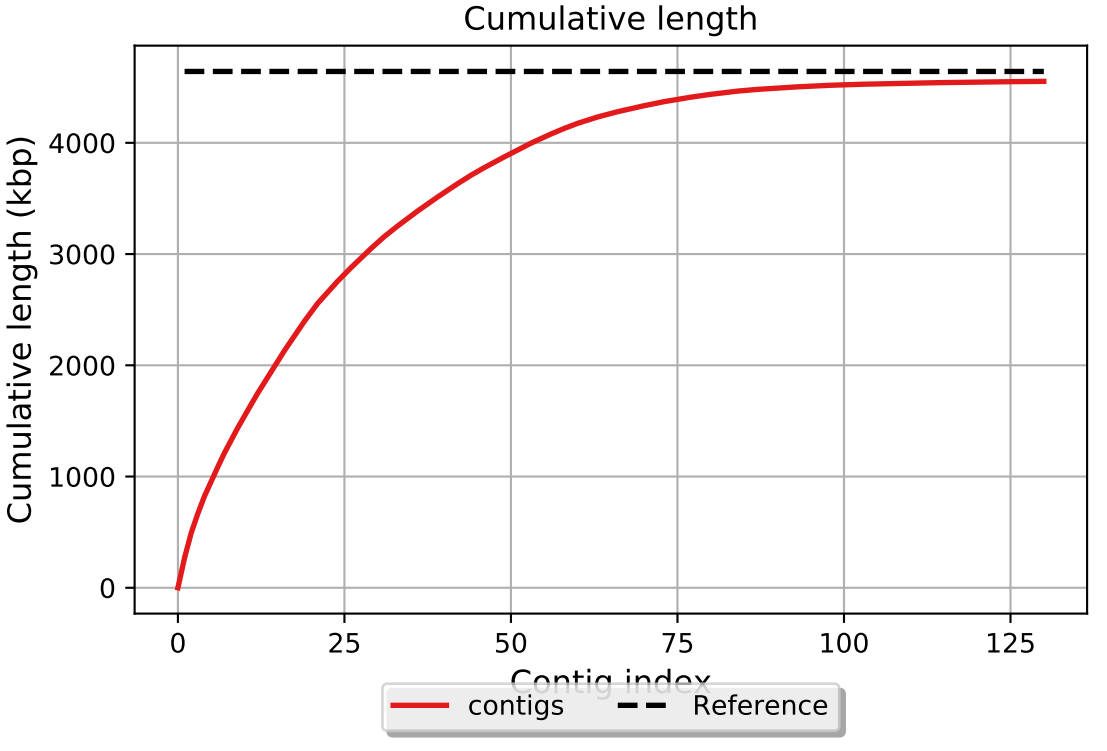
Unaligned report

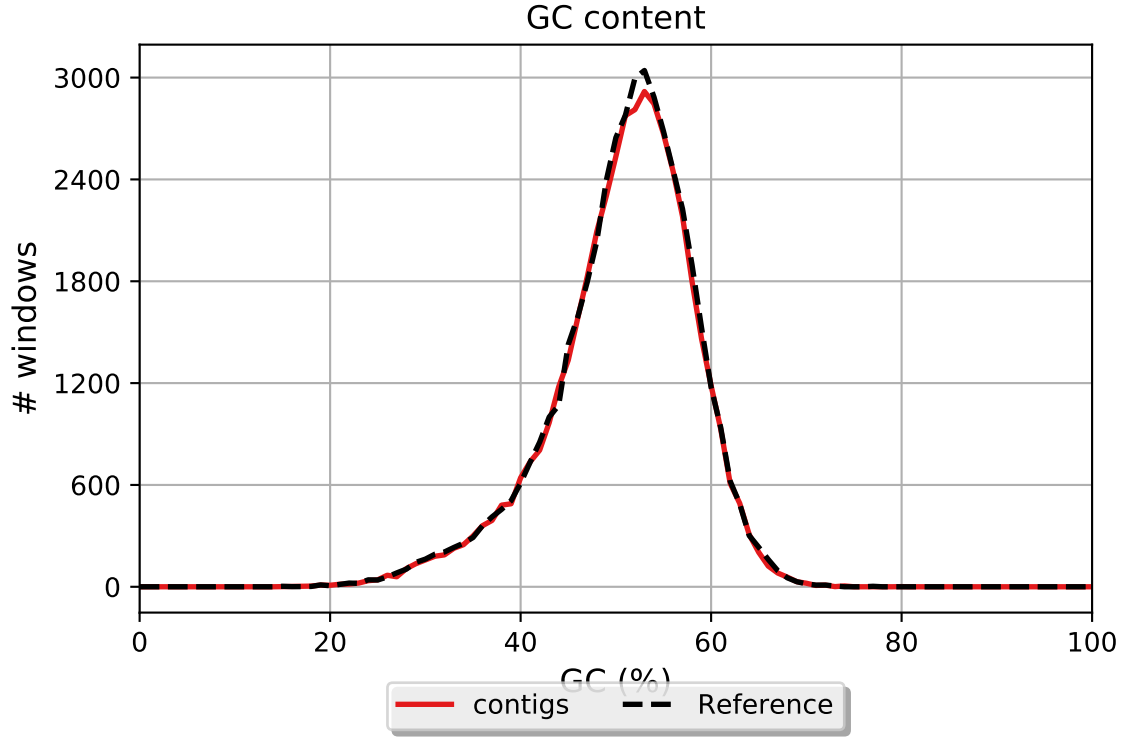
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

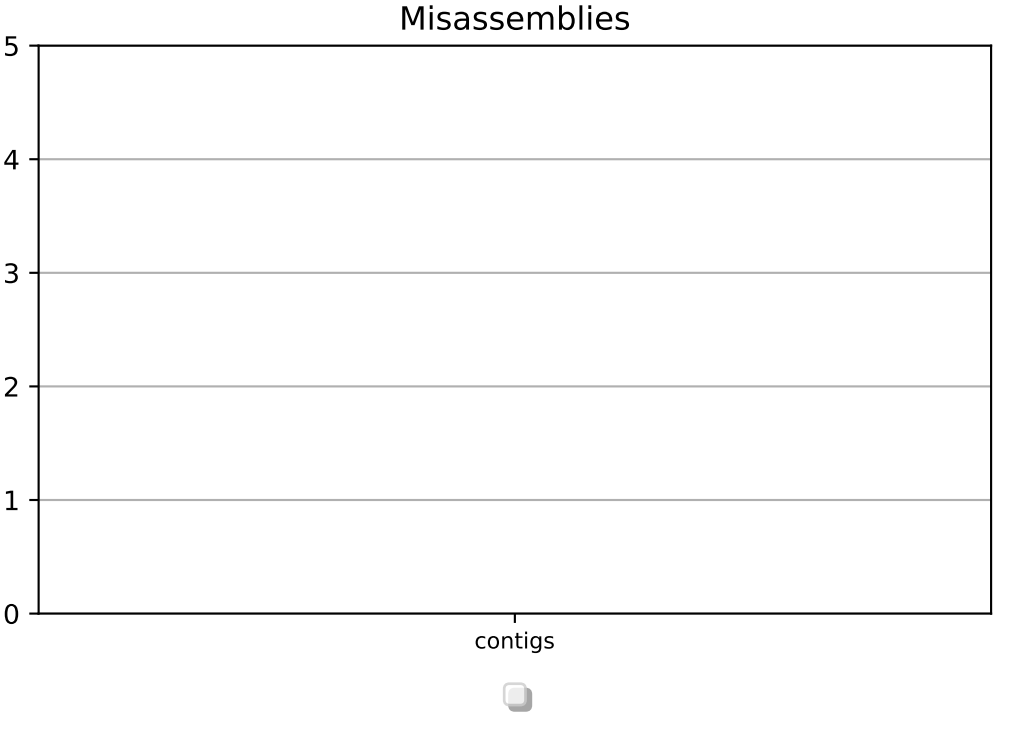
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

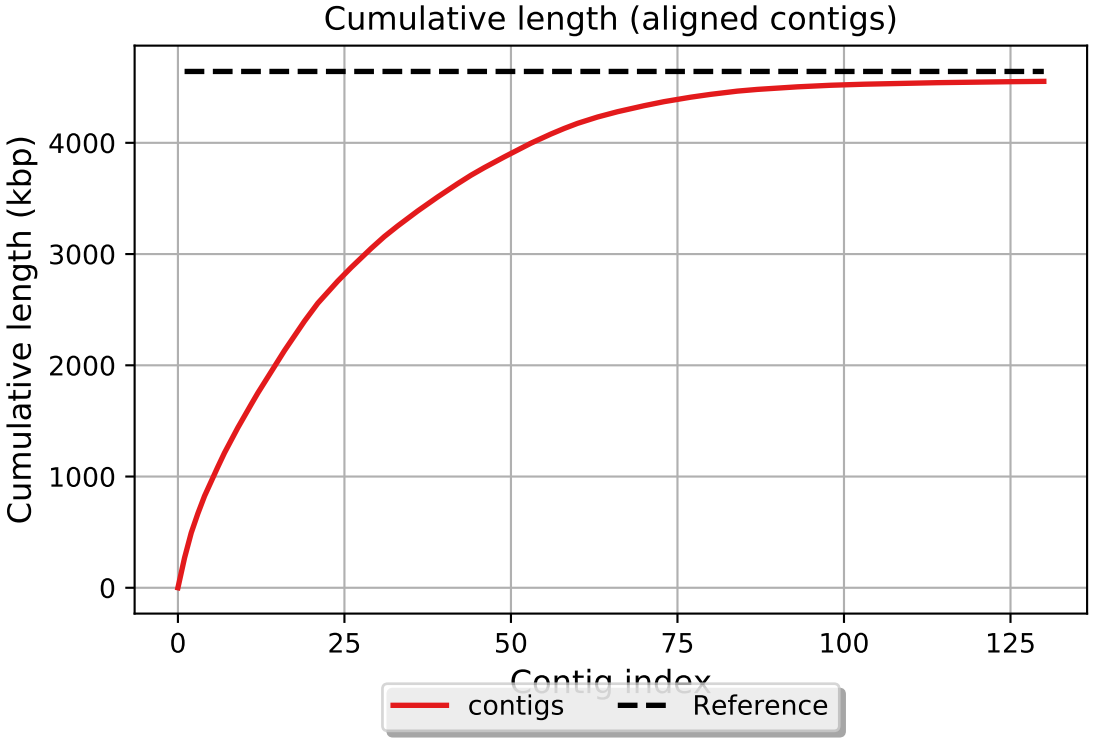

Nx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs

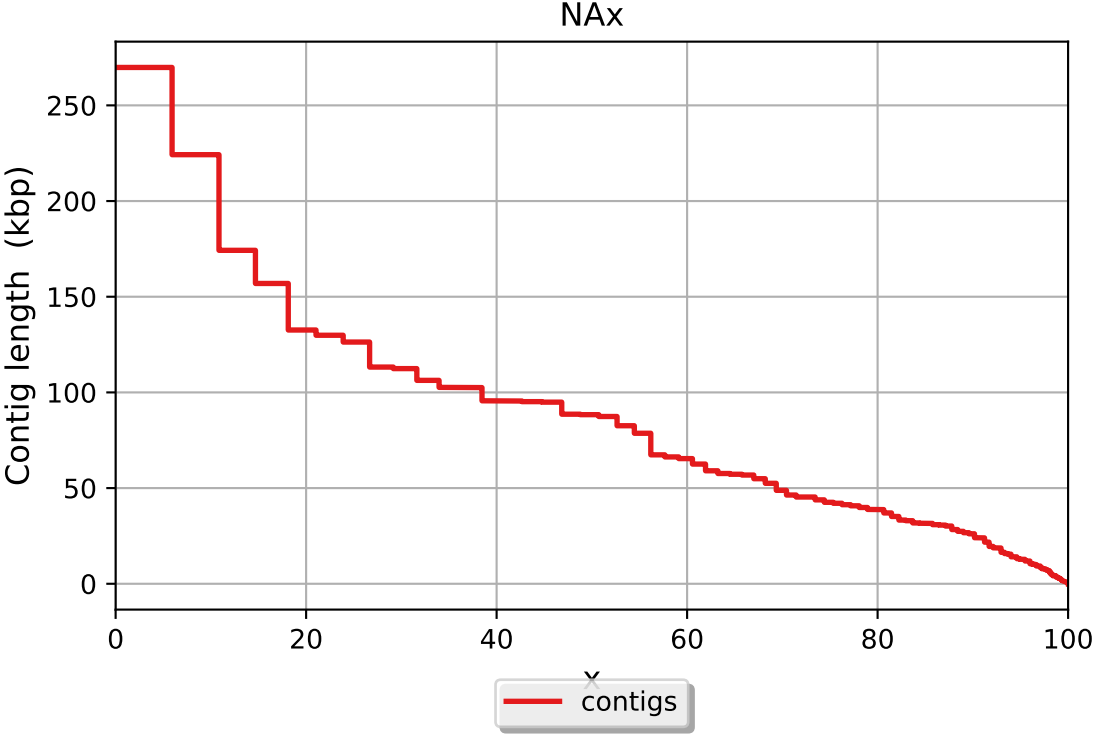

NGx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs

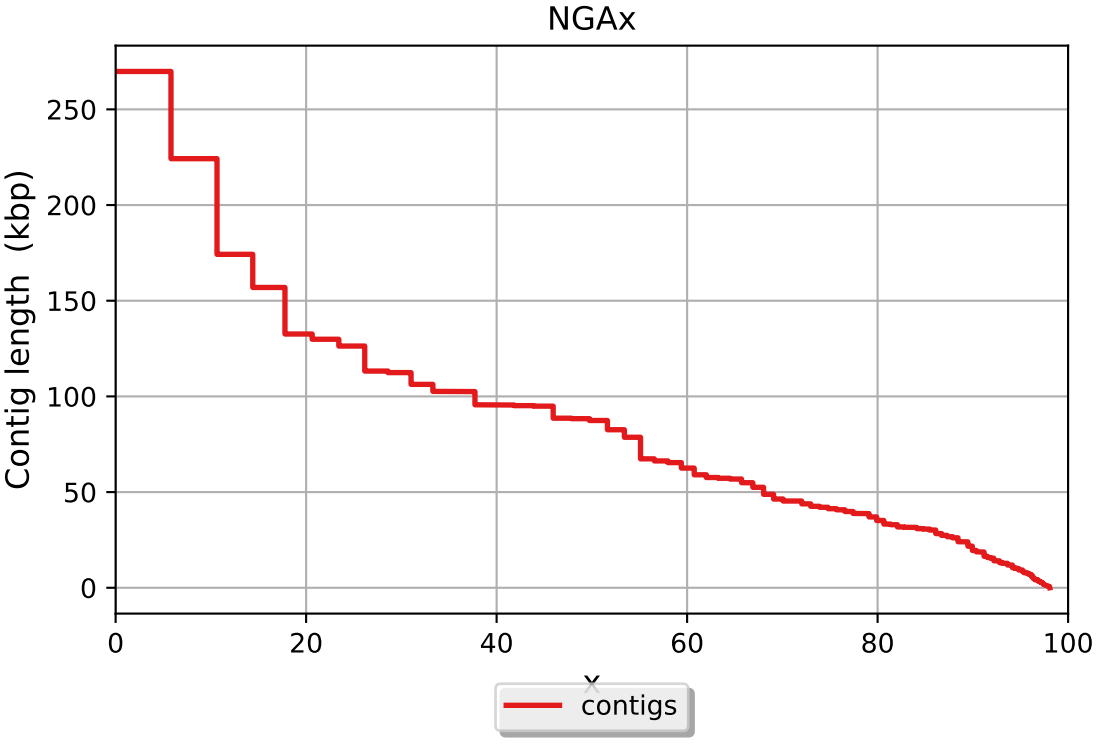

Cumulative length
Cumulative length (kbp)
4000
3000
2000
1000
0
0
25
50
75
100
125
Contig index
contigs
Reference


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


Misassemblies
5
4
3
2
1
0
contigs


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


NAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
250
200
150
100
50
0
0
20
40
60
80
100
x
contigs