Report

	contigs
# contigs (>= 0 bp)	5901
# contigs (>= 1000 bp)	404
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3003262
Total length (>= 1000 bp)	536653
Total length (>= 5000 bp)	14030
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2206
Largest contig	8377
Total length	1771258
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.79
N50	807
N75	633
L50	796
L75	1417
# misassemblies	26
# misassembled contigs	26
Misassembled contigs length	48527
# local misassemblies	1
# unaligned contigs	1 + 18 part
Unaligned length	2888
Genome fraction (%)	37.974
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1318.61
# indels per 100 kbp	2.84
Largest alignment	6837
NA50	797
NGA50	-
NA75	628
LA50	808
LA75	1434

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

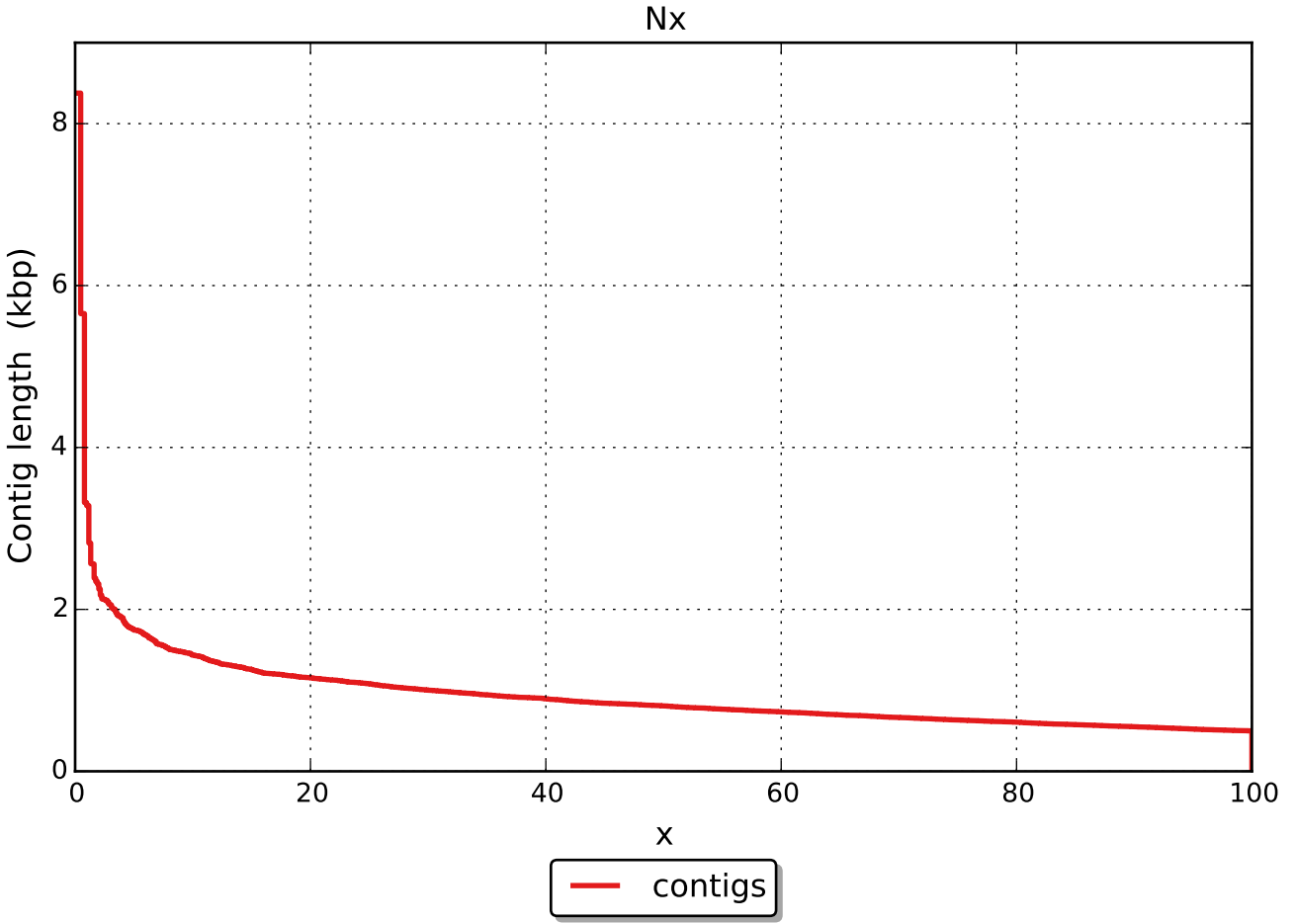
	contigs
# misassemblies	26
# relocations	26
# translocations	0
# inversions	0
# misassembled contigs	26
Misassembled contigs length	48527
# local misassemblies	1
# mismatches	23242
# indels	50
# short indels	50
# long indels	0
Indels length	58

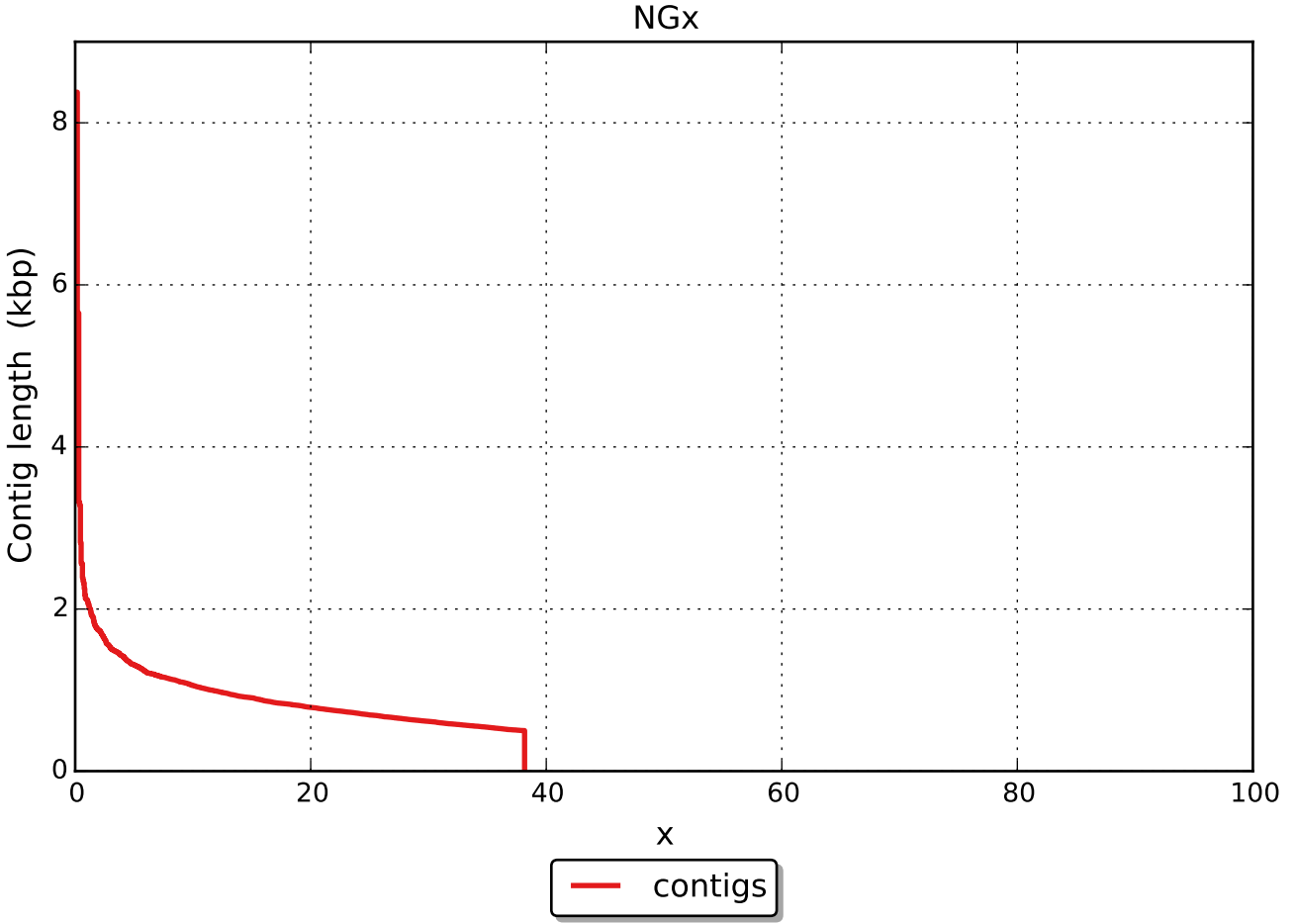
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

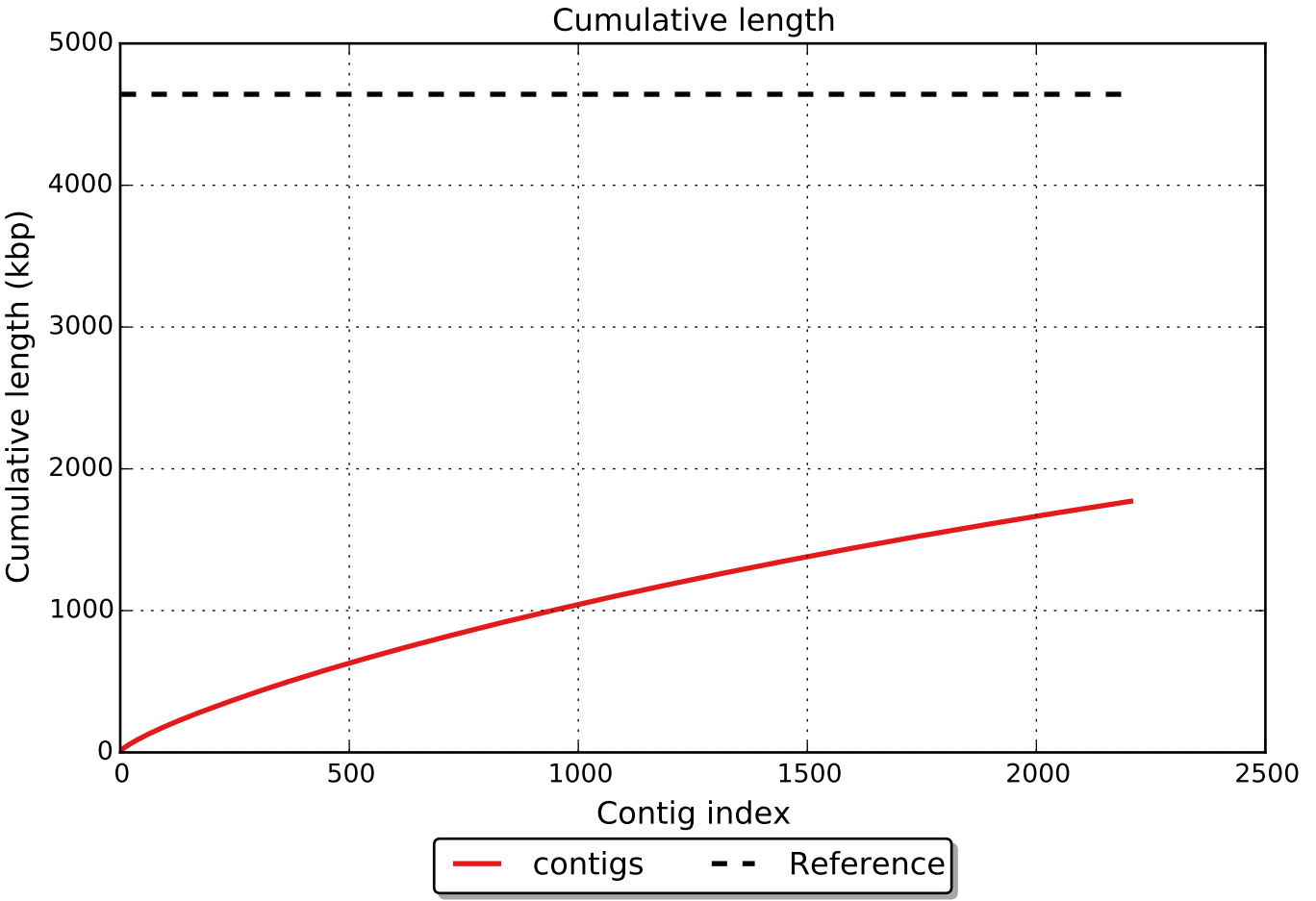
Unaligned report

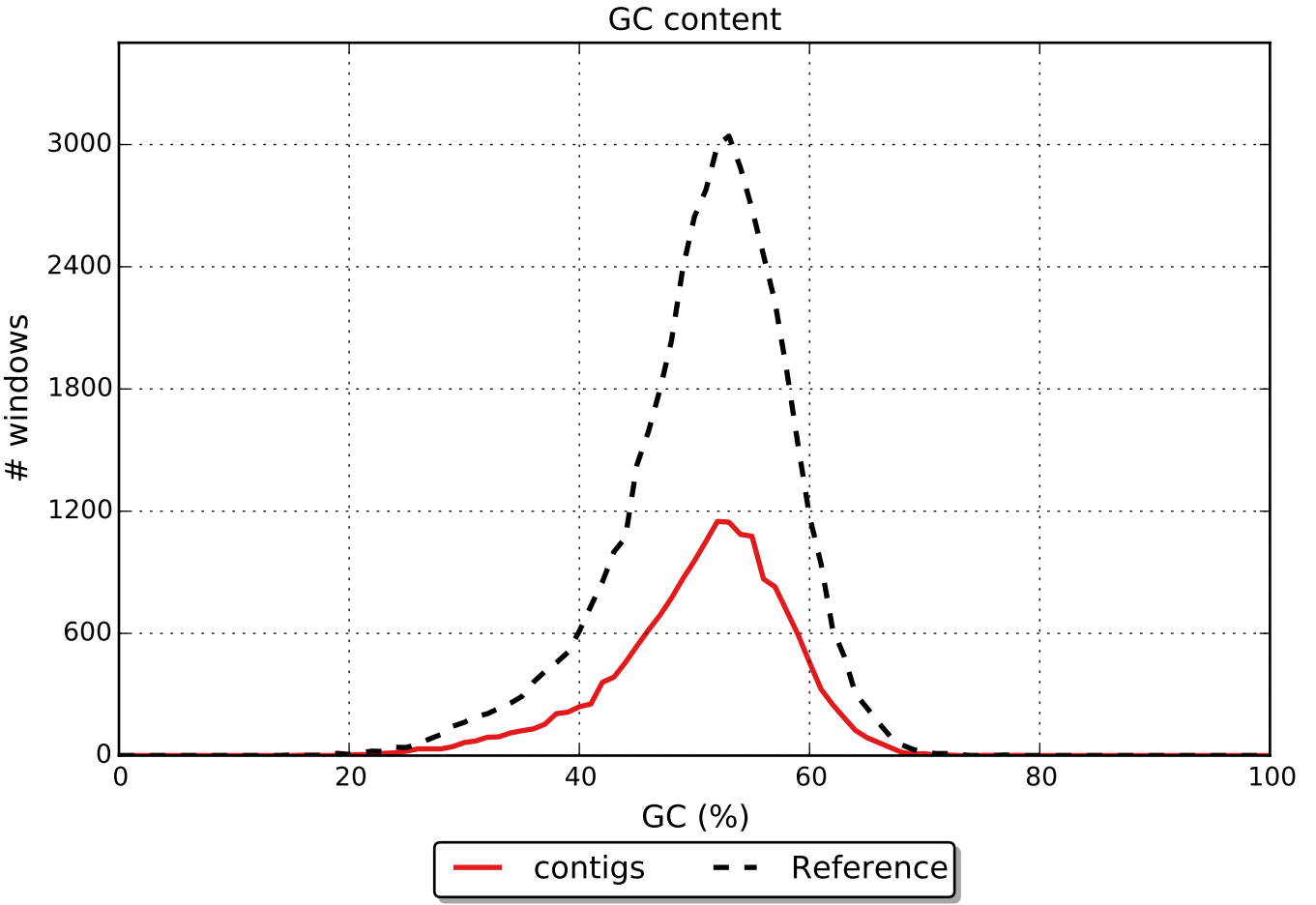
	contigs
# fully unaligned contigs	1
Fully unaligned length	1290
# partially unaligned contigs	18
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1598
# N's	0

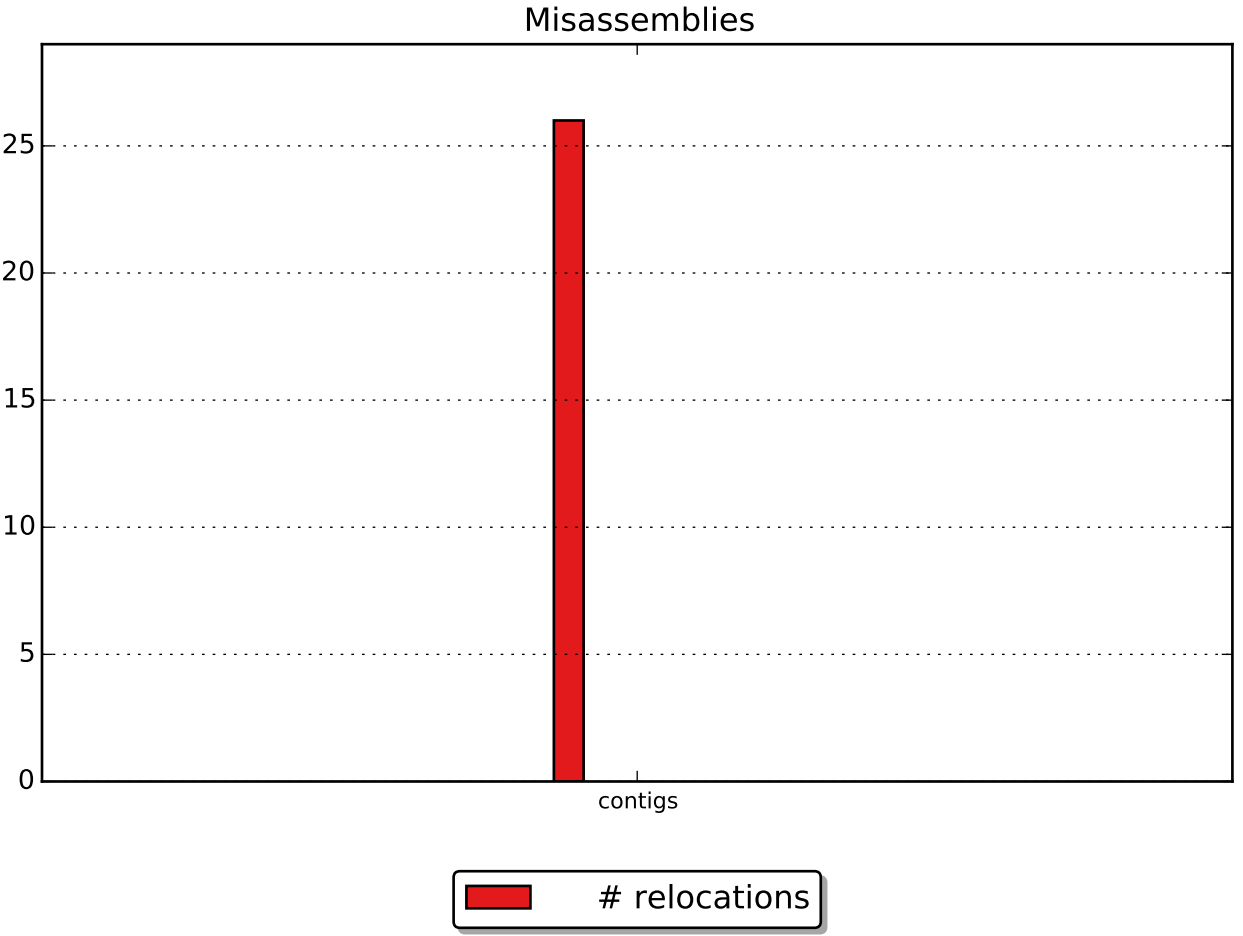
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

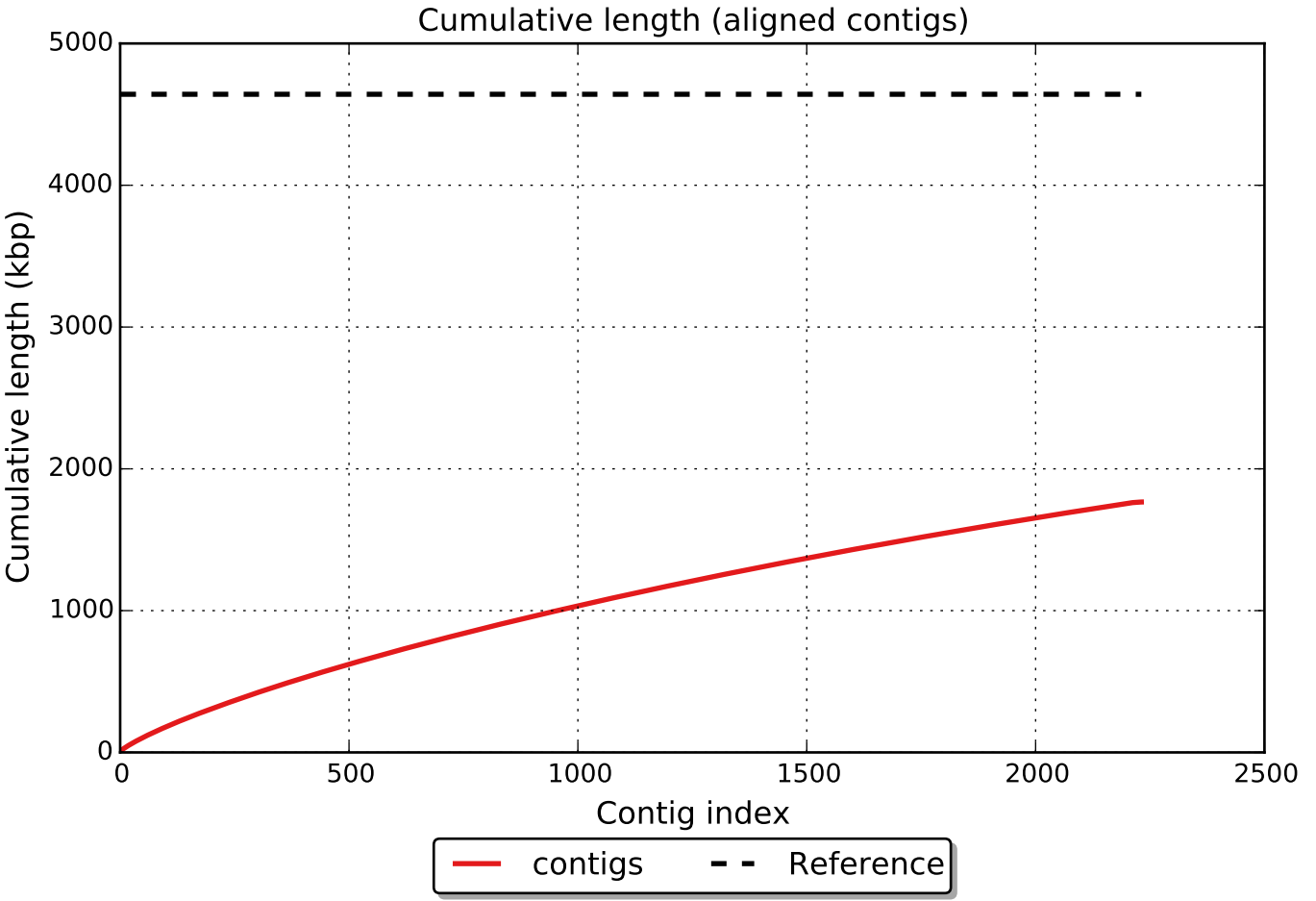

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
contigs

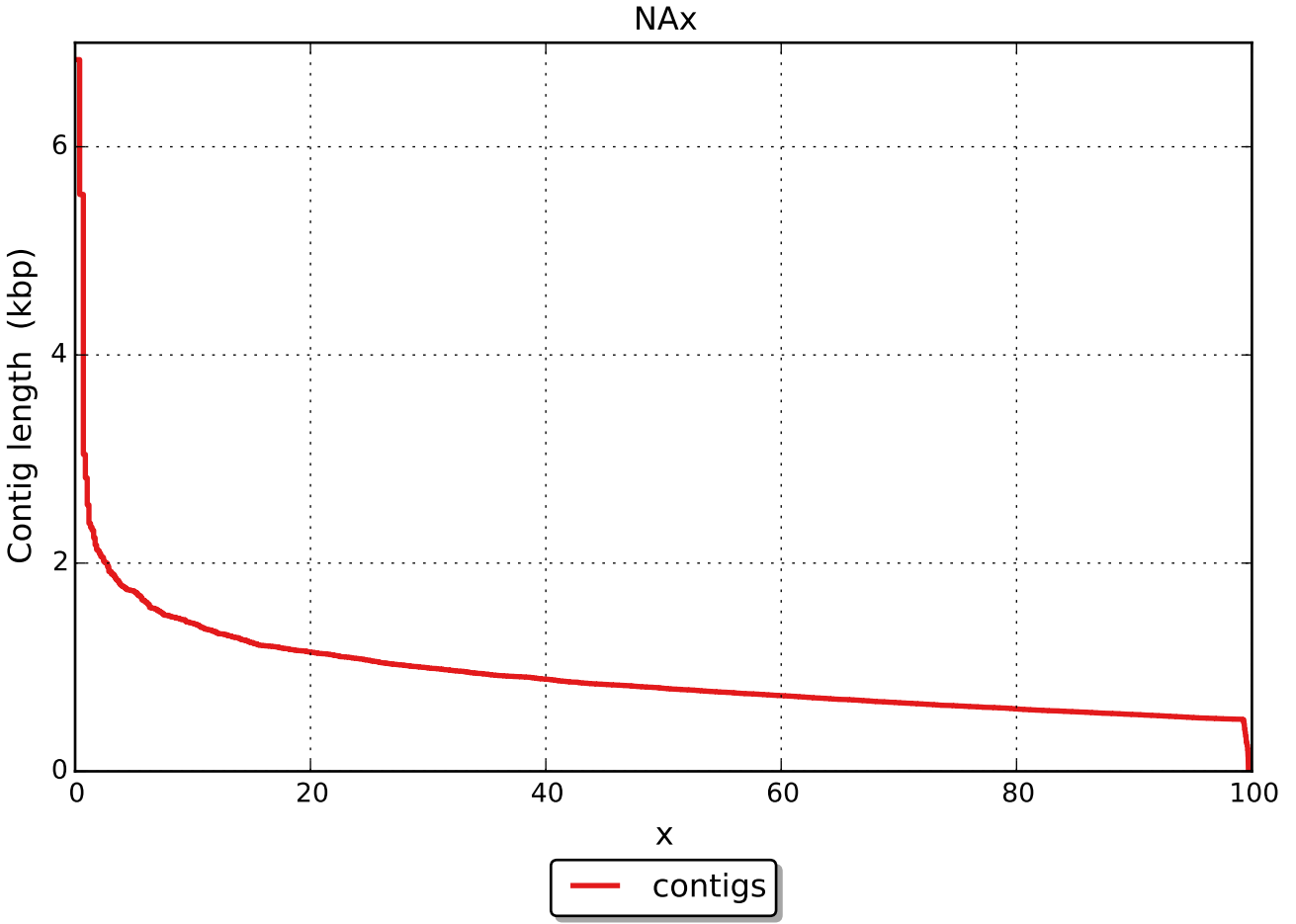

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
contigs

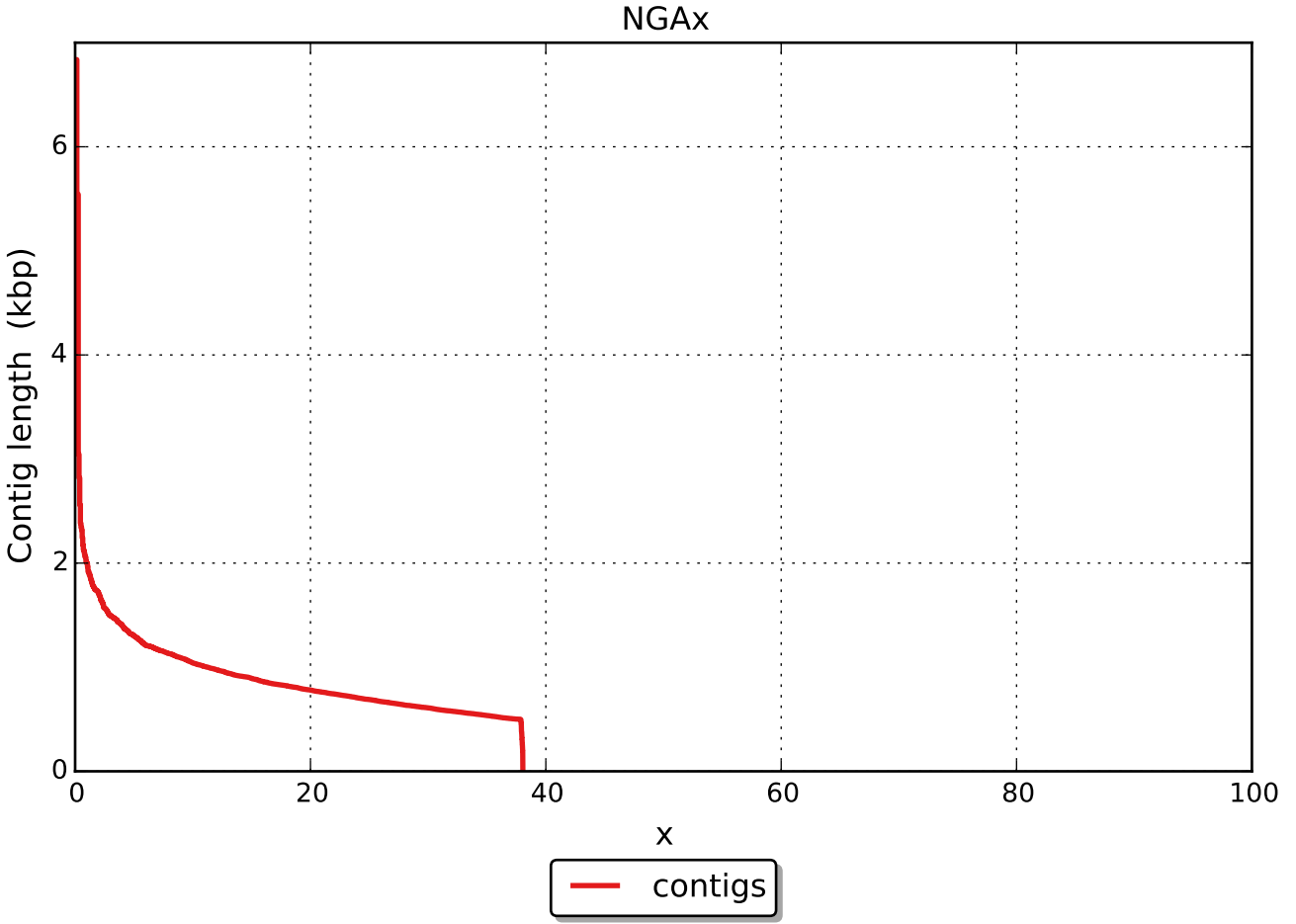

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
contigs
Reference


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


Misassemblies
25
20
15
10
5
0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
contigs