Report

	contigs
# contigs (>= 0 bp)	11095
# contigs (>= 1000 bp)	302
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4598196
Total length (>= 1000 bp)	380811
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2702
Largest contig	3259
Total length	1971634
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	719
N75	588
L50	1027
L75	1790
# misassemblies	14
# misassembled contigs	14
Misassembled contigs length	18788
# local misassemblies	3
# unaligned contigs	0 + 9 part
Unaligned length	528
Genome fraction (%)	41.549
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	998.32
# indels per 100 kbp	1.40
Largest alignment	3243
NA50	717
NGA50	-
NA75	587
LA50	1032
LA75	1797

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

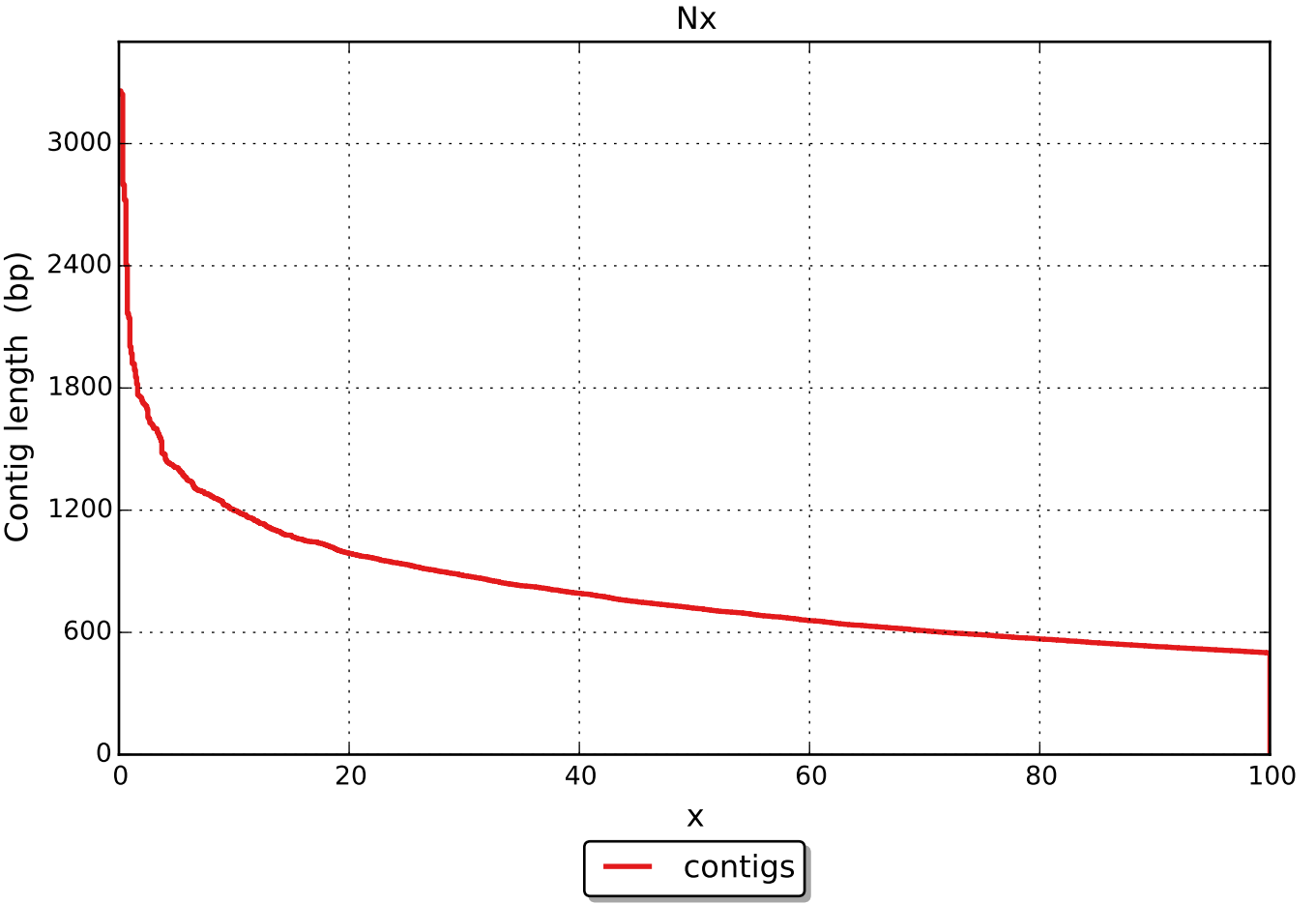
	contigs
# misassemblies	14
# relocations	14
# translocations	0
# inversions	0
# misassembled contigs	14
Misassembled contigs length	18788
# local misassemblies	3
# mismatches	19253
# indels	27
# short indels	27
# long indels	0
Indels length	27

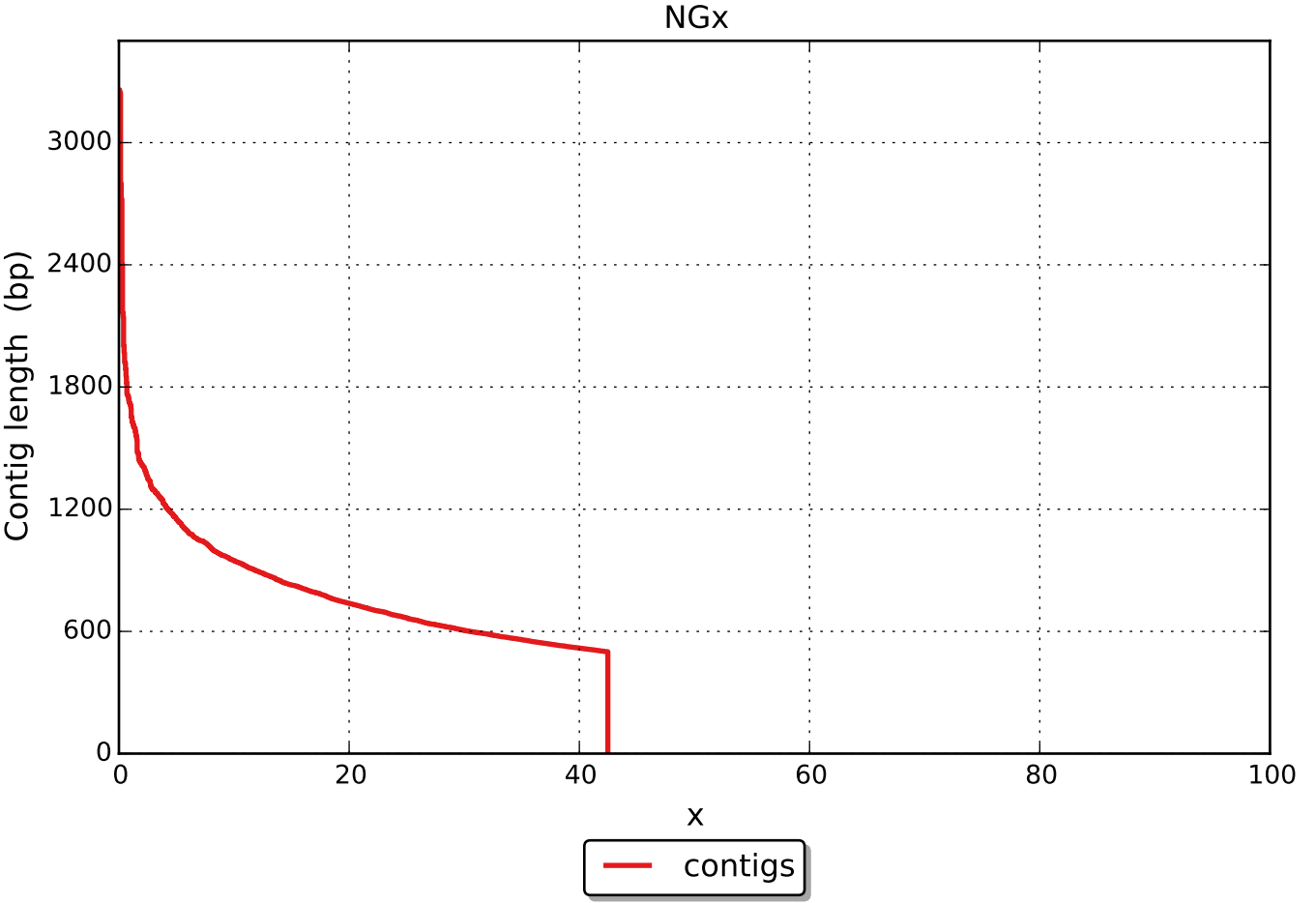
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

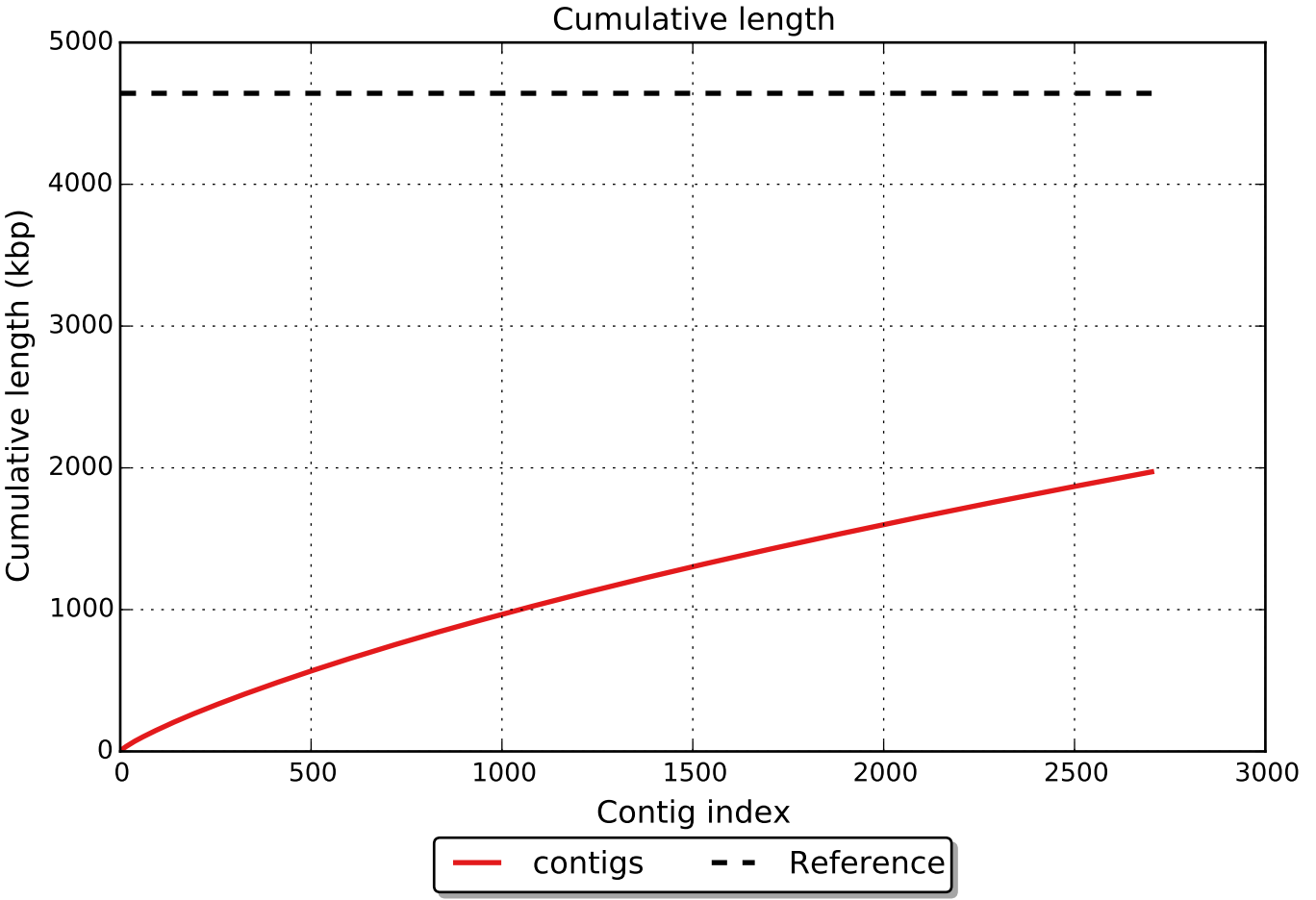
Unaligned report

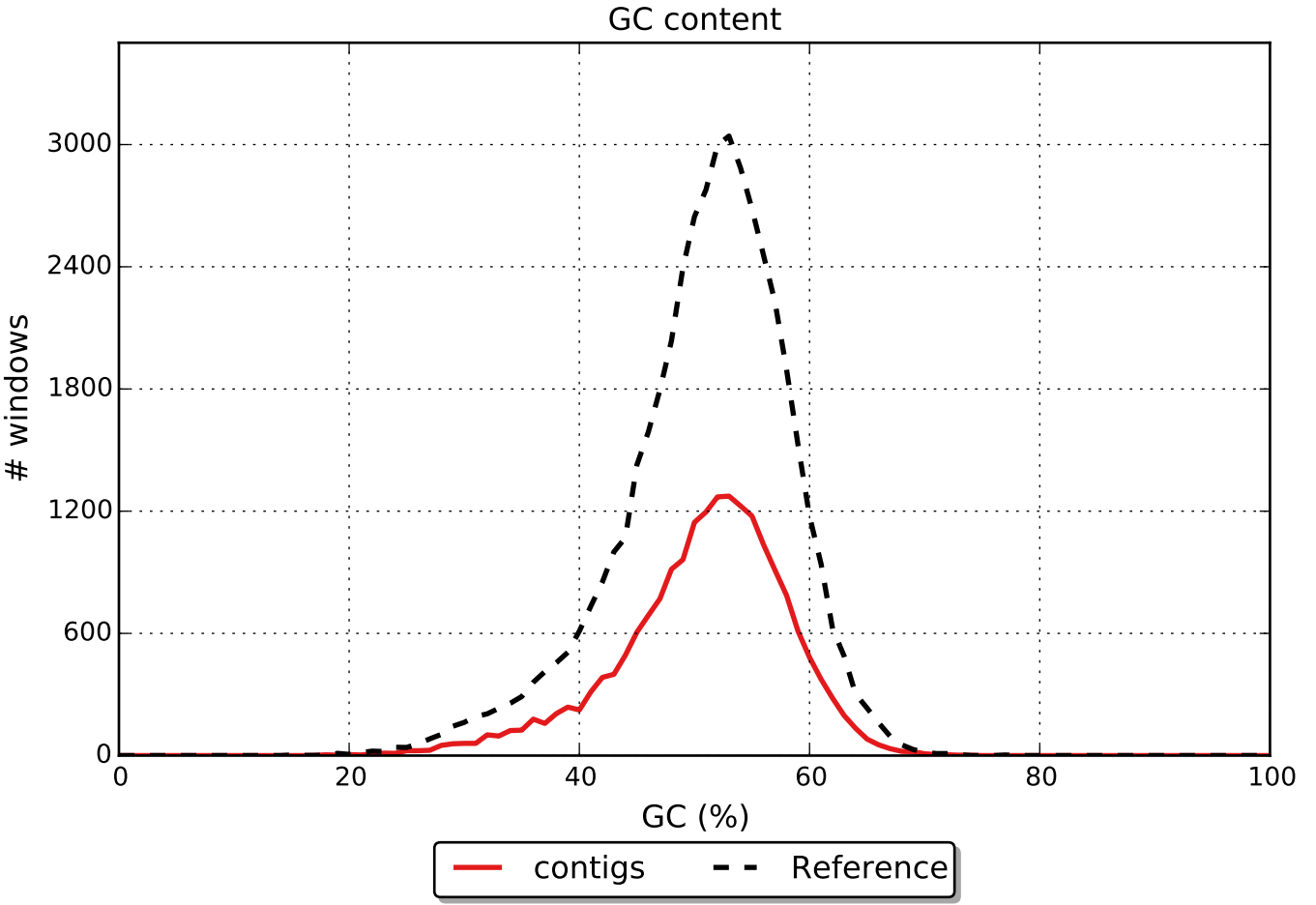
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	0
Partially unaligned length	528
# N's	0

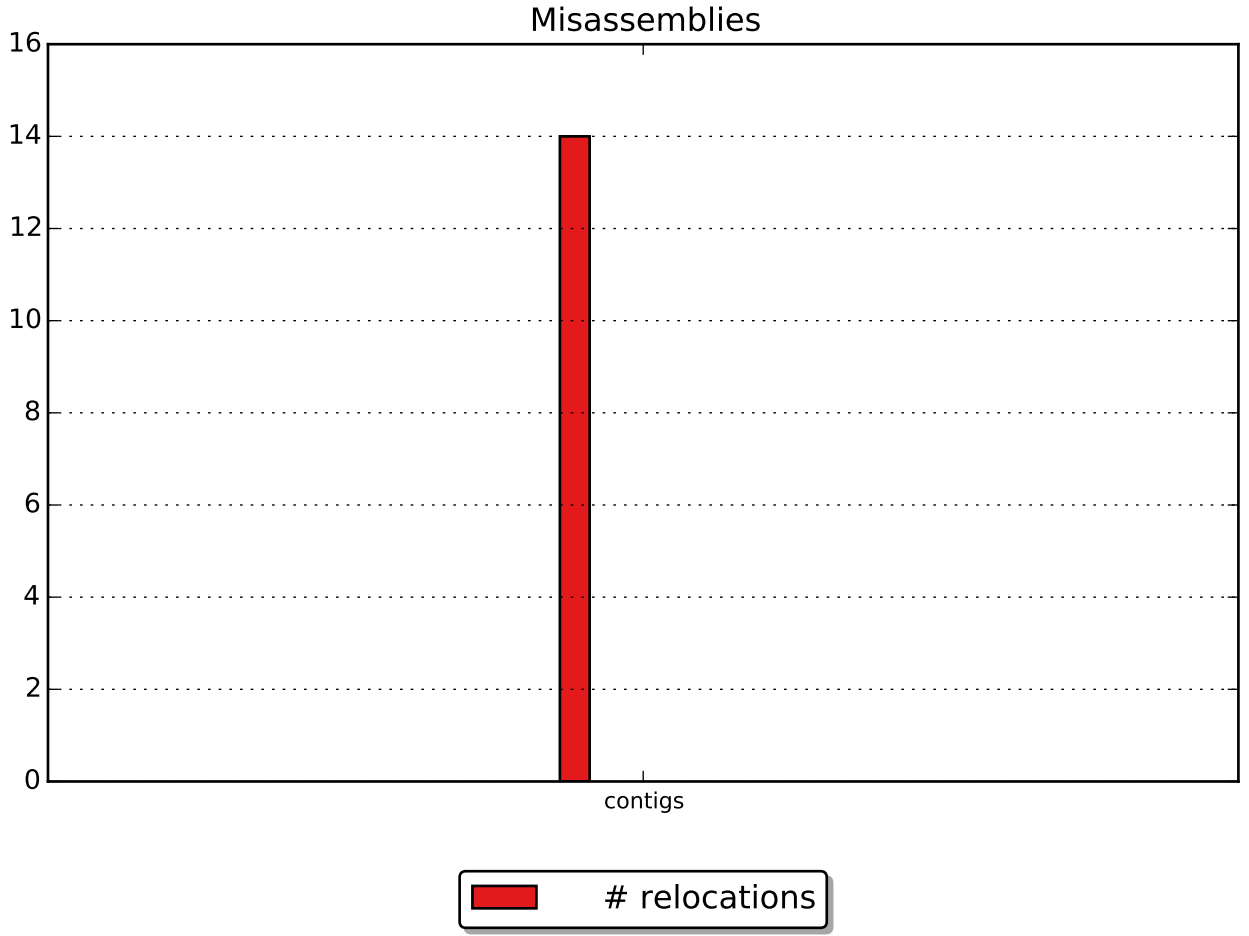
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

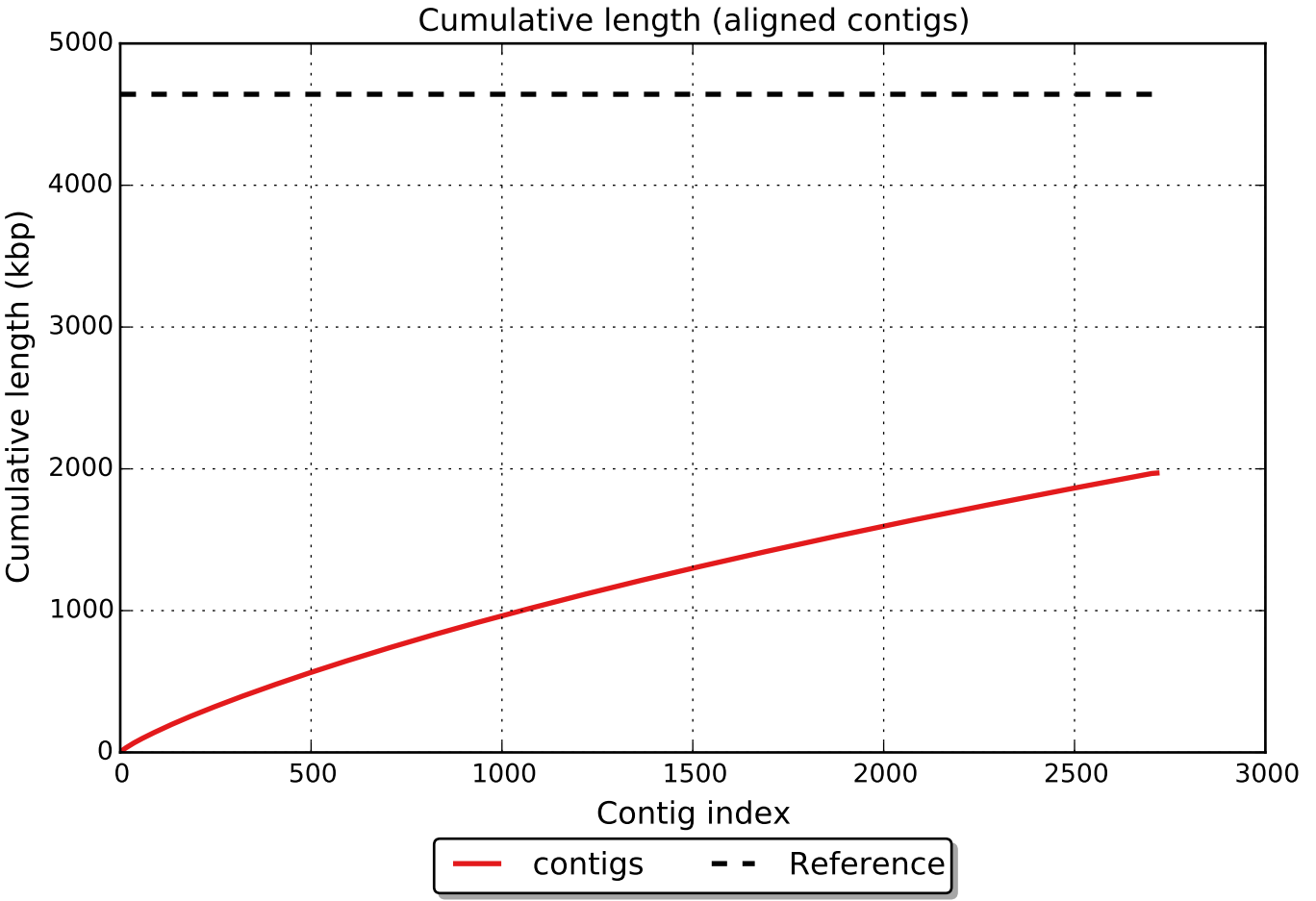

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs

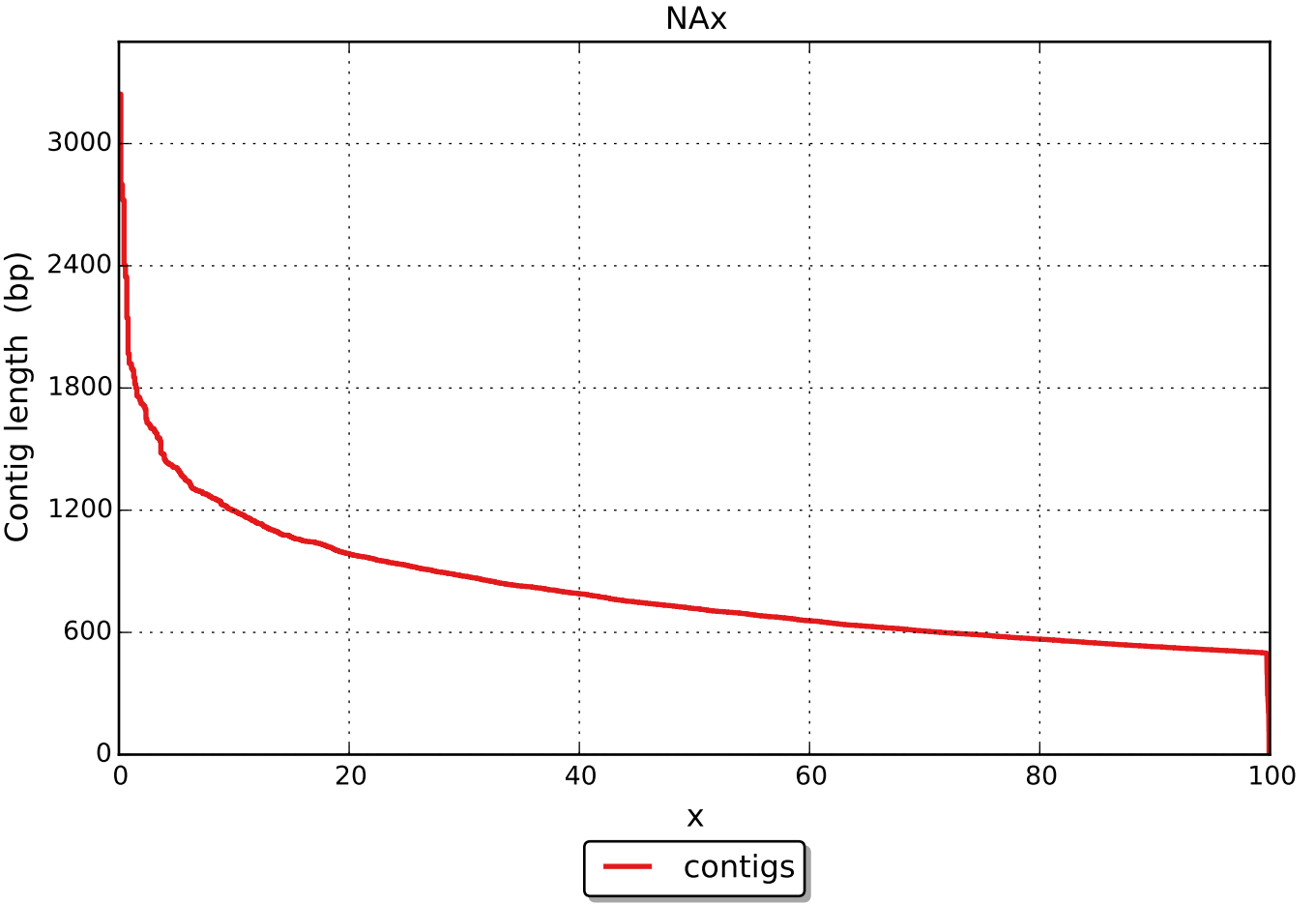

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs

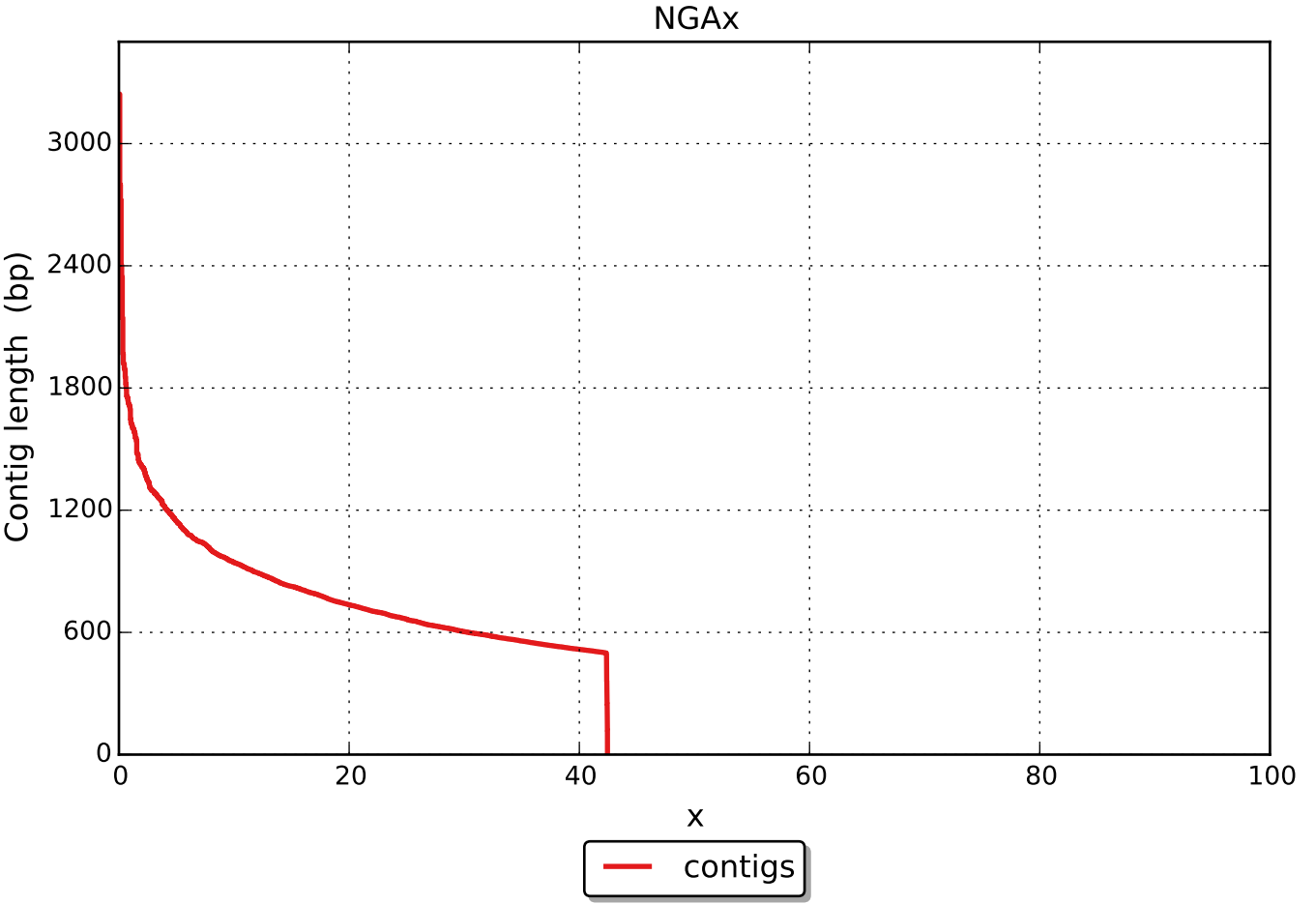

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
contigs
Reference


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


Misassemblies
16
14
12
10
8
6
4
2
0
contigs
relocations


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


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
contigs