Report

	contigs
# contigs (>= 1000 bp)	532
# contigs (>= 5000 bp)	149
# contigs (>= 10000 bp)	37
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2213088
Total length (>= 5000 bp)	1260896
Total length (>= 10000 bp)	513382
Total length (>= 25000 bp)	61000
Total length (>= 50000 bp)	0
# contigs	666
Largest contig	31499
Total length	2304257
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	5507
N75	2991
L50	129
L75	269
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	382
Genome fraction (%)	49.391
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	807.35
# indels per 100 kbp	0.83
Largest alignment	31499
NA50	5507
NGA50	-
NA75	2991
LA50	129
LA75	269

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

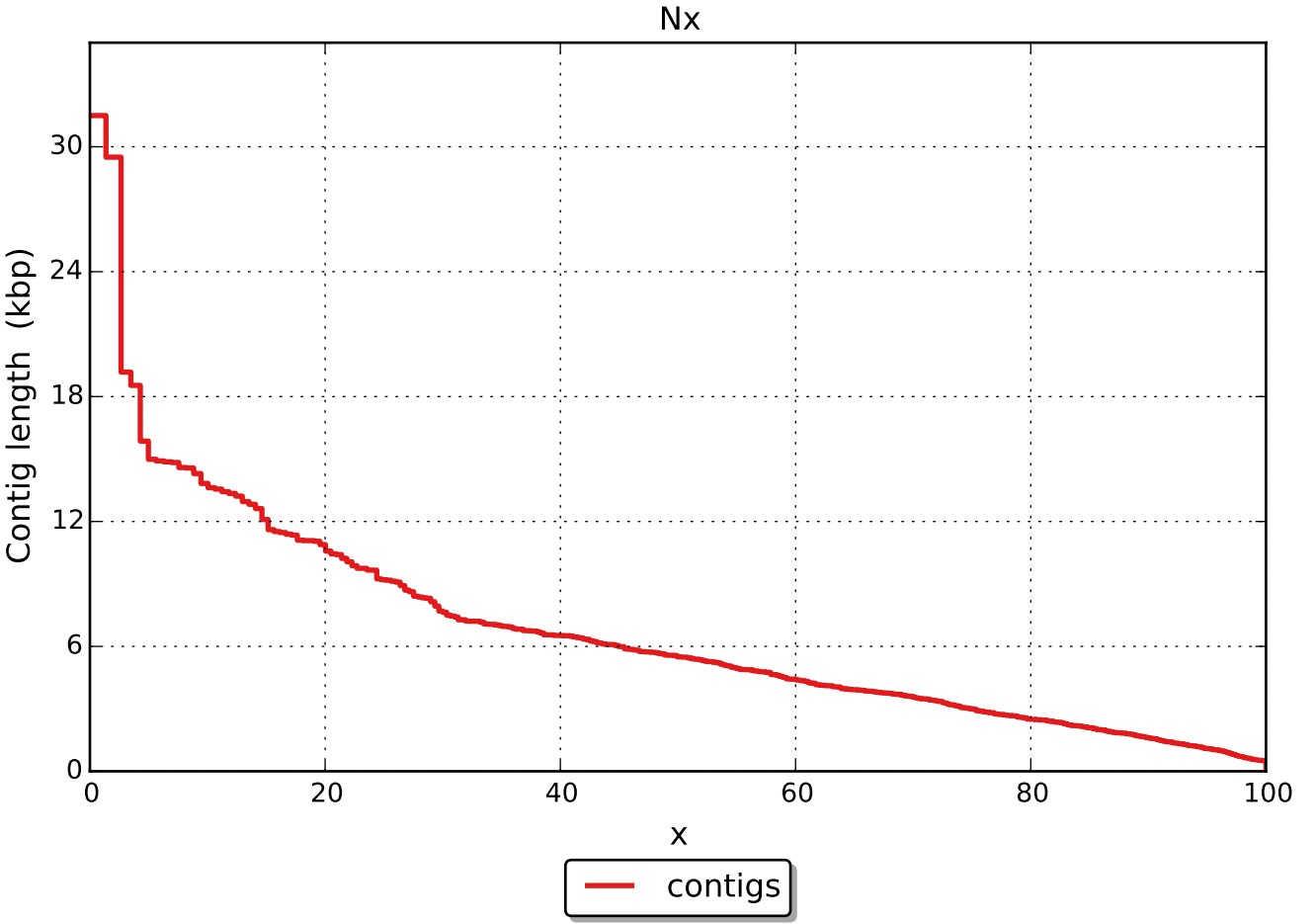
	contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	18509
# indels	19
# short indels	19
# long indels	0
Indels length	25

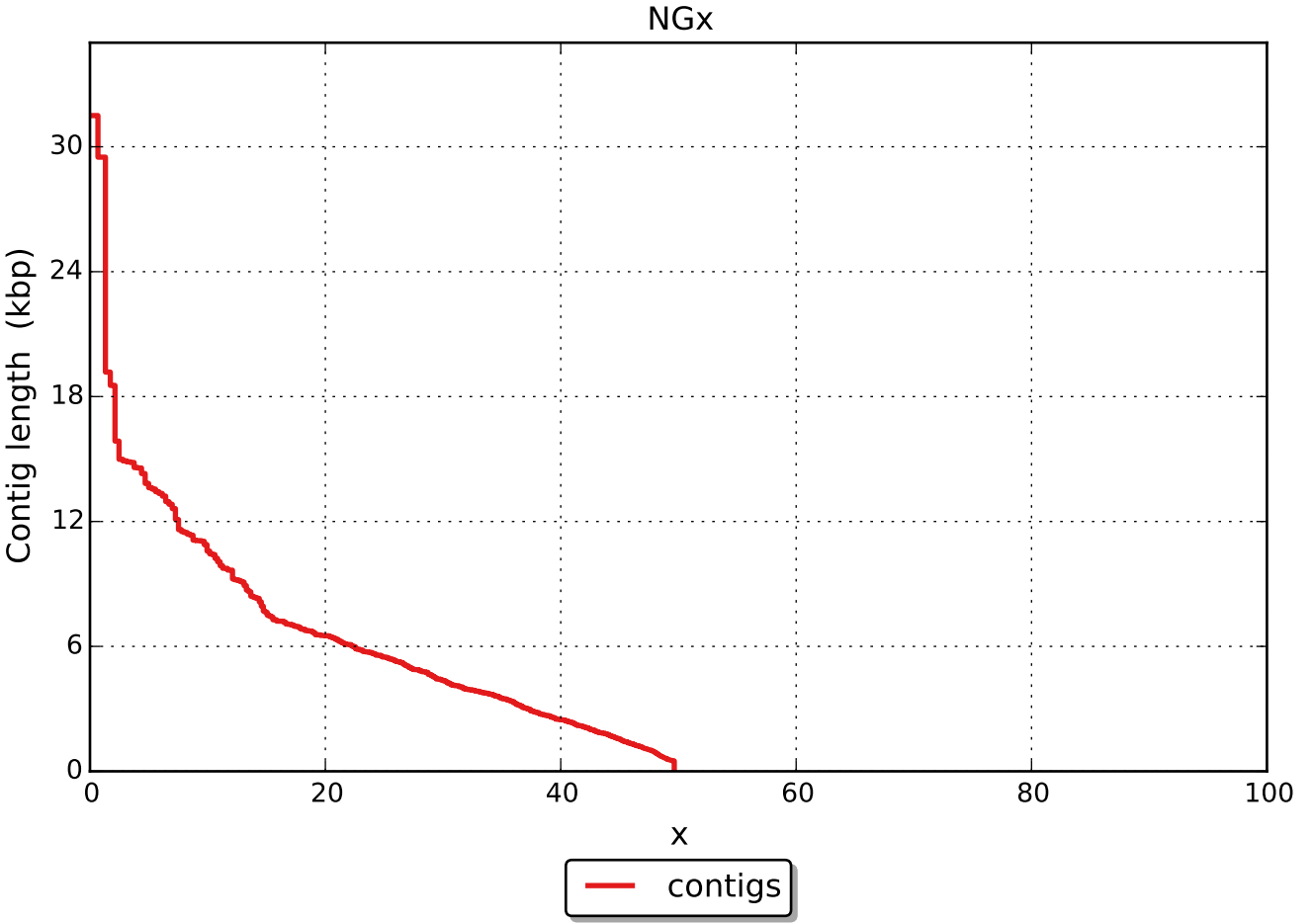
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

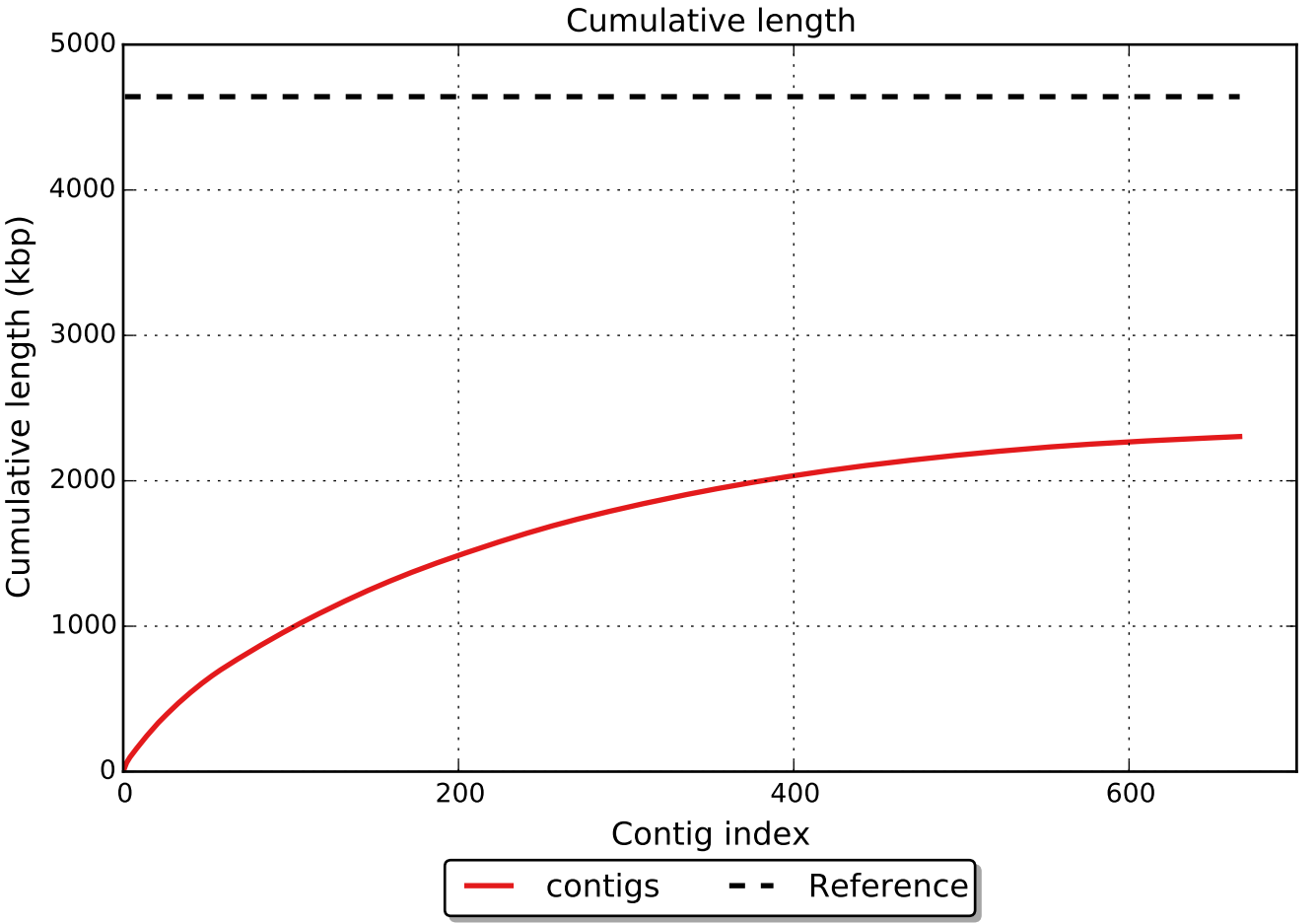
Unaligned report

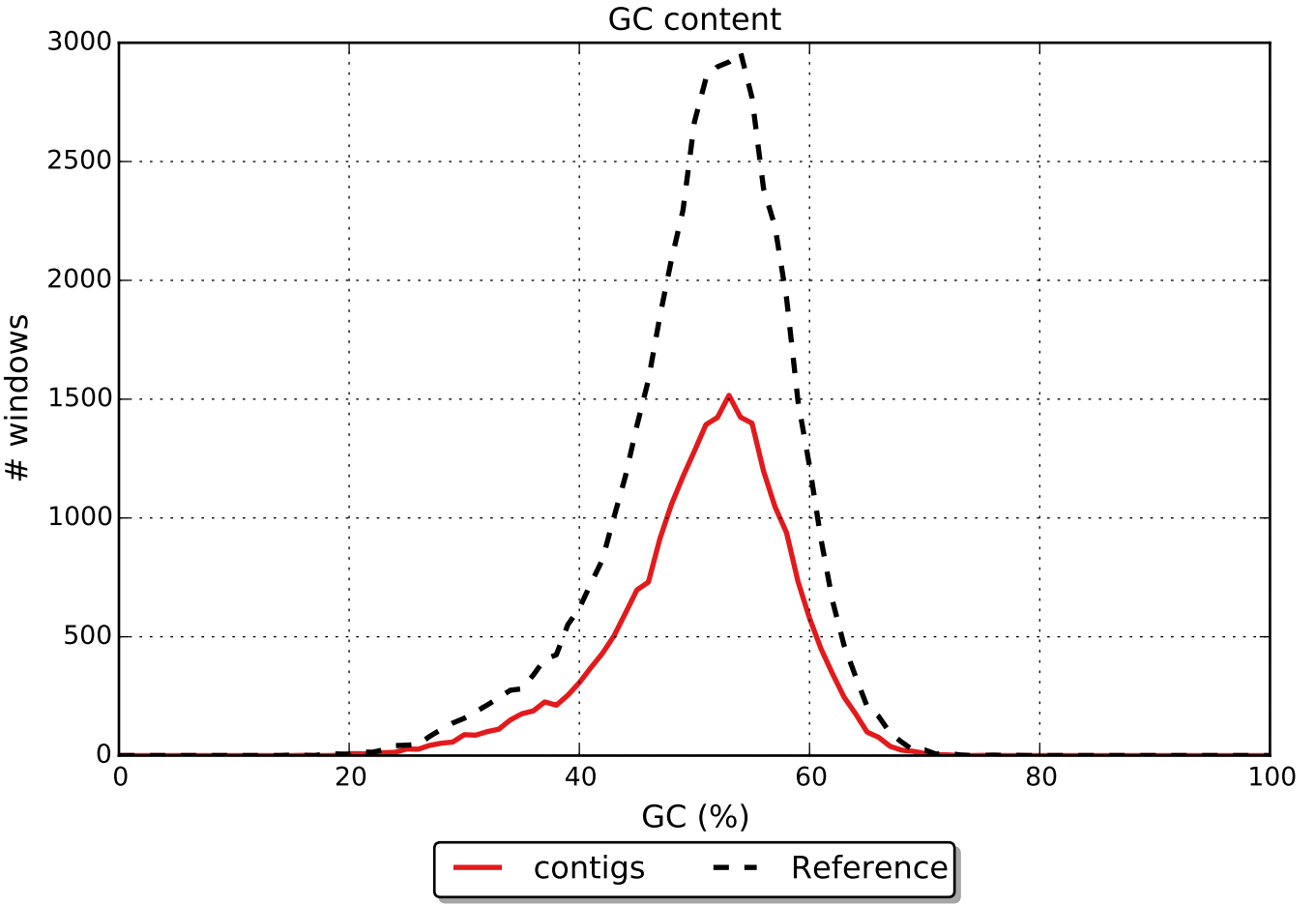
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	382
# N's	0

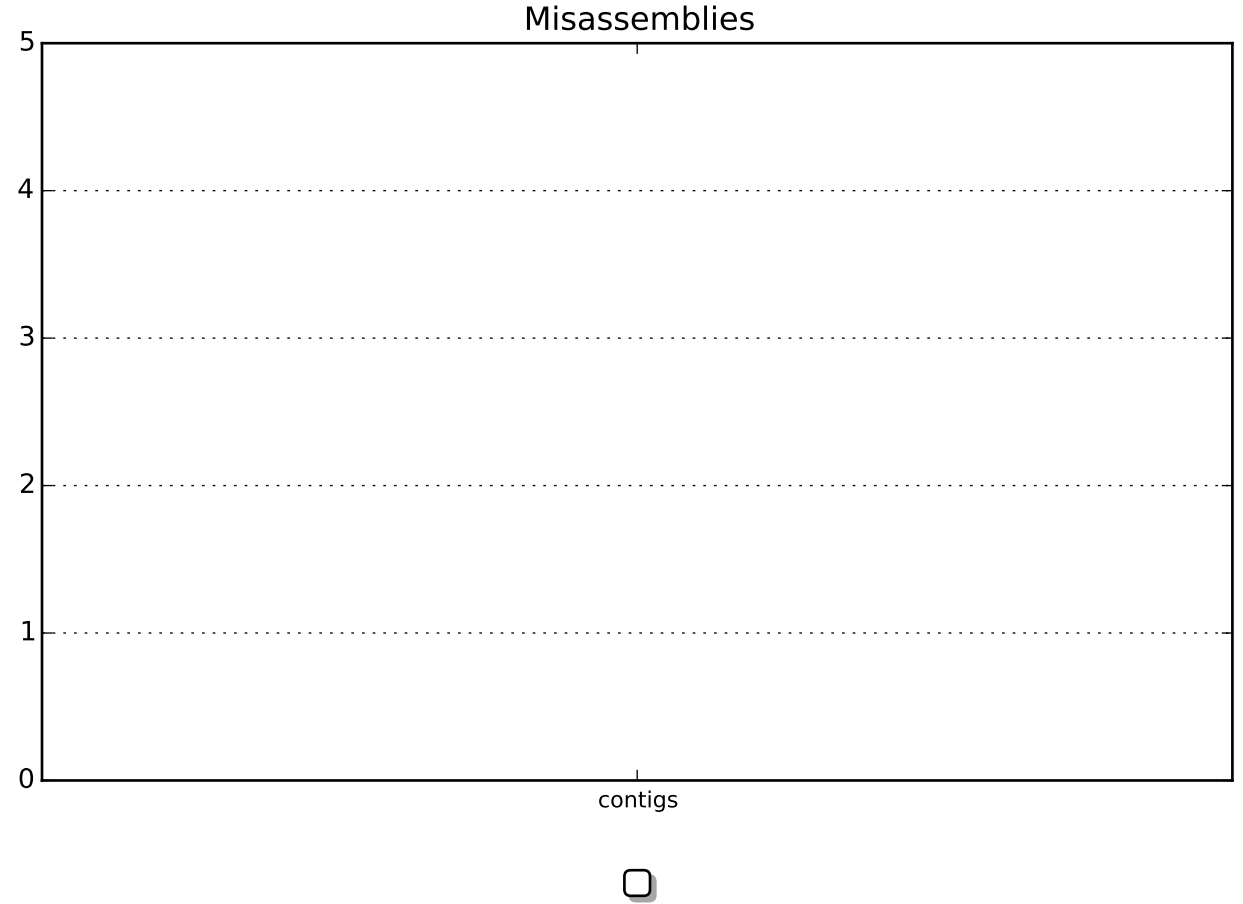
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

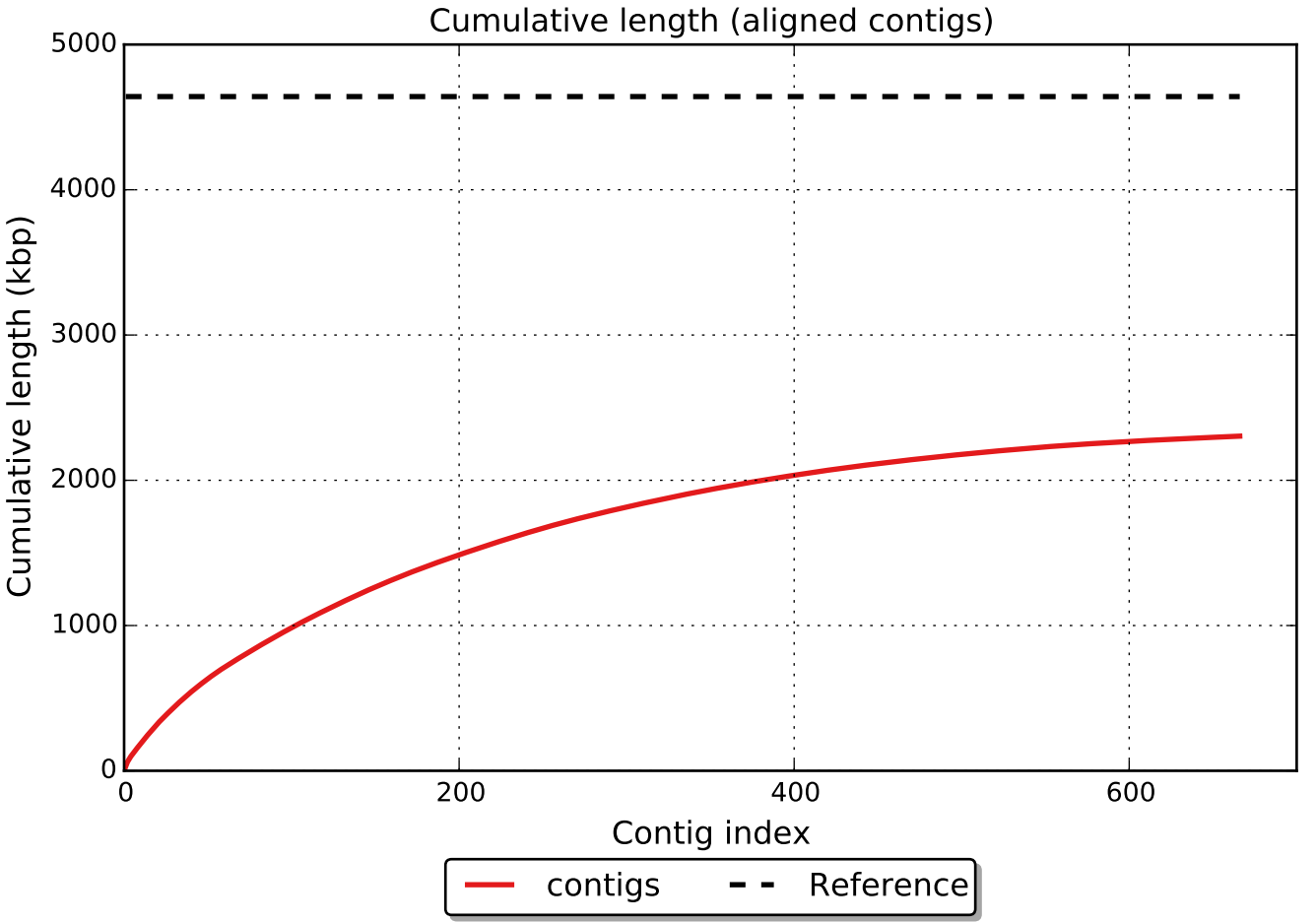

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs

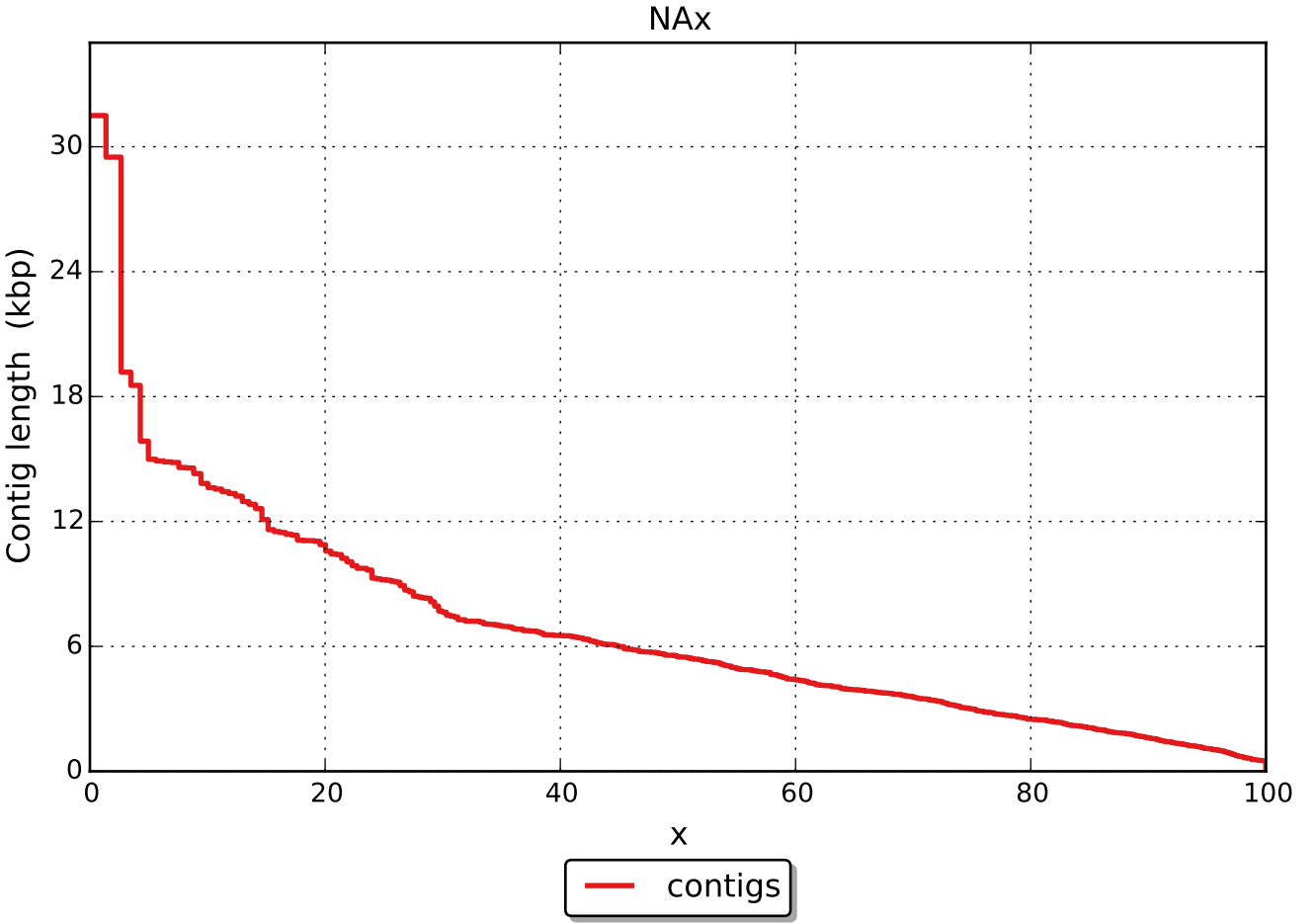

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs

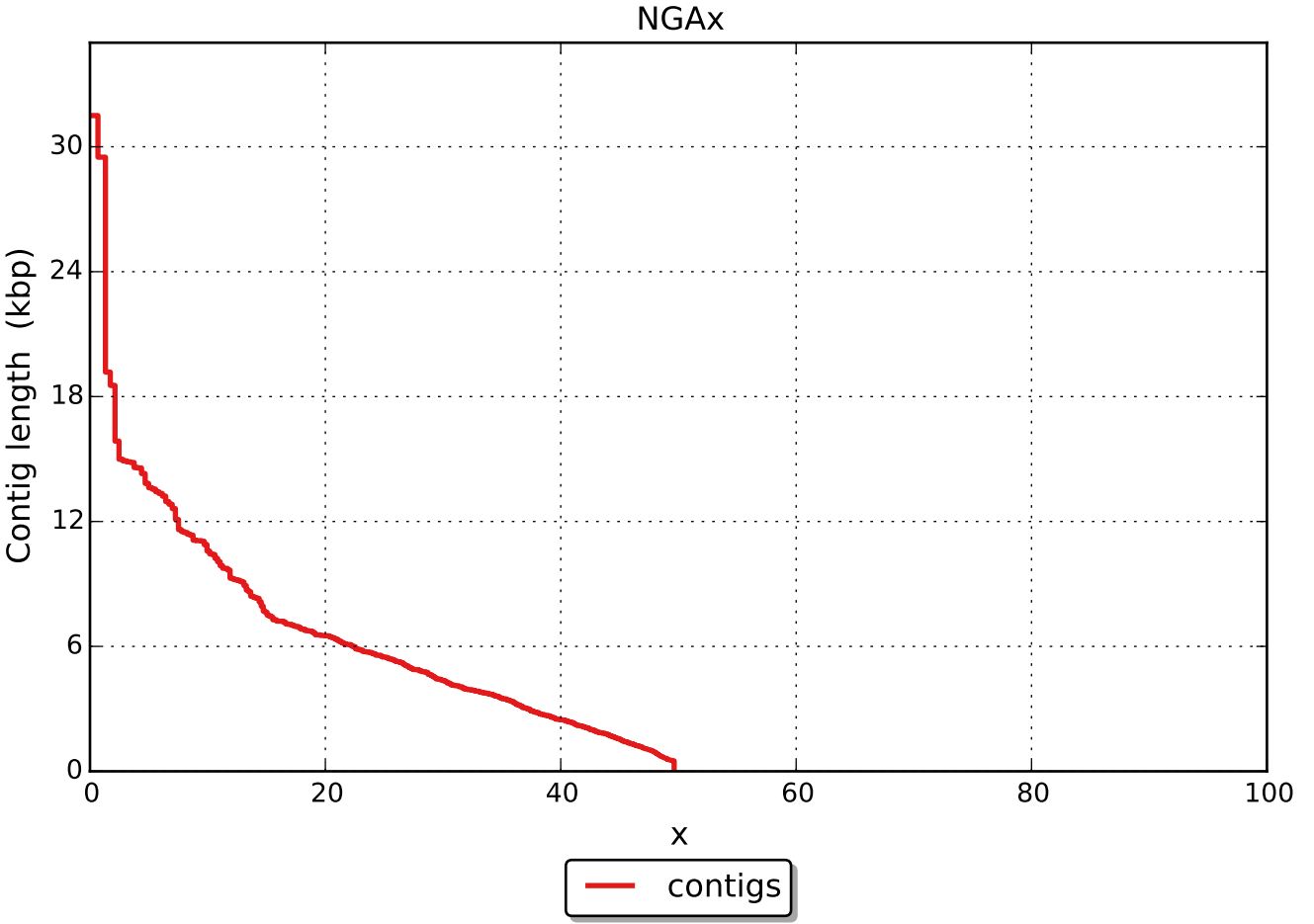

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
200
400
600
Contig index
contigs
Reference


GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
contigs
Reference


Misassemblies
5
4
3
2
1
0
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
Contig index
contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs