Report

	contigs
# contigs (>= 1000 bp)	171
# contigs (>= 5000 bp)	121
# contigs (>= 10000 bp)	79
# contigs (>= 25000 bp)	25
# contigs (>= 50000 bp)	8
Total length (>= 1000 bp)	2388941
Total length (>= 5000 bp)	2251033
Total length (>= 10000 bp)	1941351
Total length (>= 25000 bp)	1106637
Total length (>= 50000 bp)	531188
# contigs	183
Largest contig	108881
Total length	2396038
Reference length	4641652
GC (%)	50.68
Reference GC (%)	50.79
N50	23315
NG50	3800
N75	12110
L50	29
LG50	138
L75	66
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	50.449
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	832.52
# indels per 100 kbp	0.56
Largest alignment	108881
NA50	23073
NGA50	3780
NA75	11853
LA50	31
LGA50	141
LA75	69

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

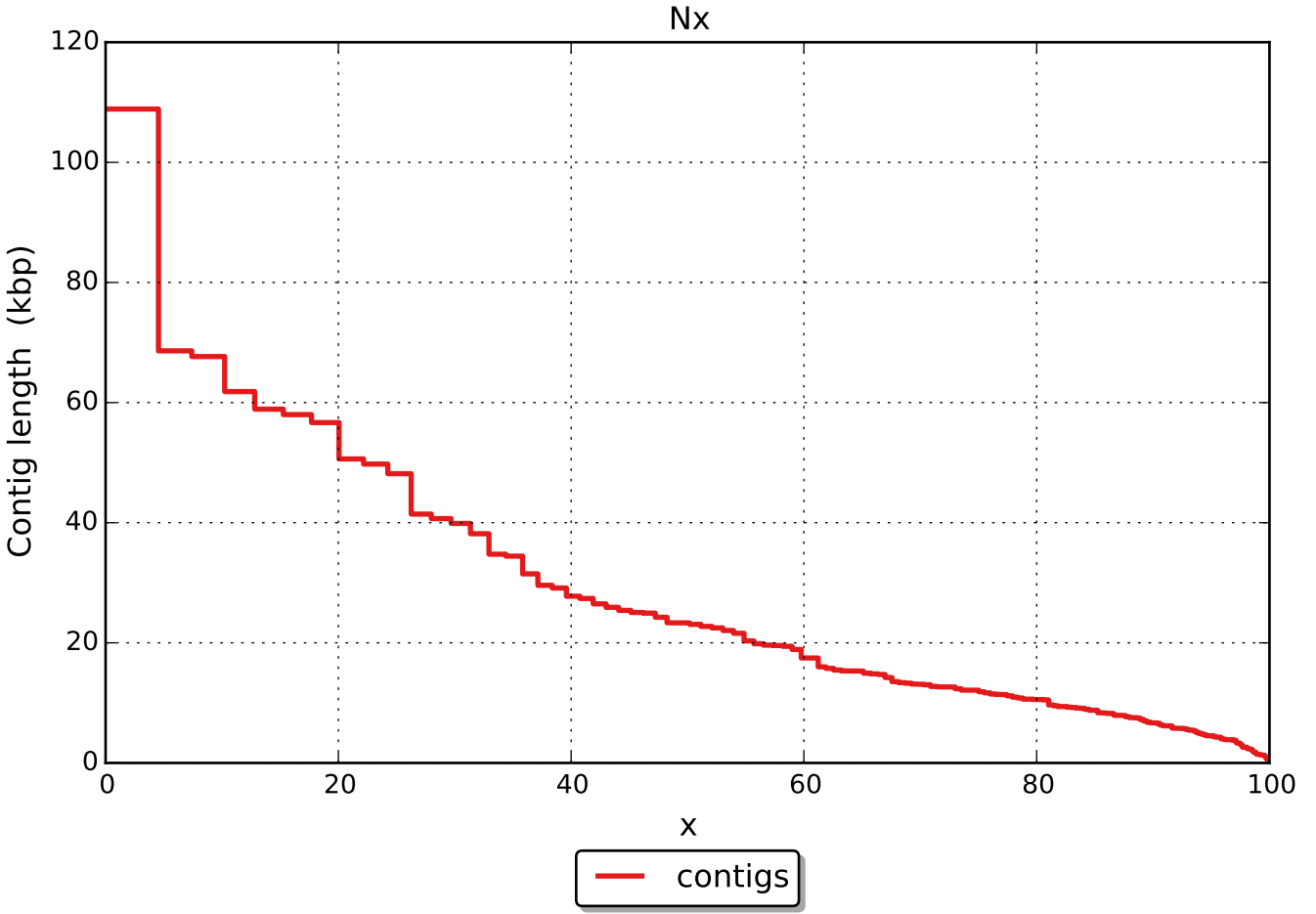
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# mismatches	19495
# indels	13
# short indels	13
# long indels	0
Indels length	19

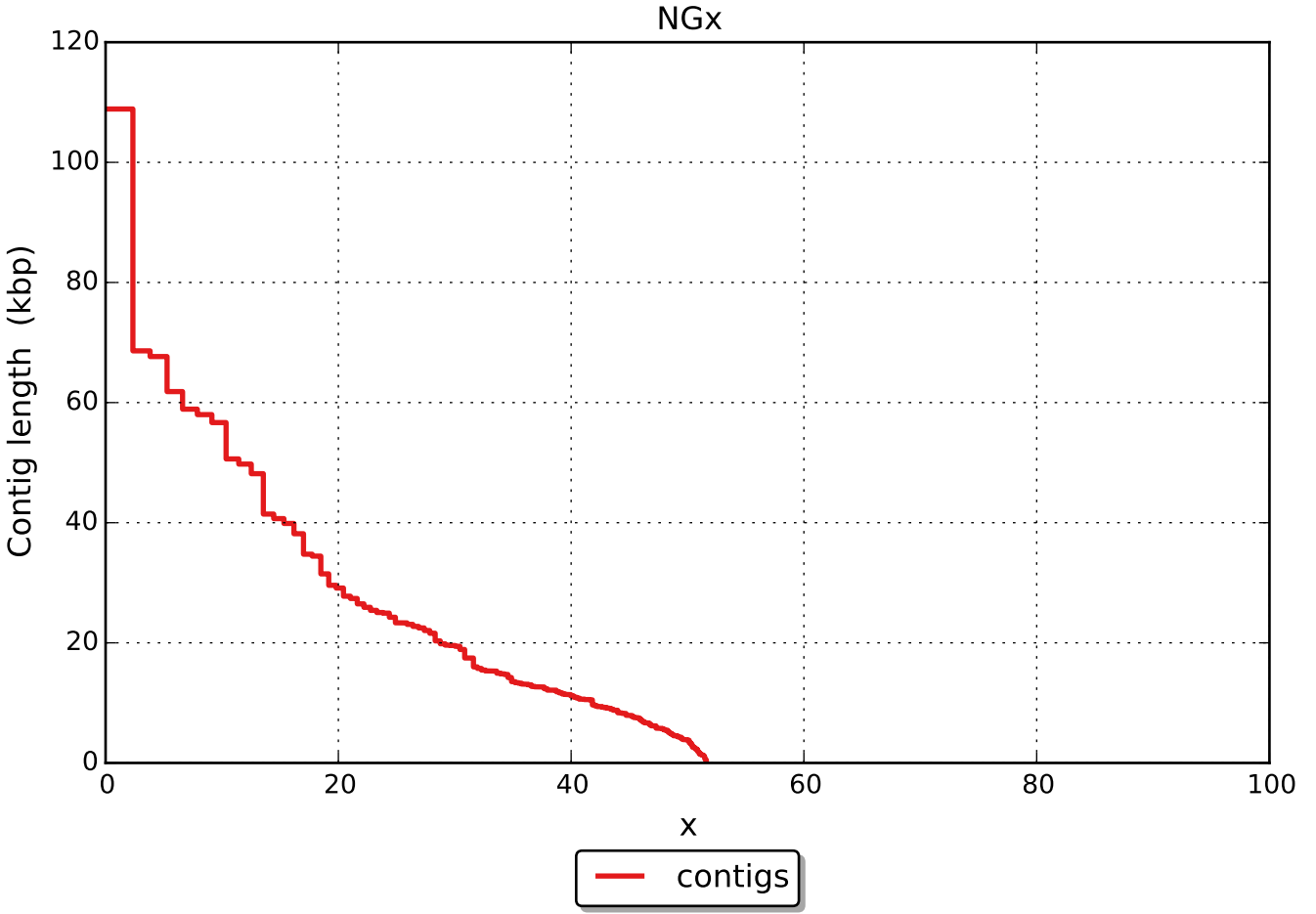
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

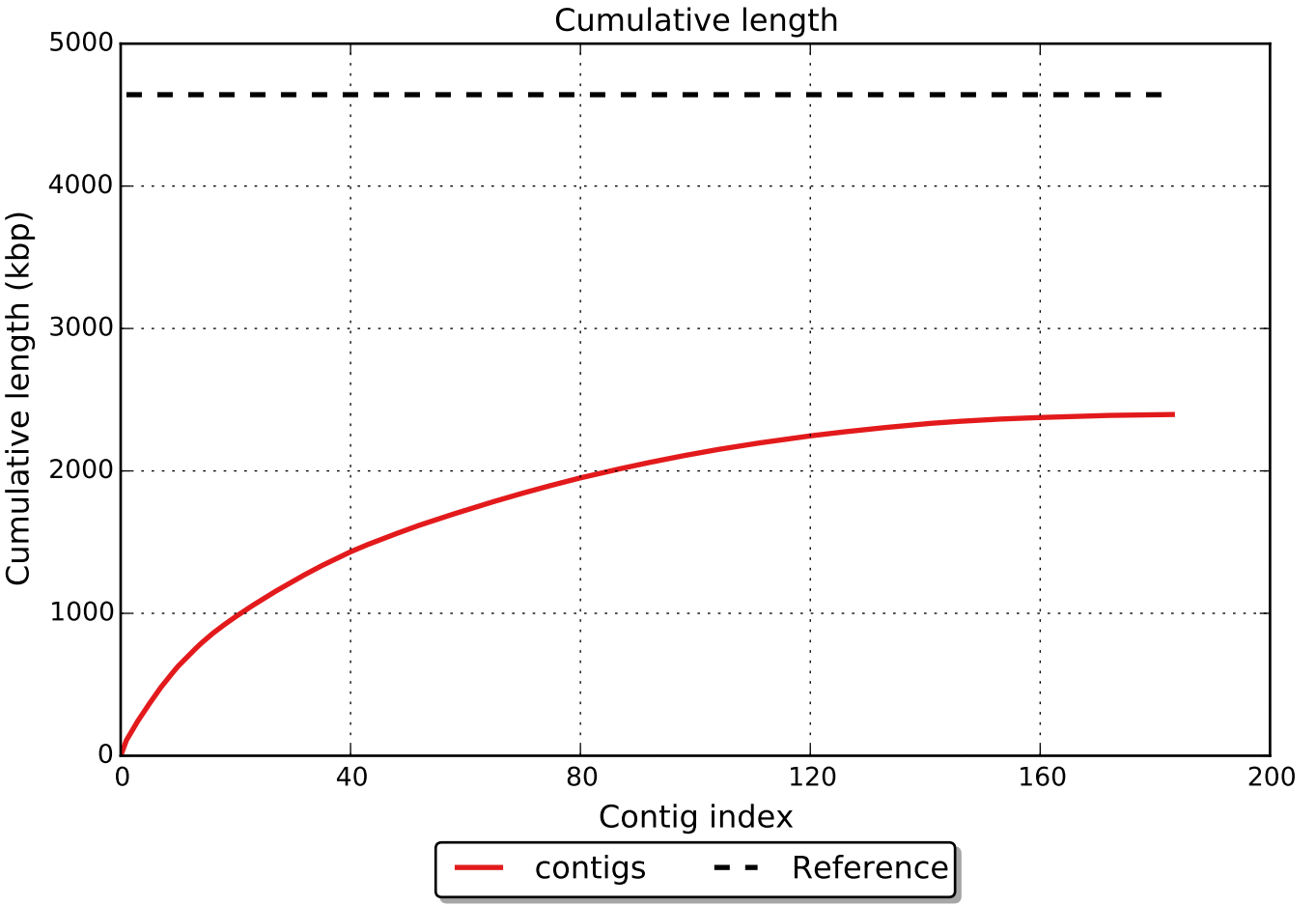
Unaligned report

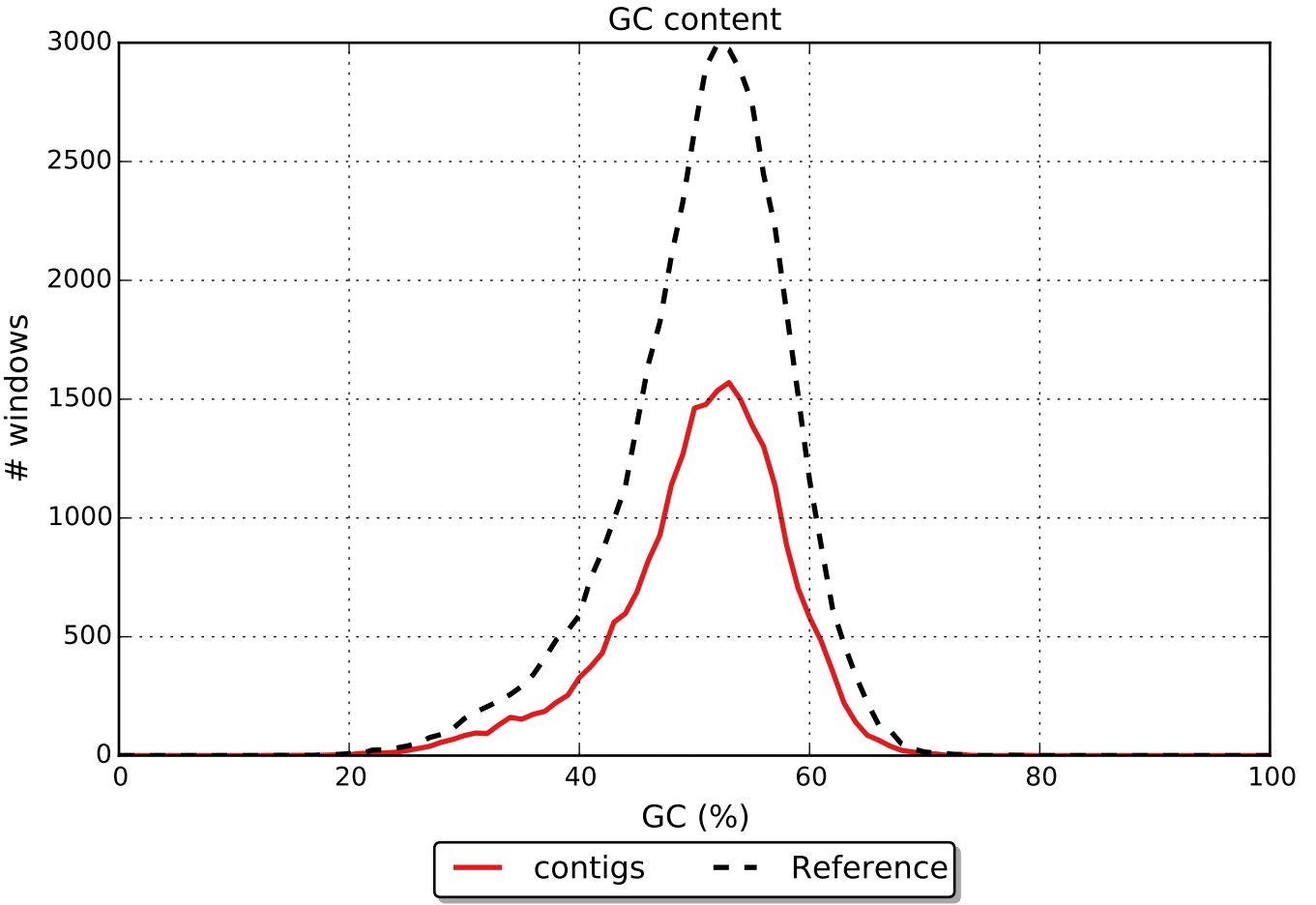
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

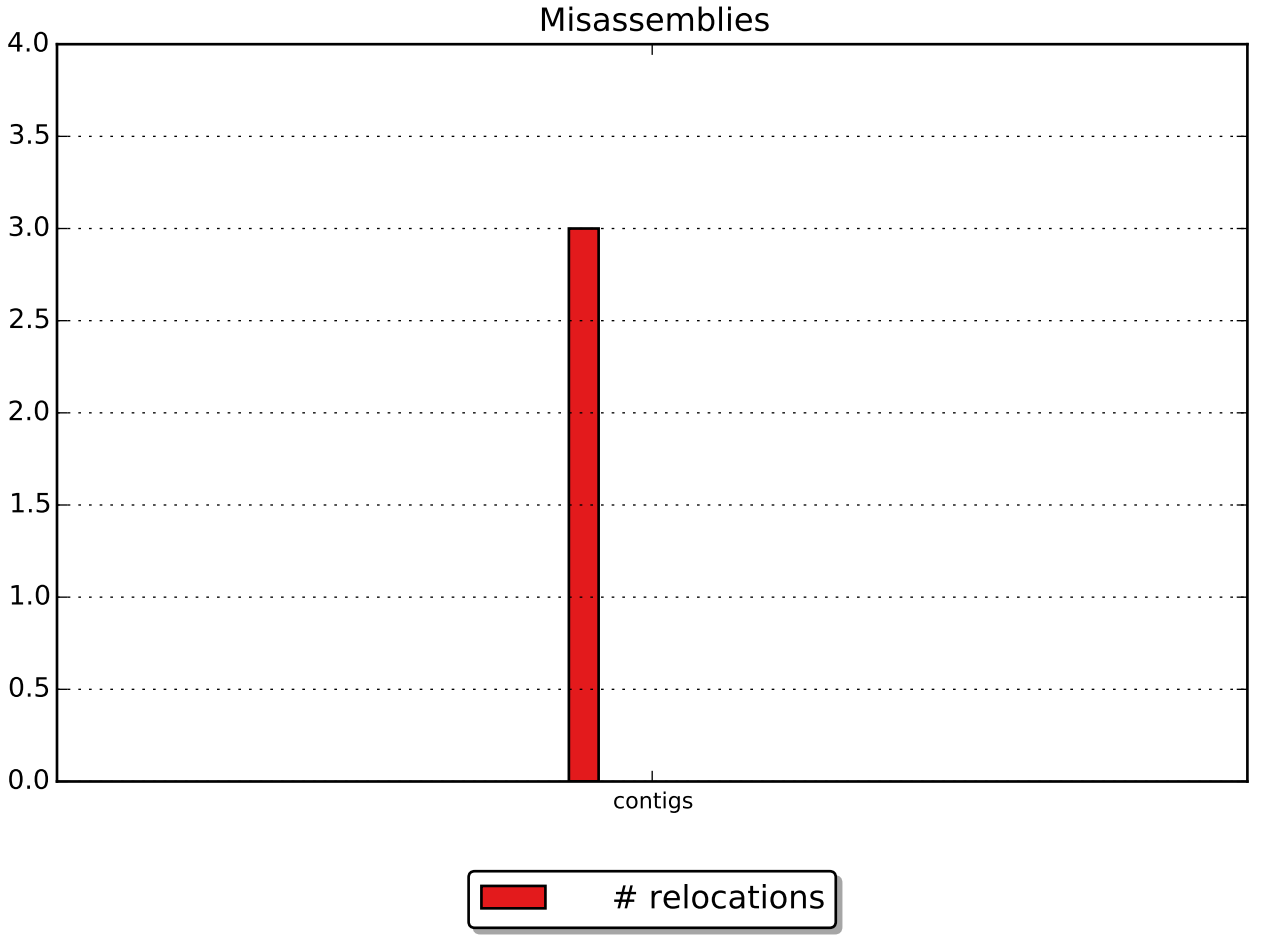
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

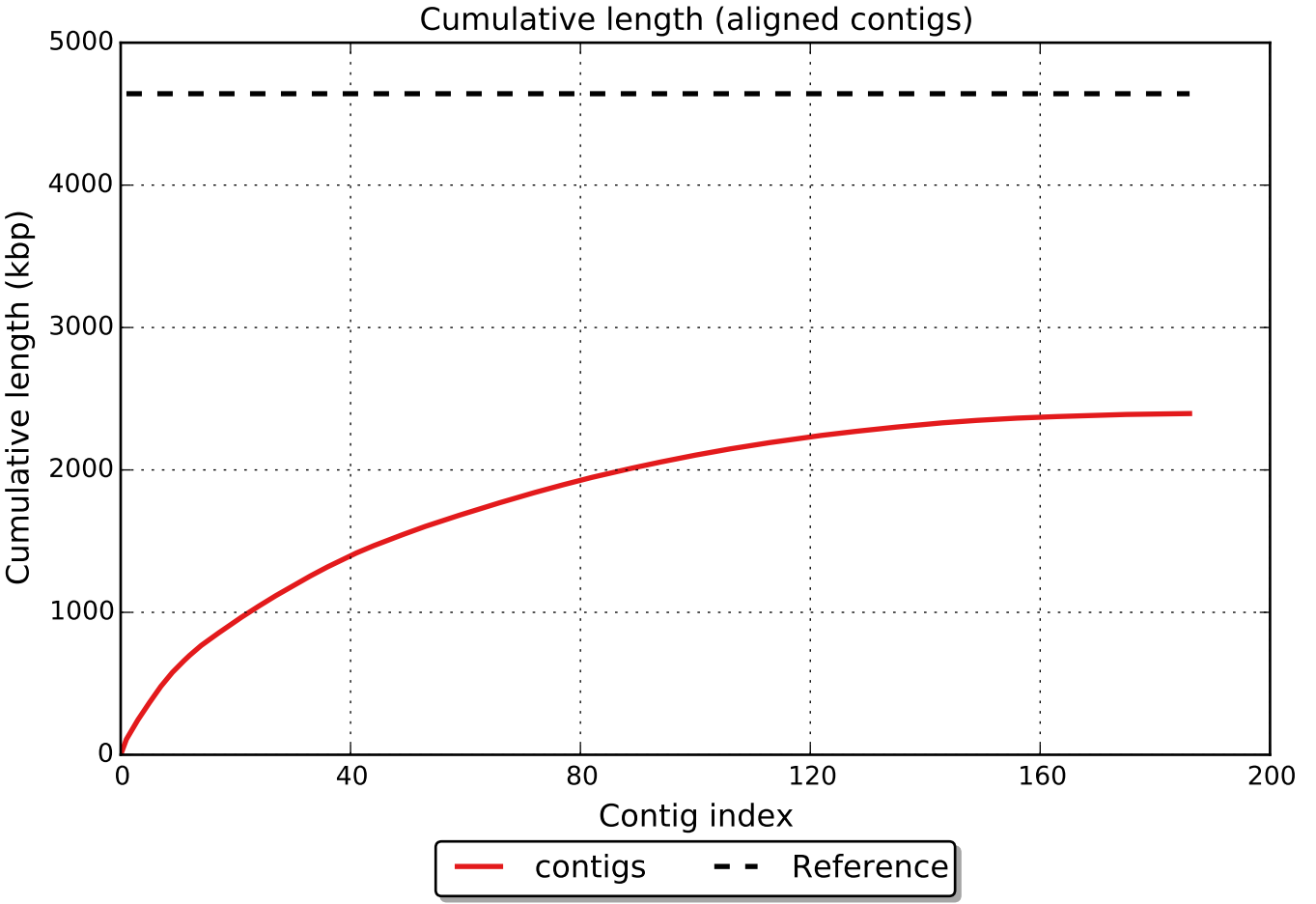

Nx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

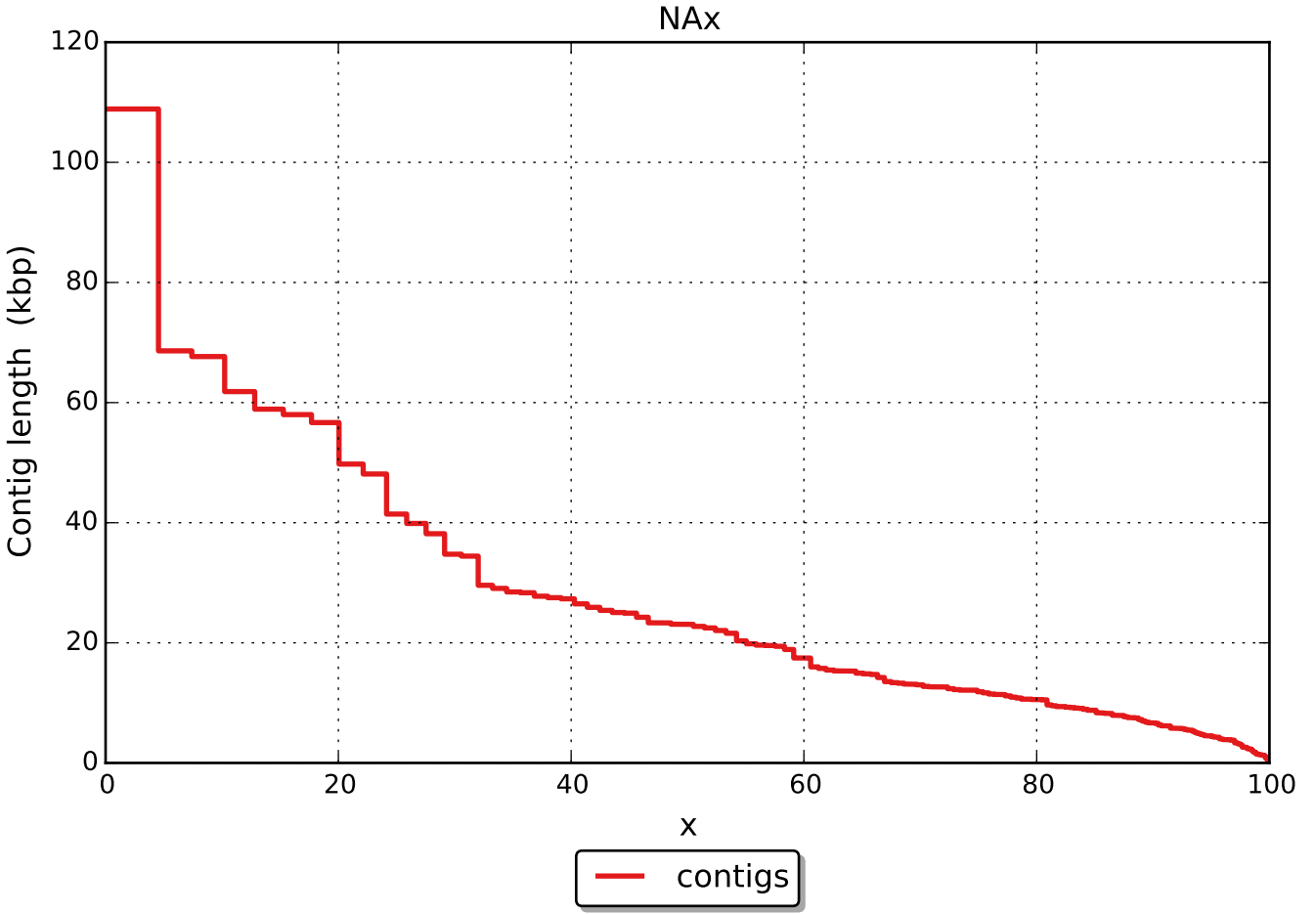

NGx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

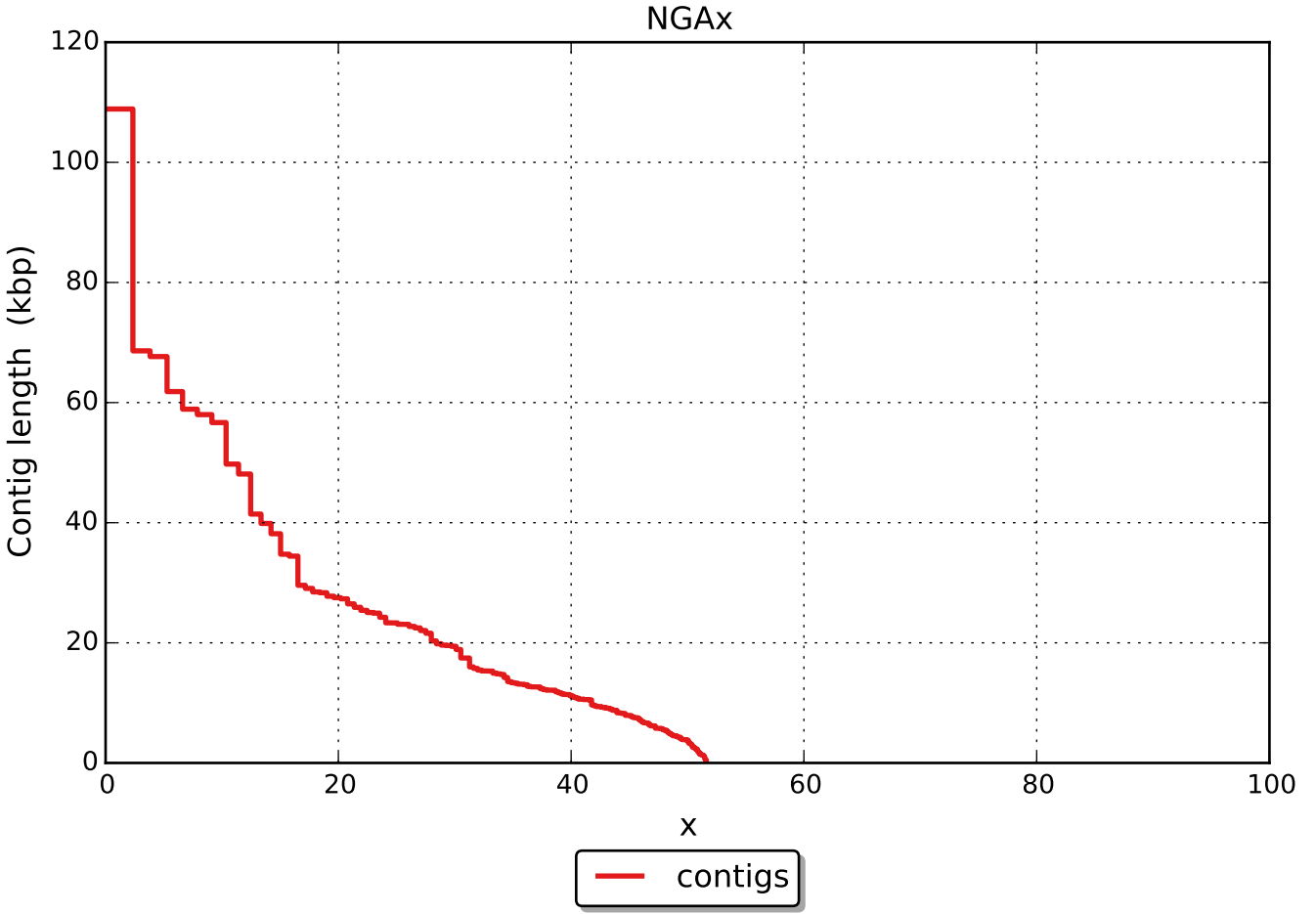

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
40
80
120
160
200
Contig index
contigs
Reference


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


Misassemblies
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
40
80
120
160
200
Contig index
contigs
Reference


NAx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs


NGAx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs