Report

	contigs
# contigs (>= 1000 bp)	200
# contigs (>= 5000 bp)	149
# contigs (>= 10000 bp)	98
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	23
Total length (>= 1000 bp)	3788316
Total length (>= 5000 bp)	3638218
Total length (>= 10000 bp)	3253284
Total length (>= 25000 bp)	2523887
Total length (>= 50000 bp)	1644099
# contigs	213
Largest contig	130415
Total length	3797254
Reference length	4641652
GC (%)	50.65
Reference GC (%)	50.78
N50	40191
NG50	32043
N75	14328
NG75	7430
L50	29
LG50	41
L75	65
LG75	125
# misassemblies	5
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.904
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	744.31
# indels per 100 kbp	0.45
Largest alignment	122264
NA50	37528
NGA50	31478
NA75	13877
NGA75	7182
LA50	32
LGA50	44
LA75	69
LGA75	130

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

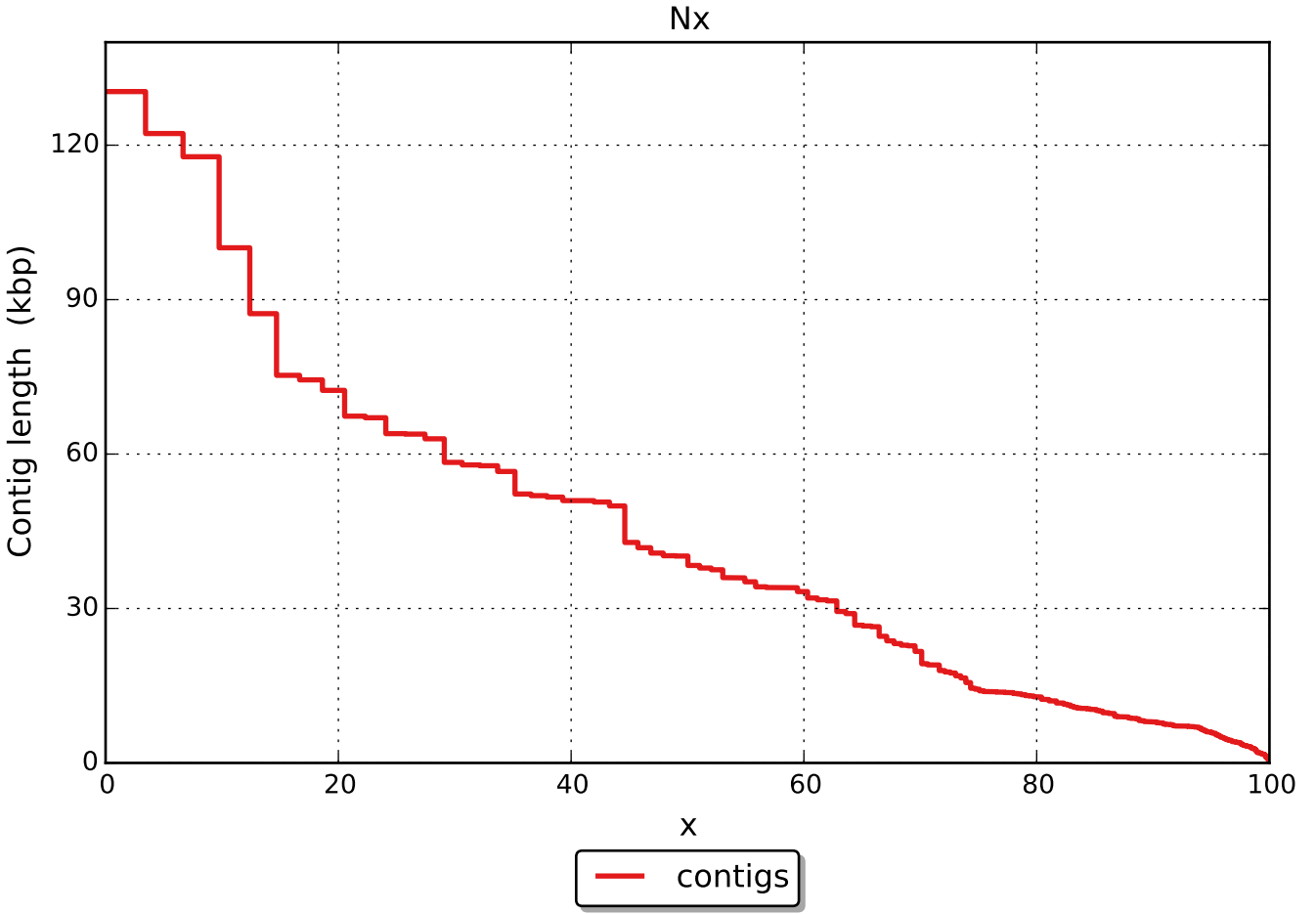
	contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	339551
# local misassemblies	3
# mismatches	27951
# indels	17
# short indels	17
# long indels	0
Indels length	23

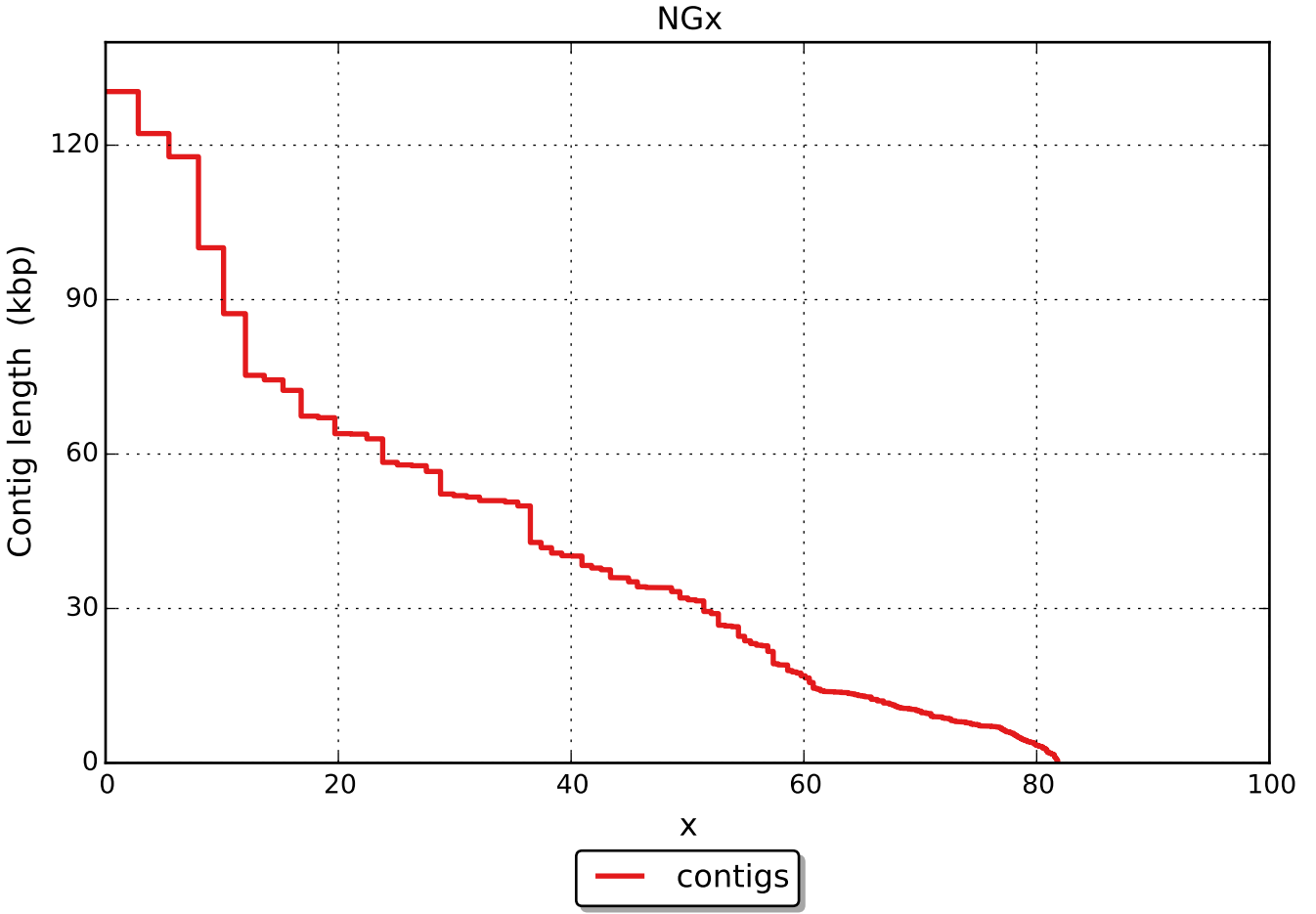
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

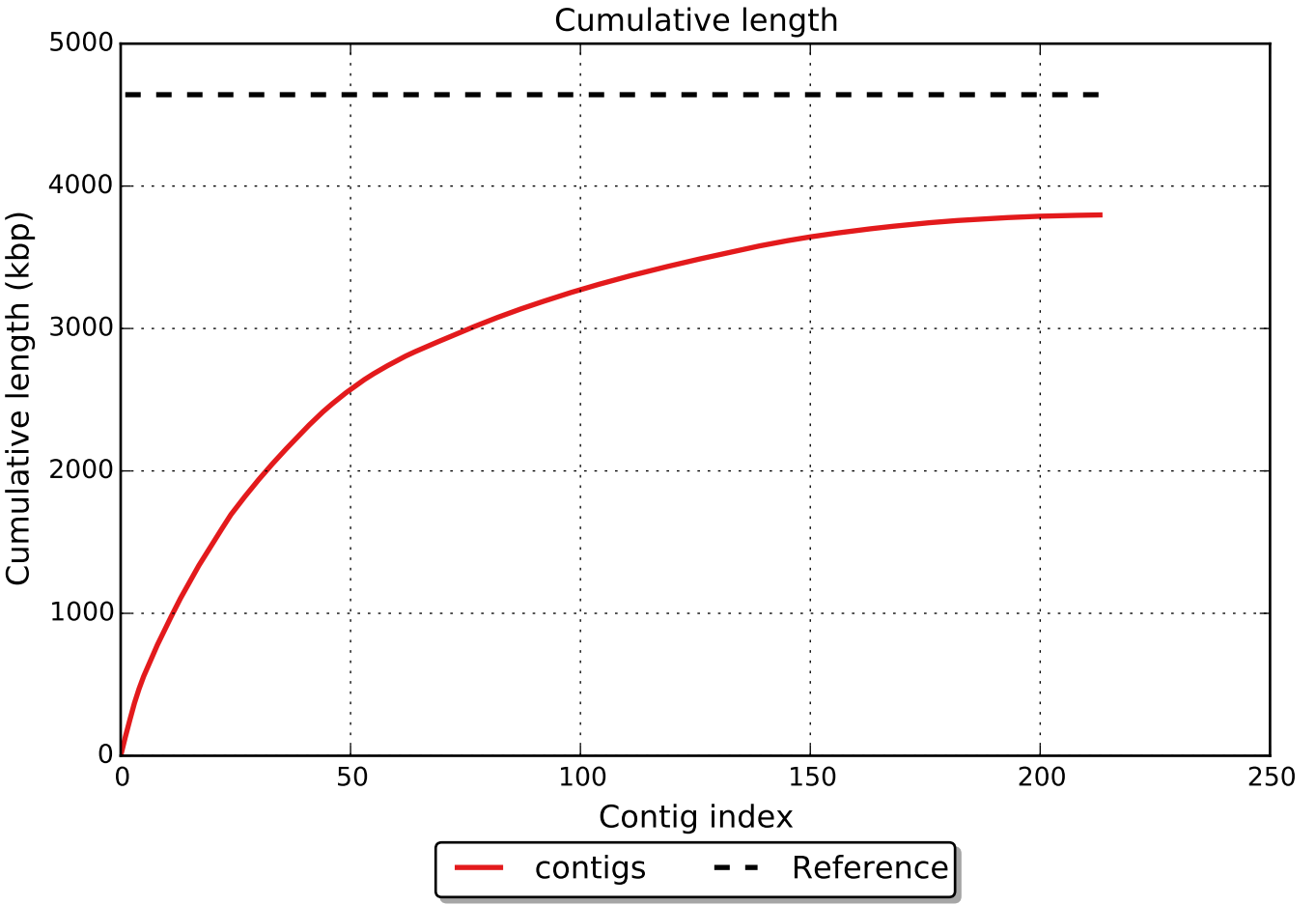
Unaligned report

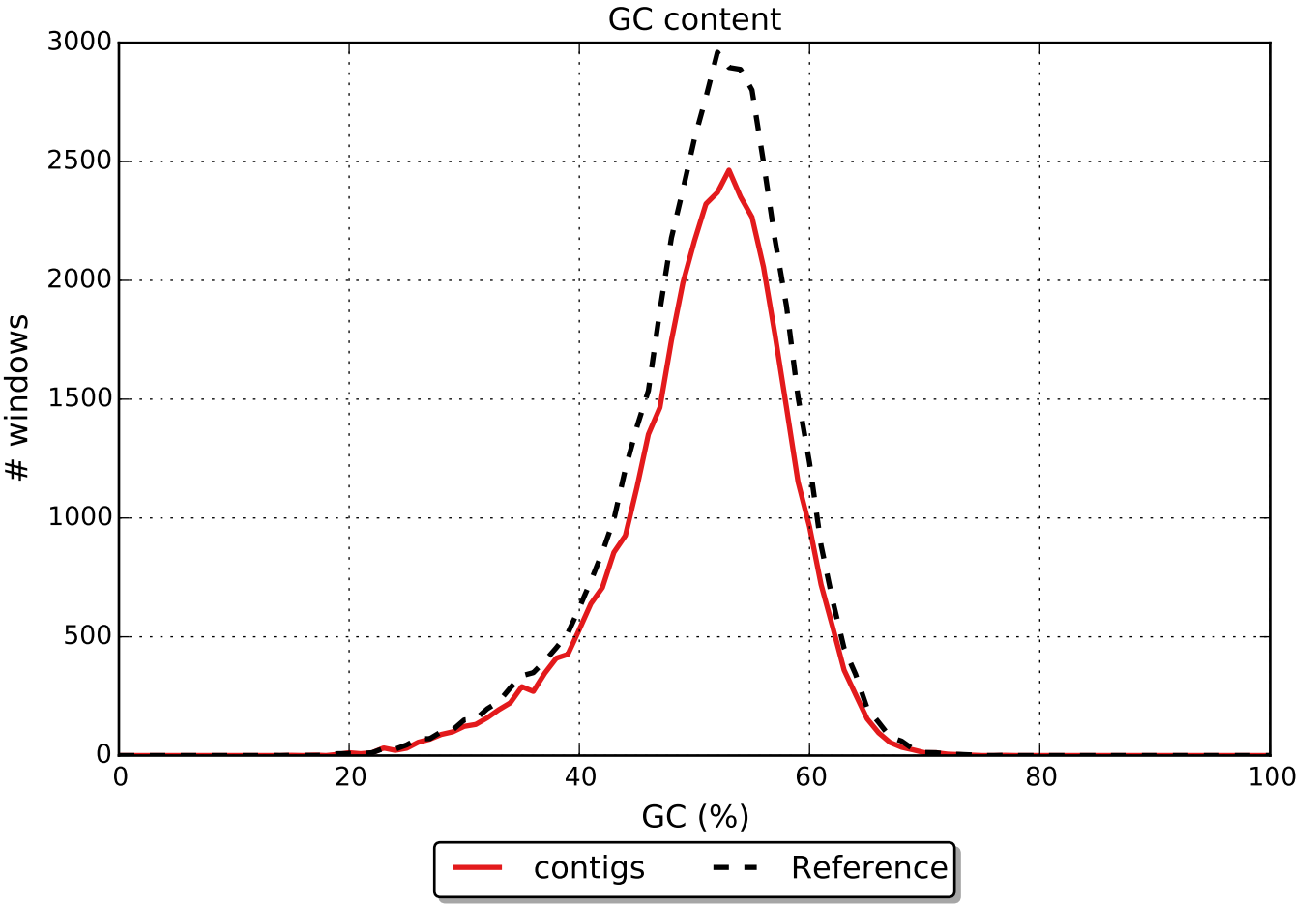
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

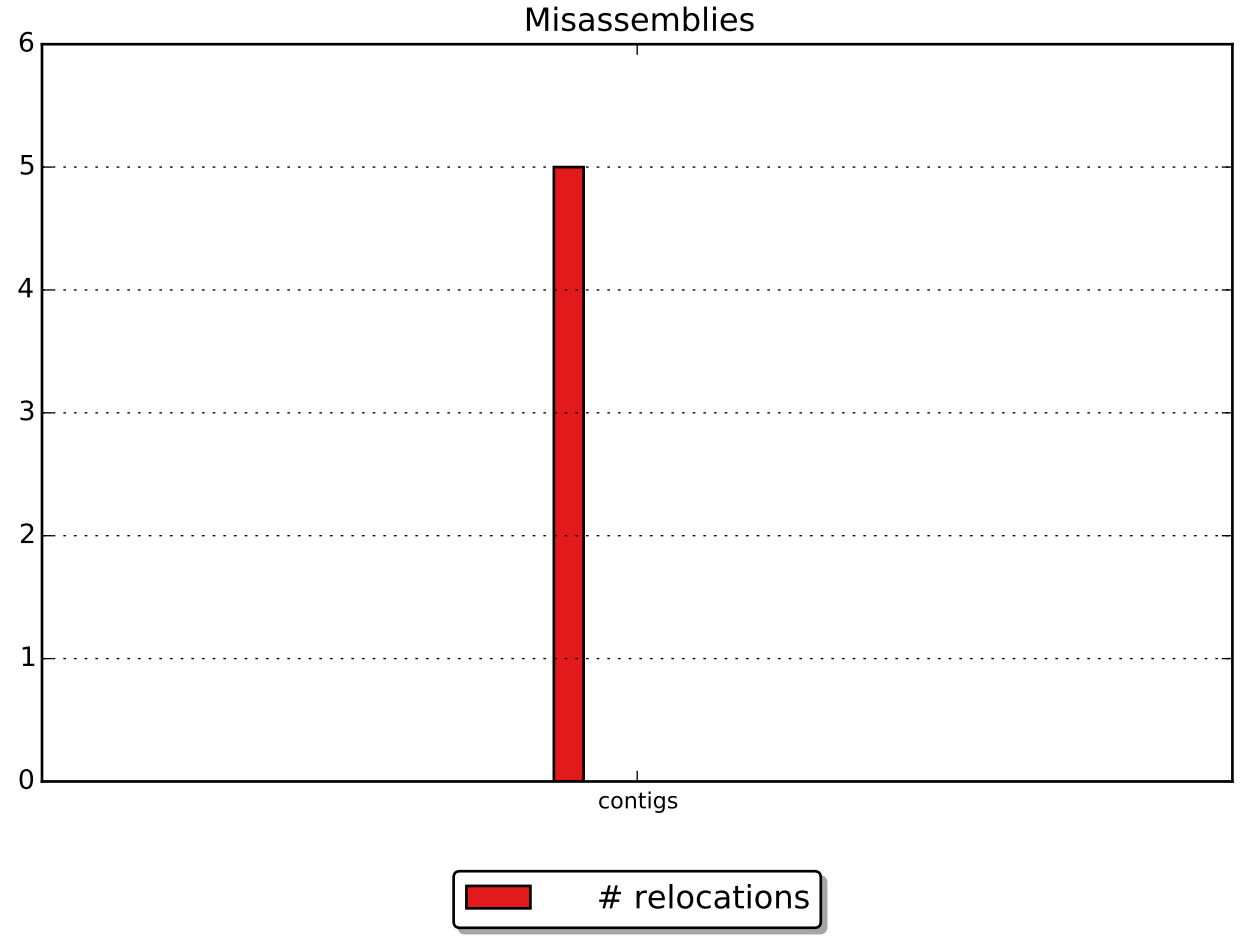
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

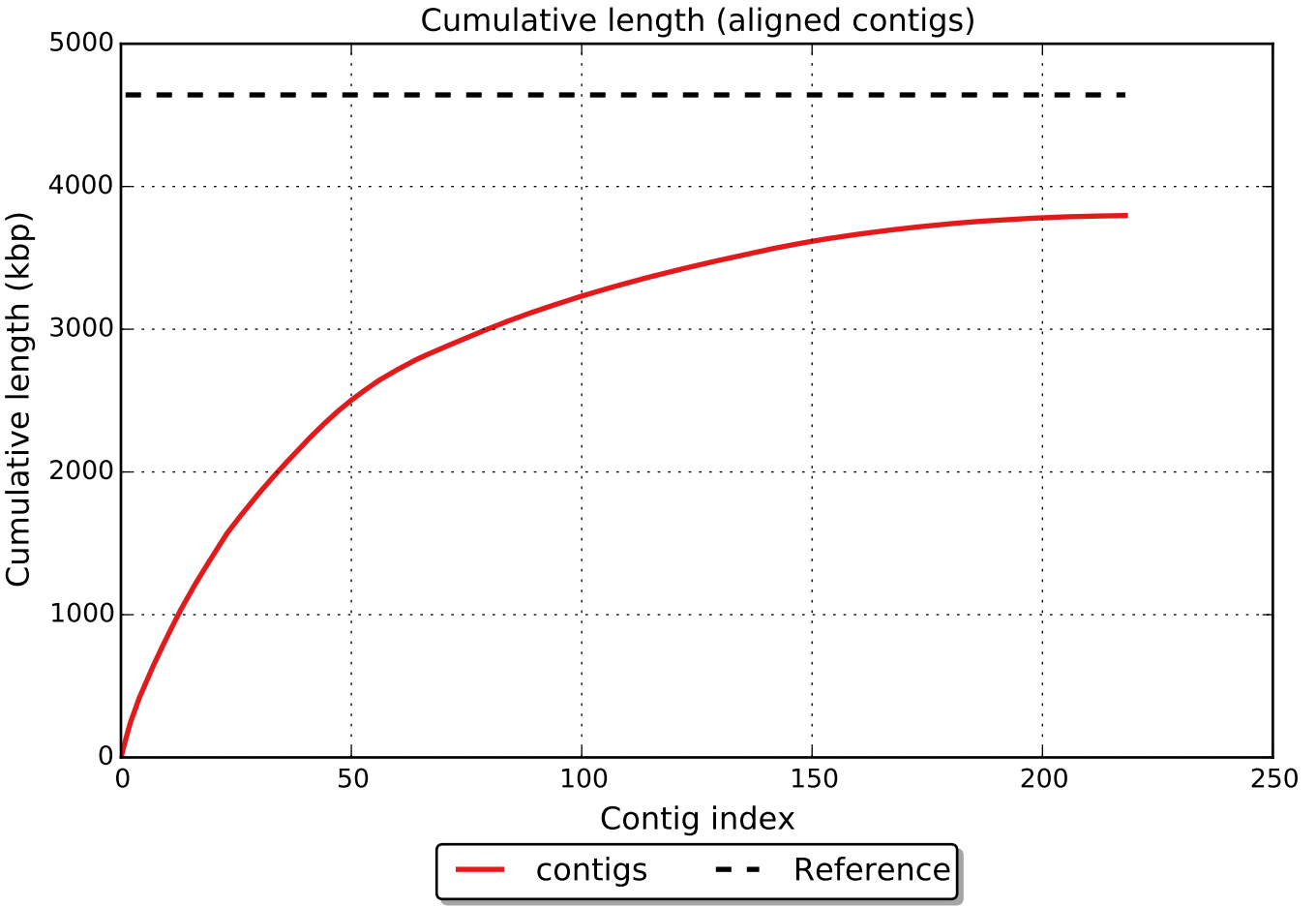

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
contigs

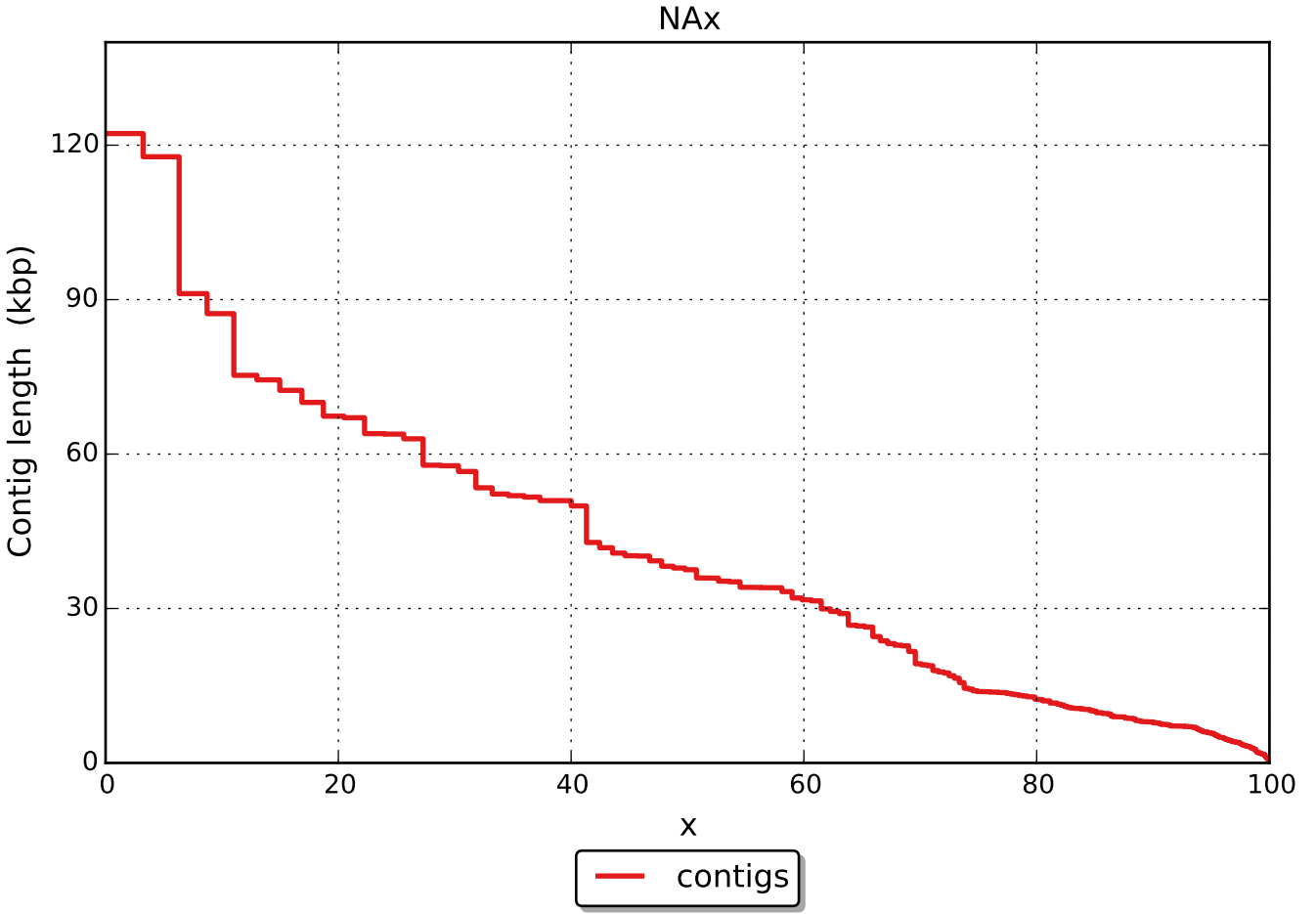

NGx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
contigs

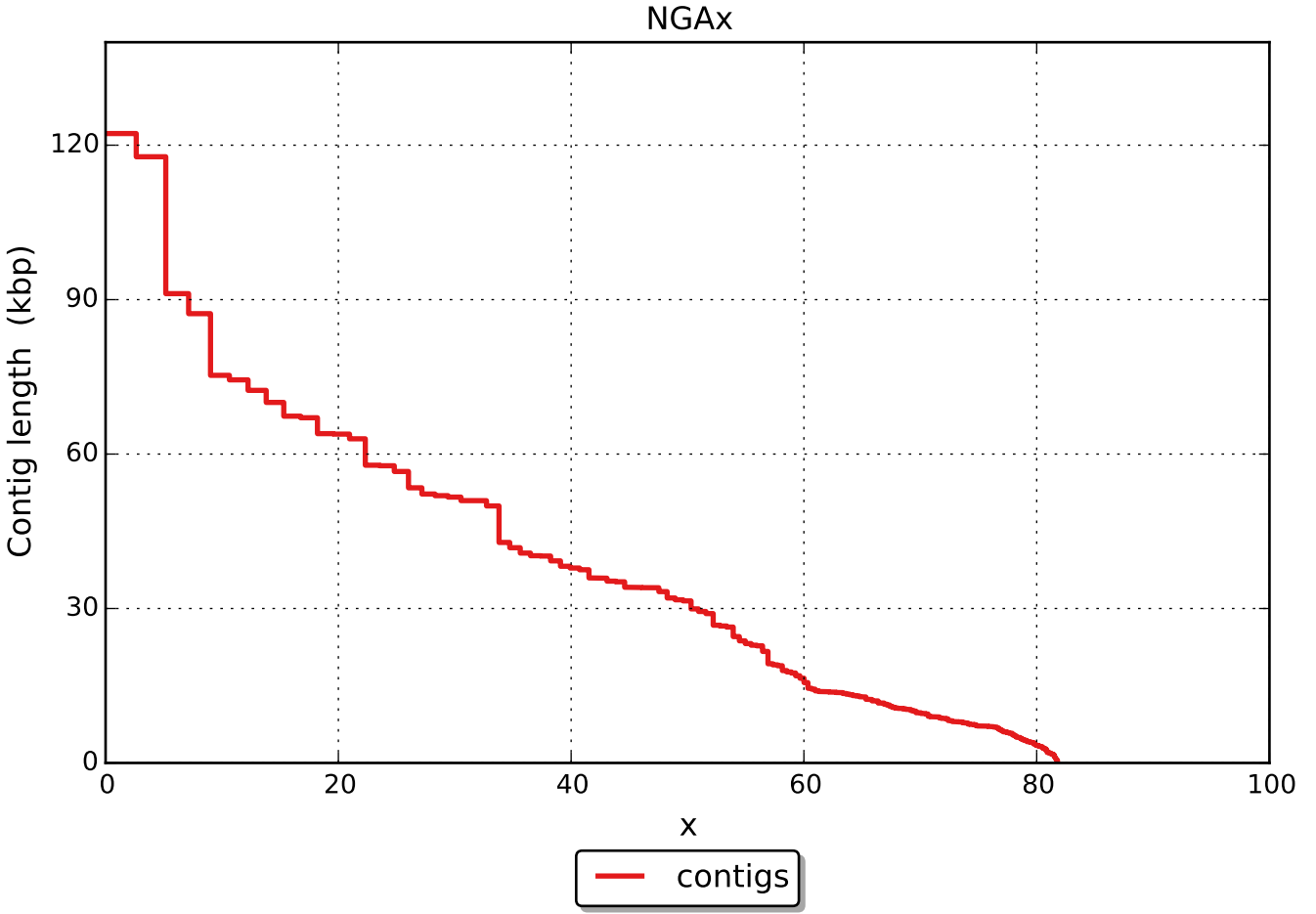

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
contigs
Reference


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


Misassemblies
6
5
4
3
2
1
0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Contig index
contigs
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
contigs