Report

	contigs
# contigs (>= 1000 bp)	309
# contigs (>= 5000 bp)	210
# contigs (>= 10000 bp)	135
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4070650
Total length (>= 5000 bp)	3791693
Total length (>= 10000 bp)	3244250
Total length (>= 25000 bp)	1887006
Total length (>= 50000 bp)	627151
# contigs	333
Largest contig	119434
Total length	4086674
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	22735
NG50	17754
N75	11709
NG75	7899
L50	52
LG50	66
L75	119
LG75	162
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.427
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	905.78
# indels per 100 kbp	0.40
Largest alignment	119434
NA50	22049
NGA50	17466
NA75	11669
NGA75	7839
LA50	53
LGA50	67
LA75	120
LGA75	164

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

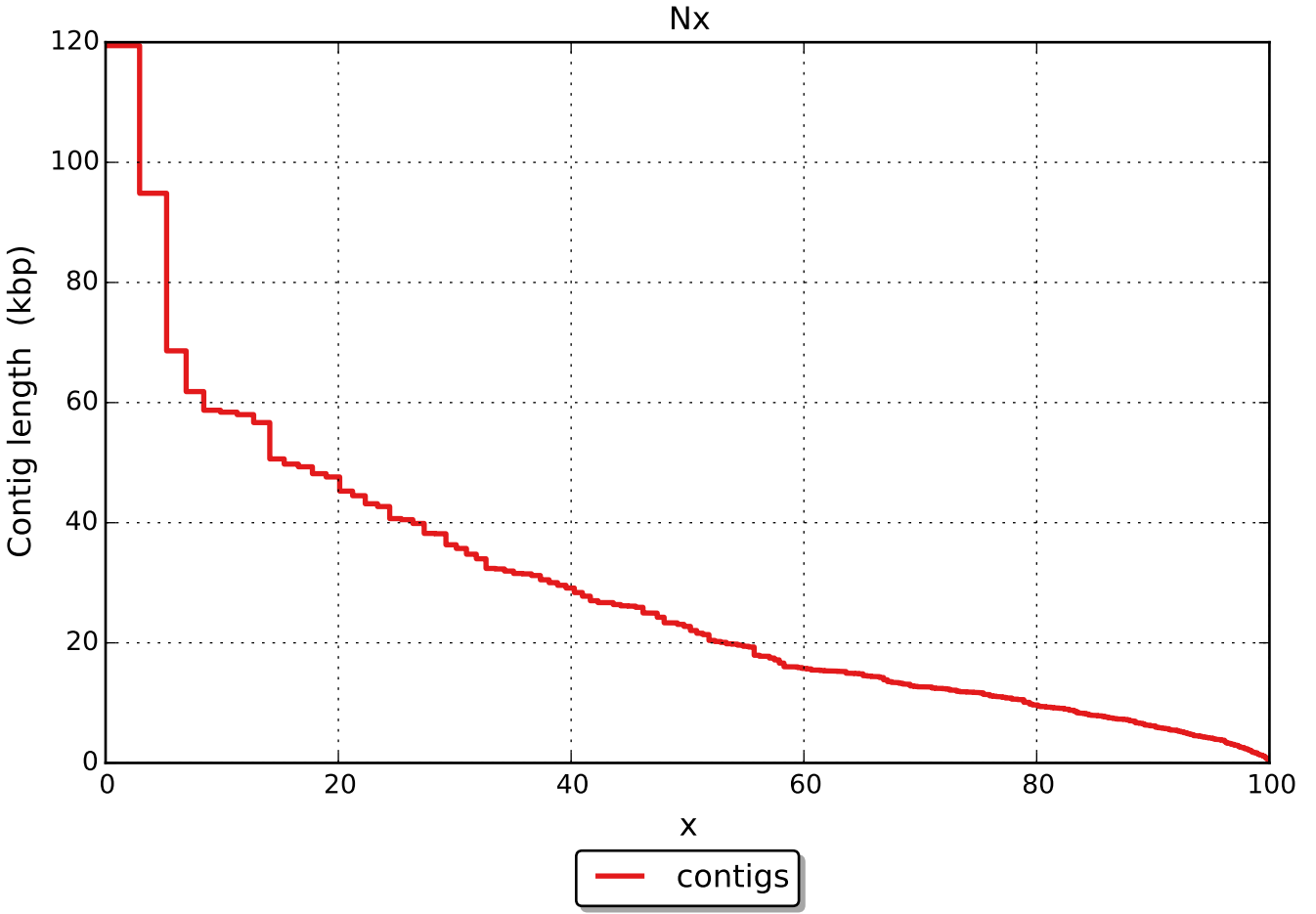
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# mismatches	35916
# indels	16
# short indels	16
# long indels	0
Indels length	24

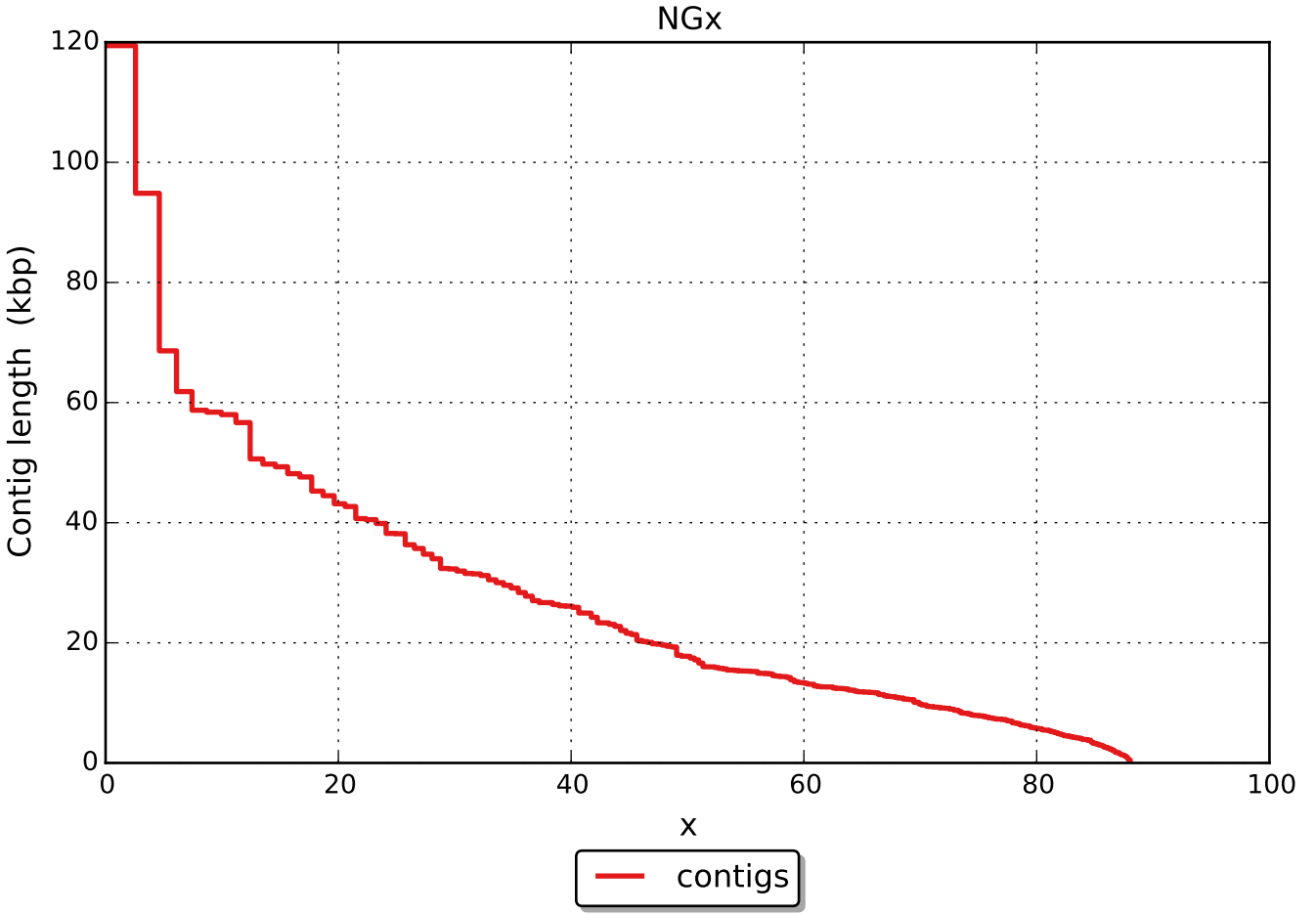
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

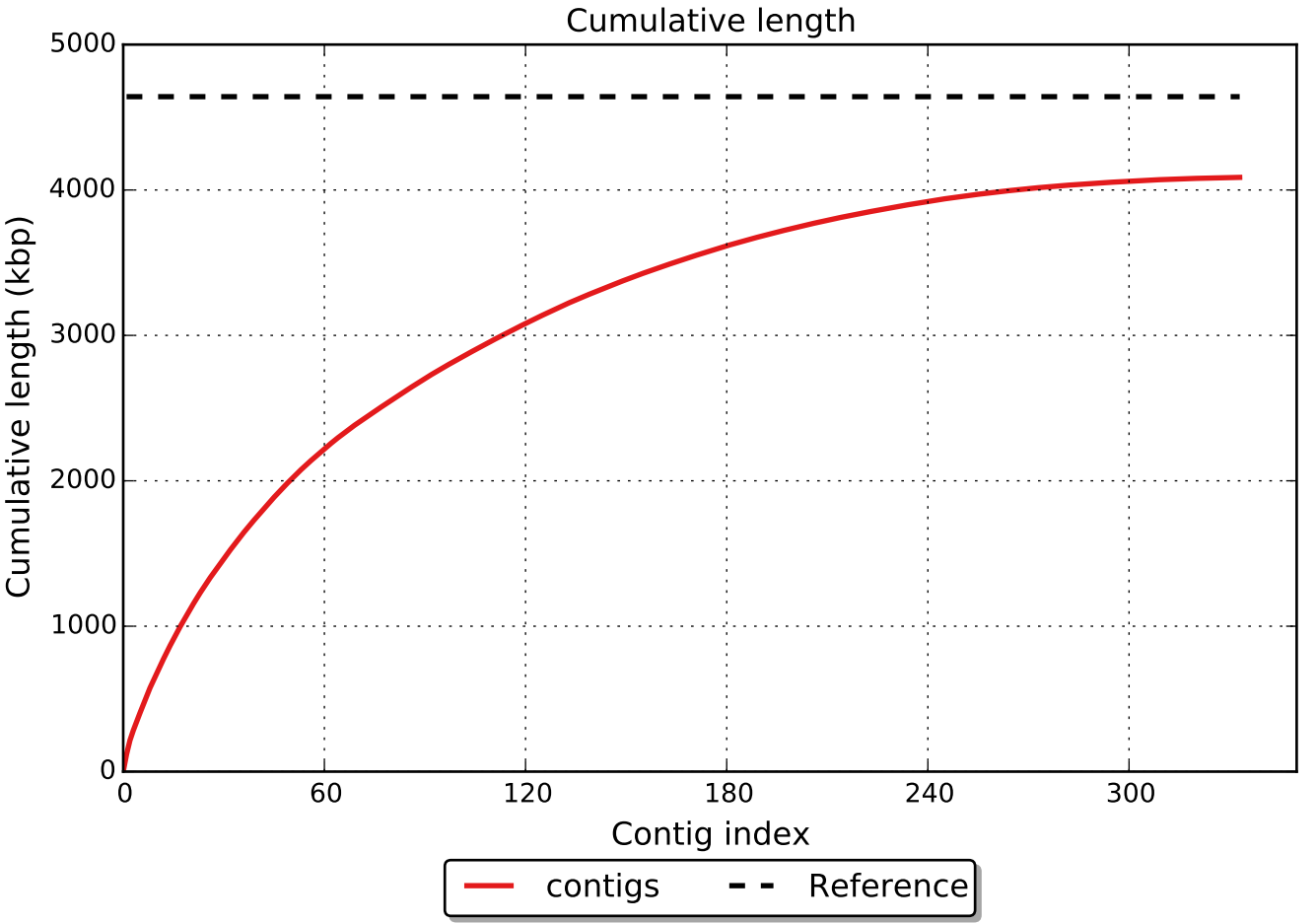
Unaligned report

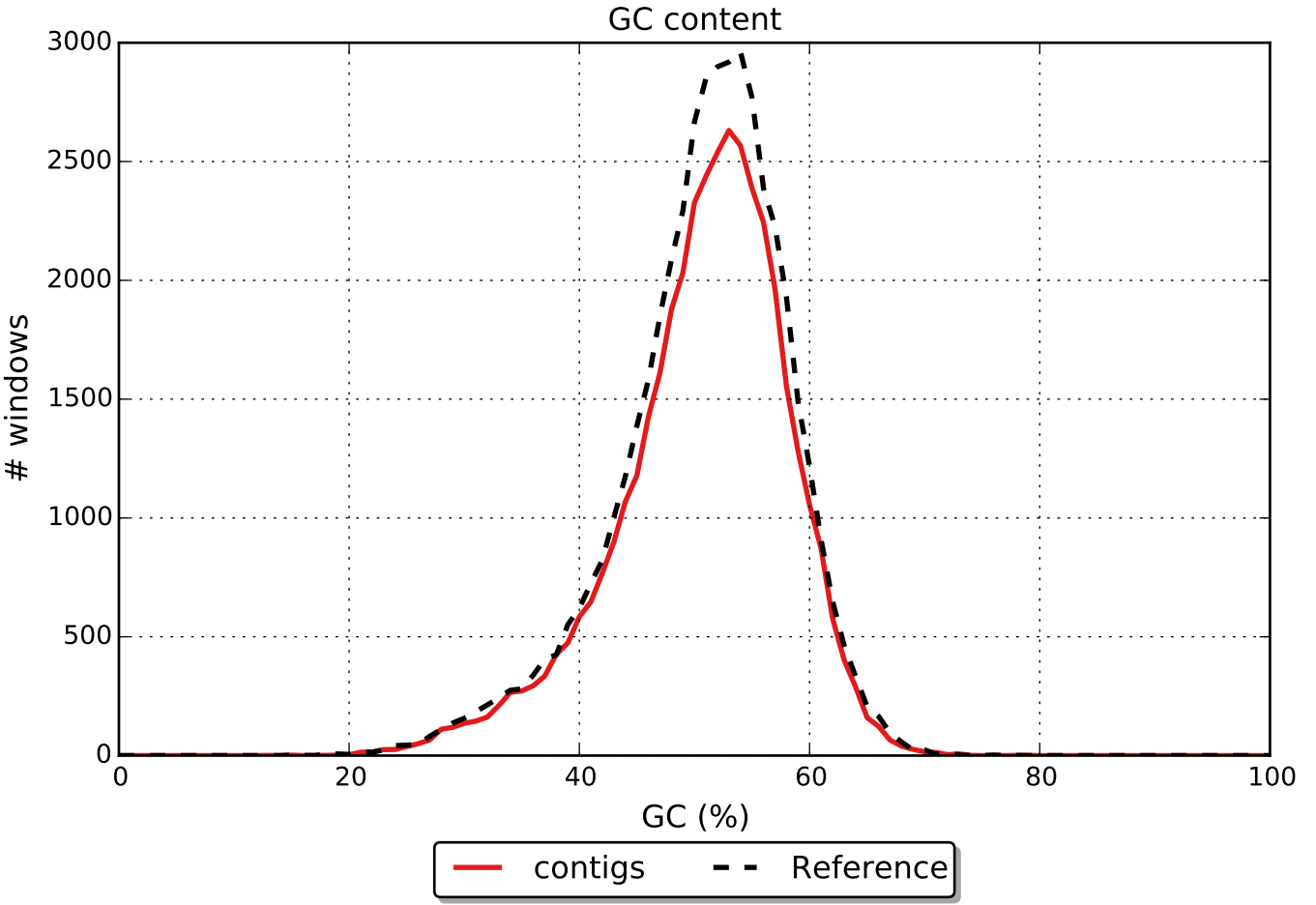
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

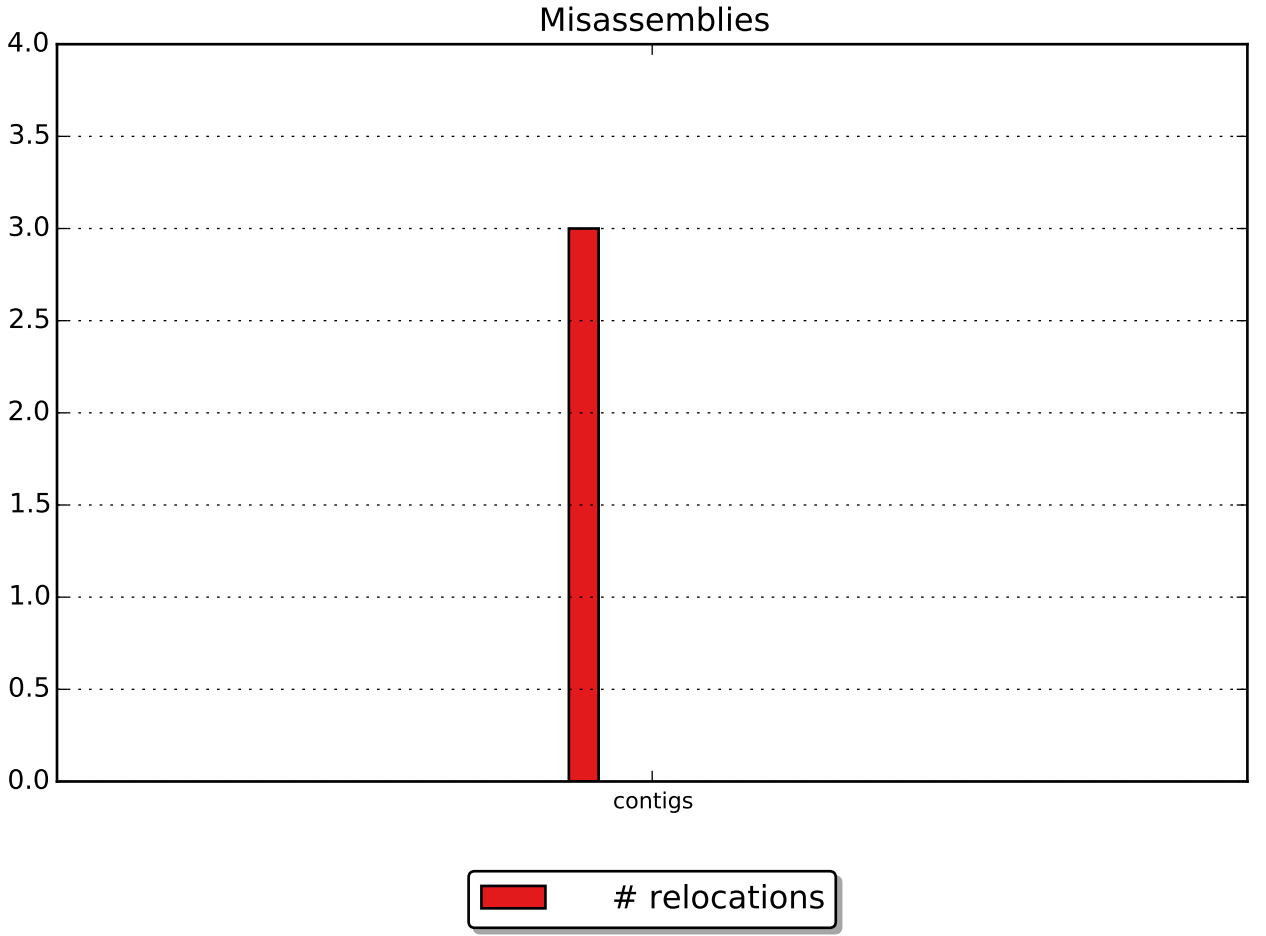
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

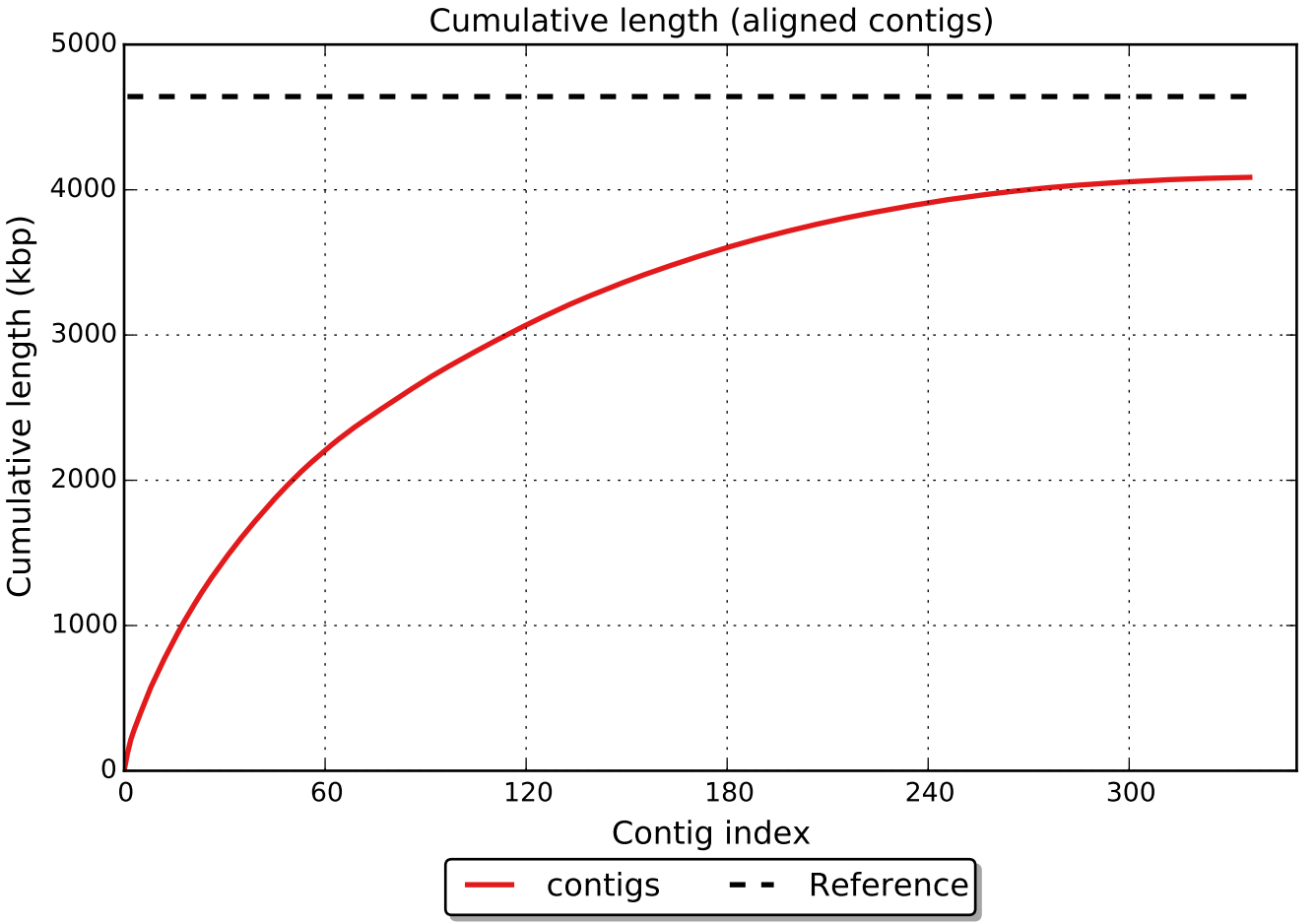

Nx
Contig length (kbp)
120
100
80
60
40
20
0
0
20
40
60
80
100
x
contigs

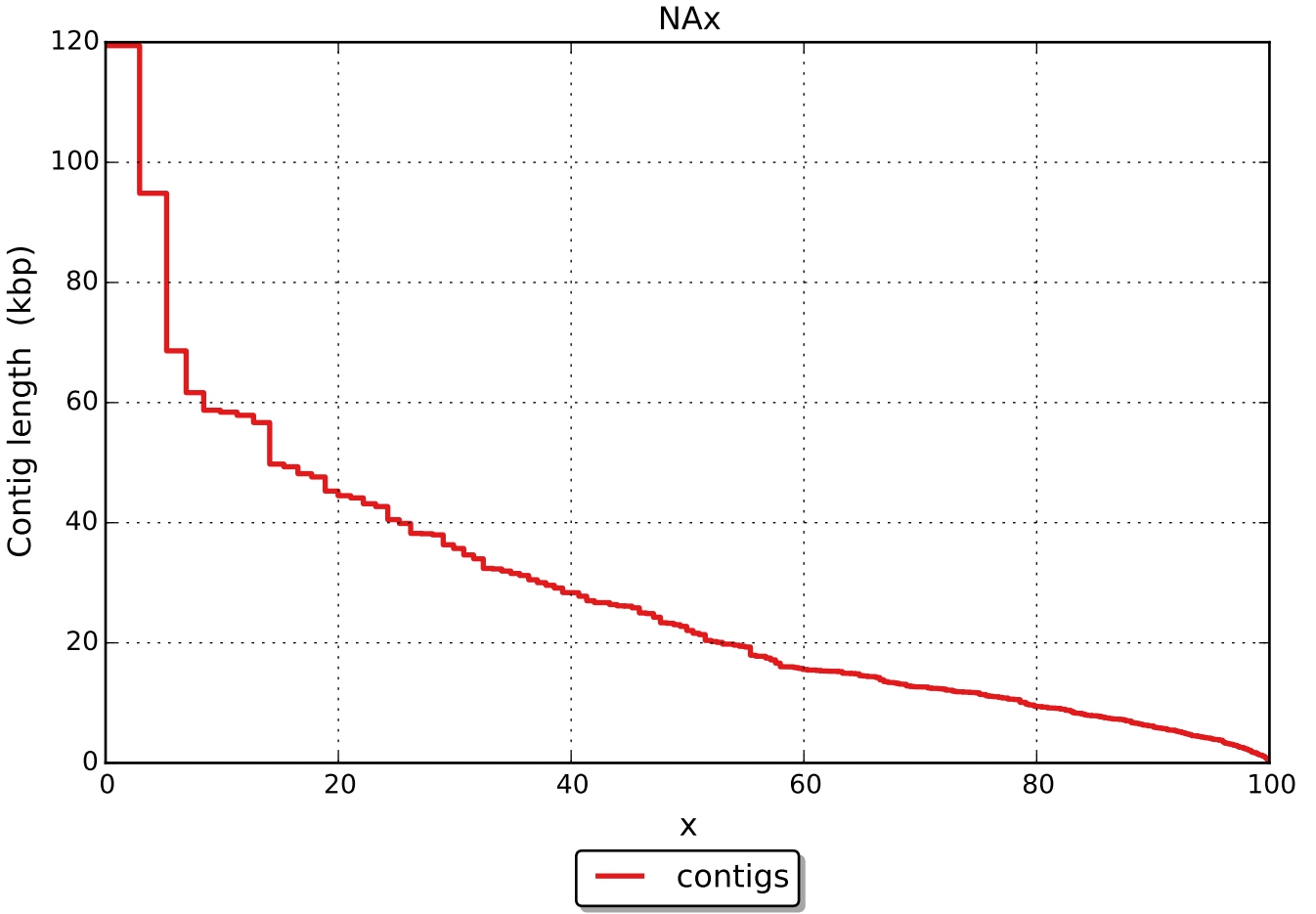

NGx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

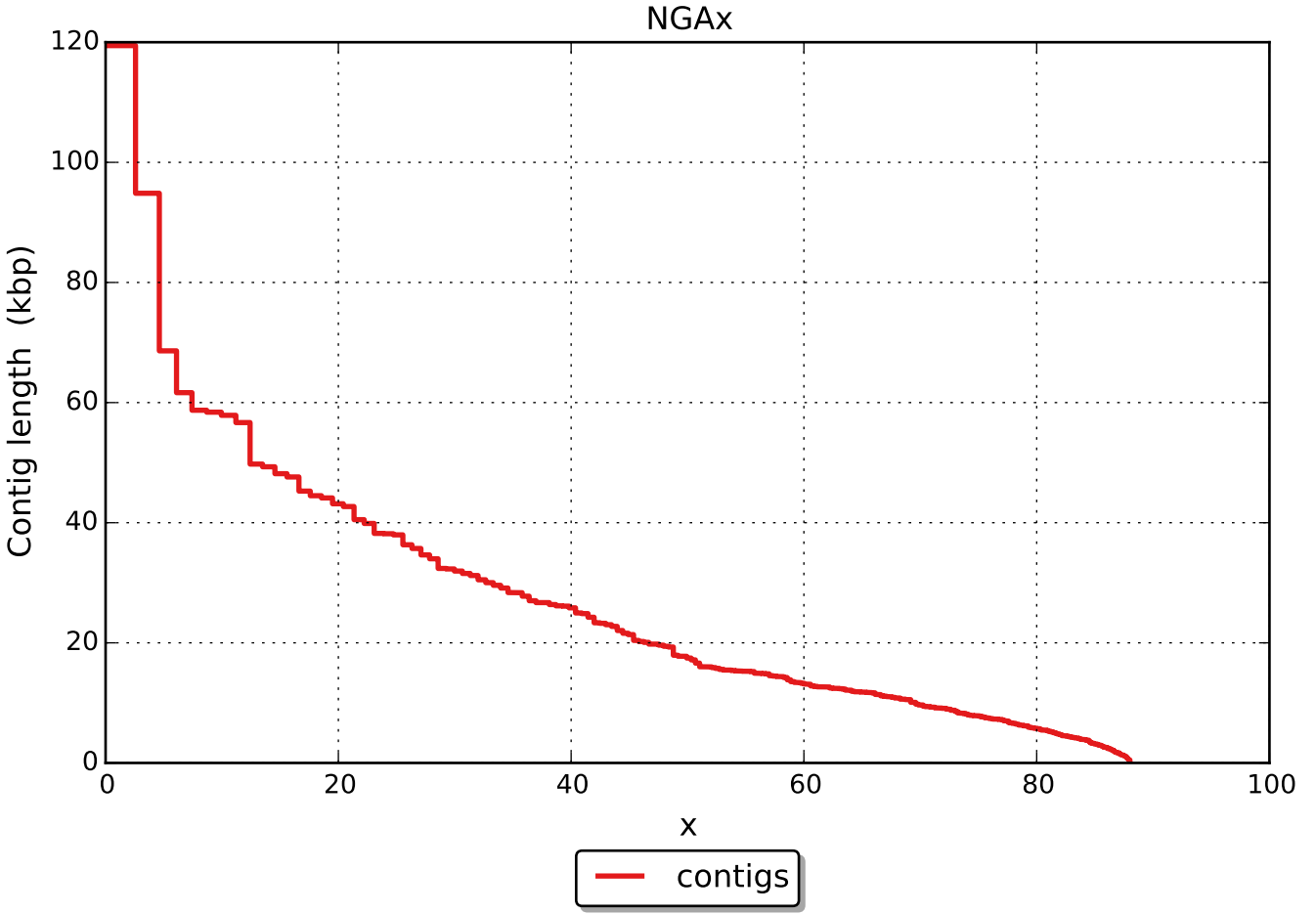

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
contigs
Reference


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
60
120
180
240
300
Contig index
contigs
Reference


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


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