Report

	contigs
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	55
# contigs (>= 10000 bp)	50
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4474008
Total length (>= 5000 bp)	4434113
Total length (>= 10000 bp)	4397044
Total length (>= 25000 bp)	4241448
Total length (>= 50000 bp)	3927769
# contigs	97
Largest contig	431470
Total length	4488888
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.78
N50	105688
NG50	105224
N75	69219
NG75	63924
L50	10
LG50	11
L75	23
LG75	25
# misassemblies	7
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.326
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	947.49
# indels per 100 kbp	1.04
Largest alignment	431470
NA50	105224
NGA50	96103
NA75	63527
NGA75	60735
LA50	10
LGA50	11
LA75	24
LGA75	26

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

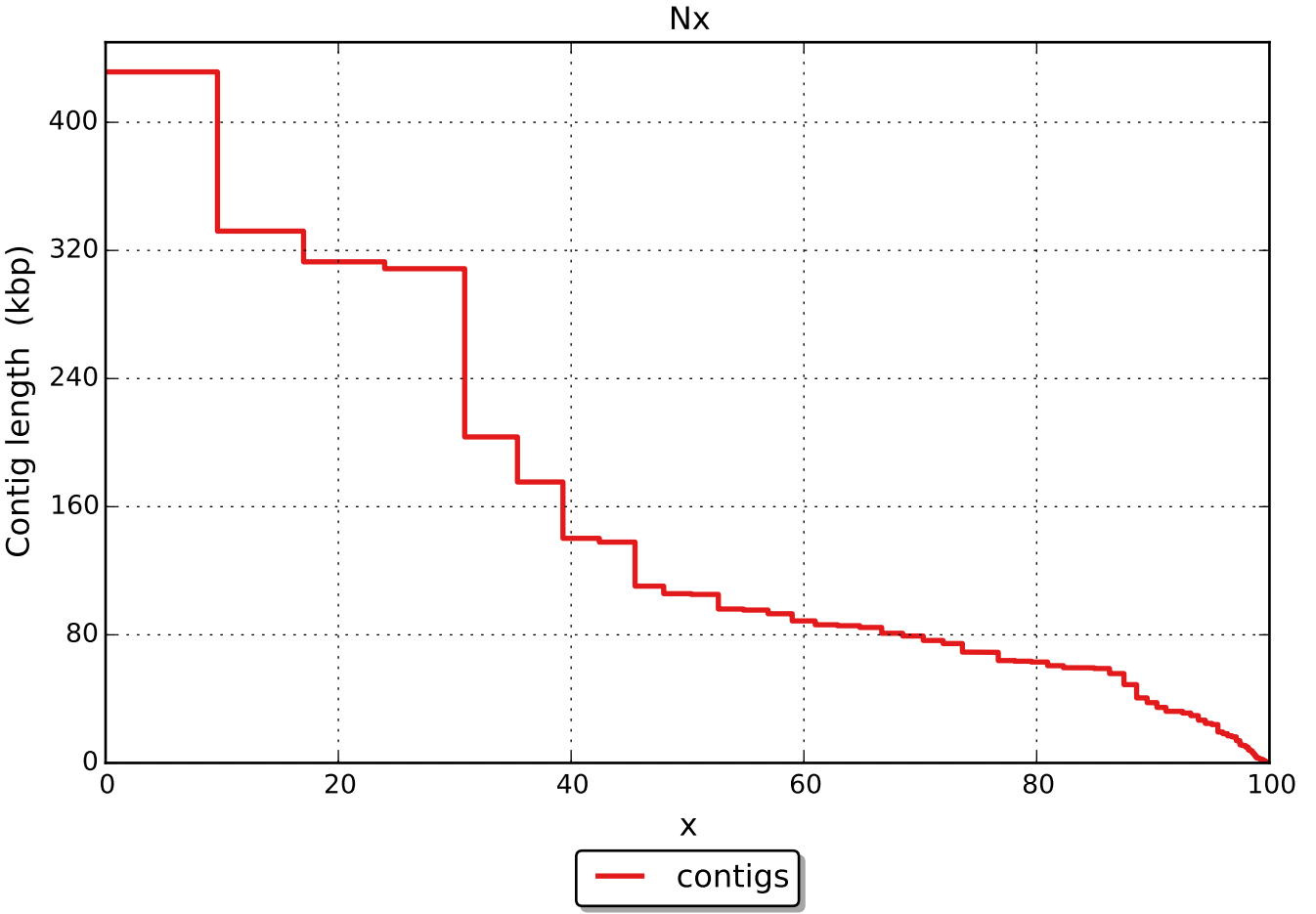
	contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	198850
# local misassemblies	5
# mismatches	41044
# indels	45
# short indels	44
# long indels	1
Indels length	54

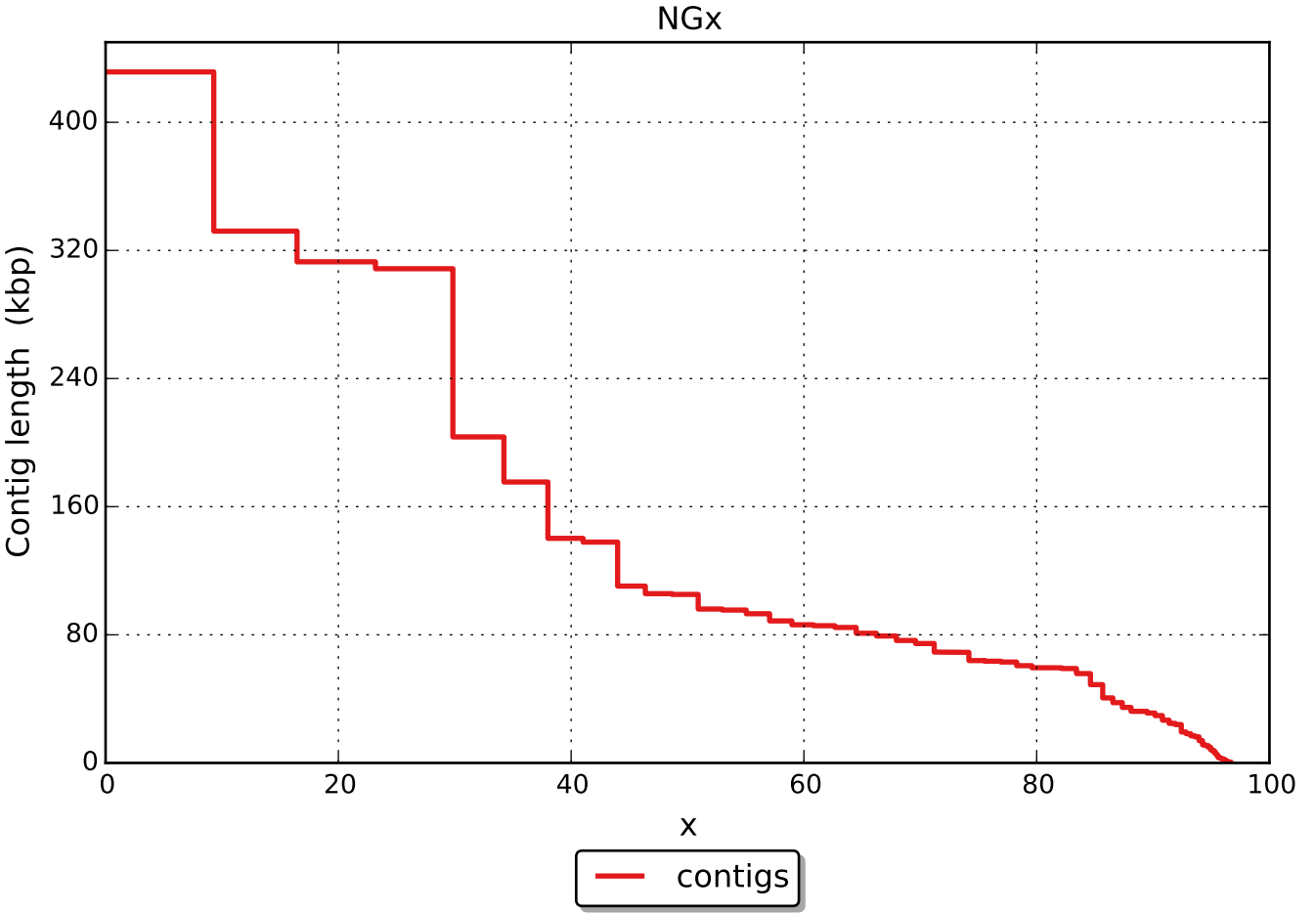
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

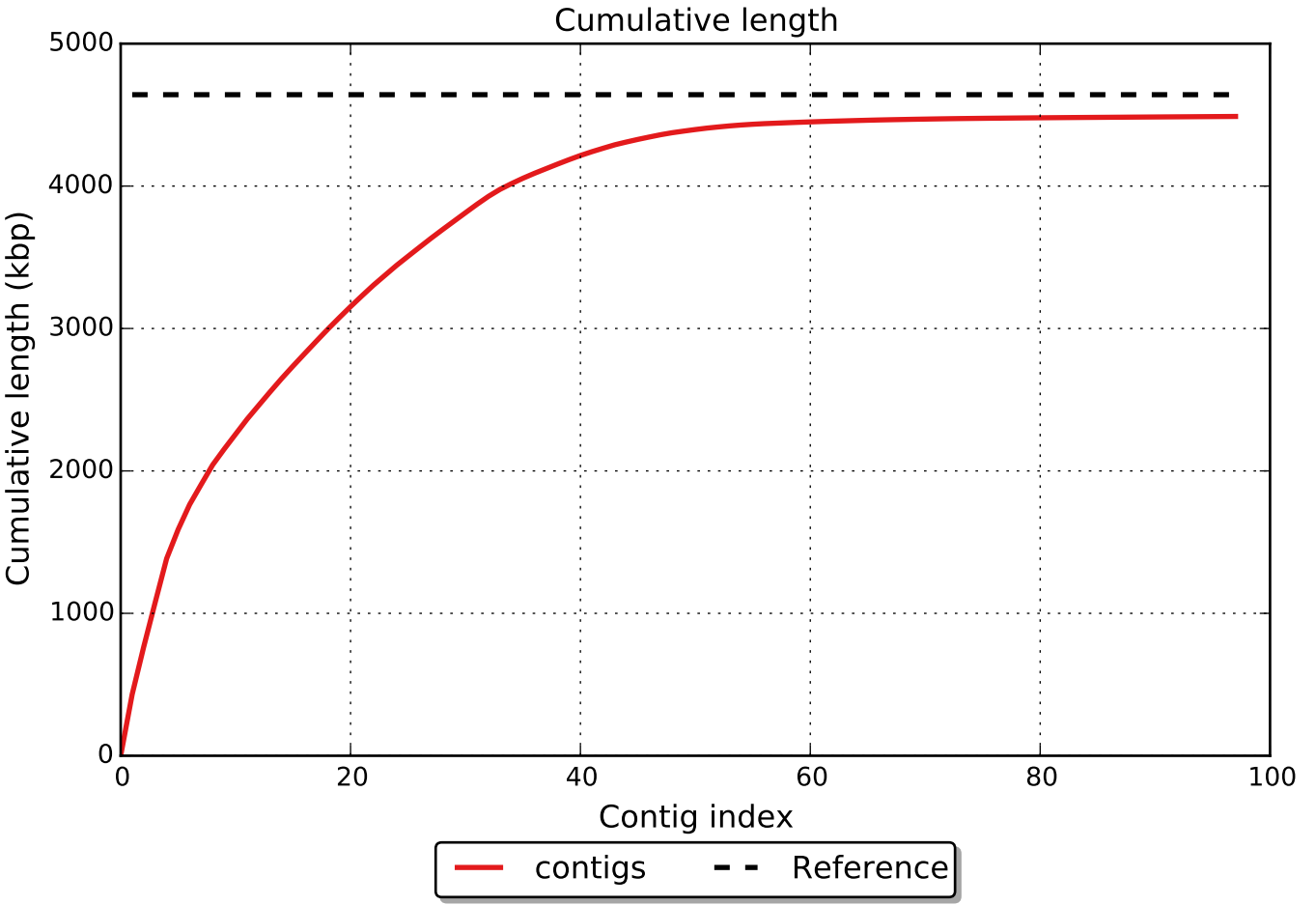
Unaligned report

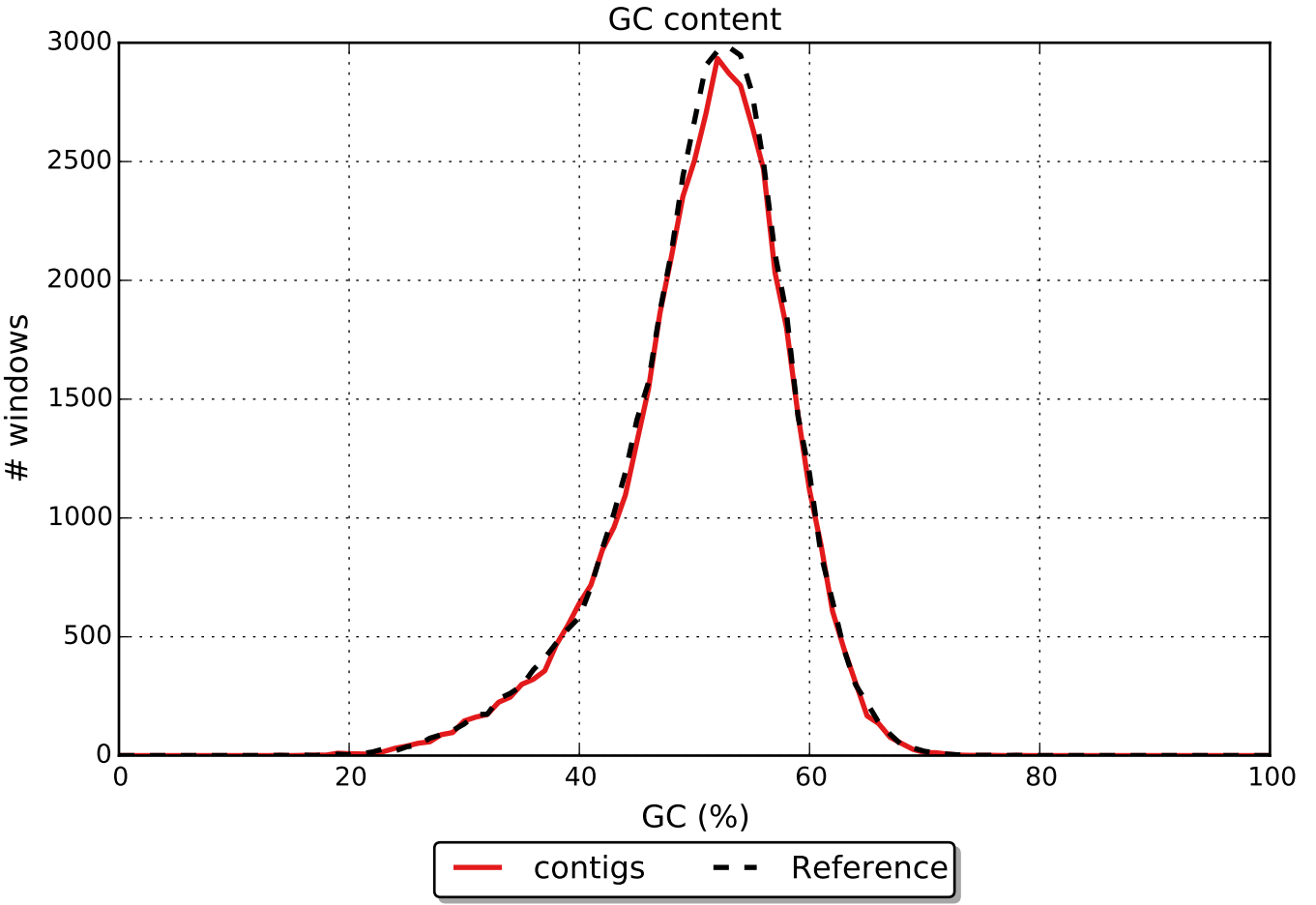
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

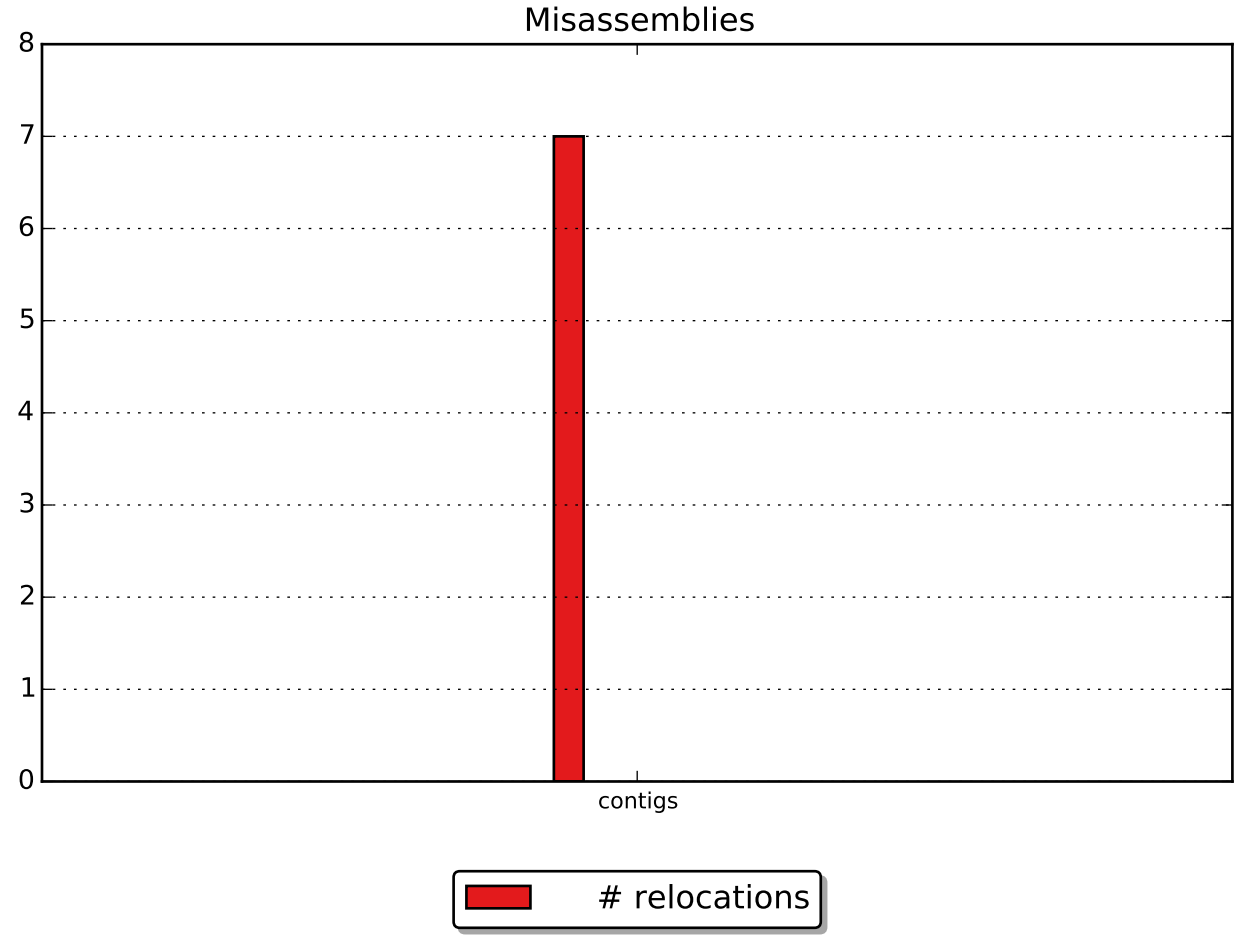
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

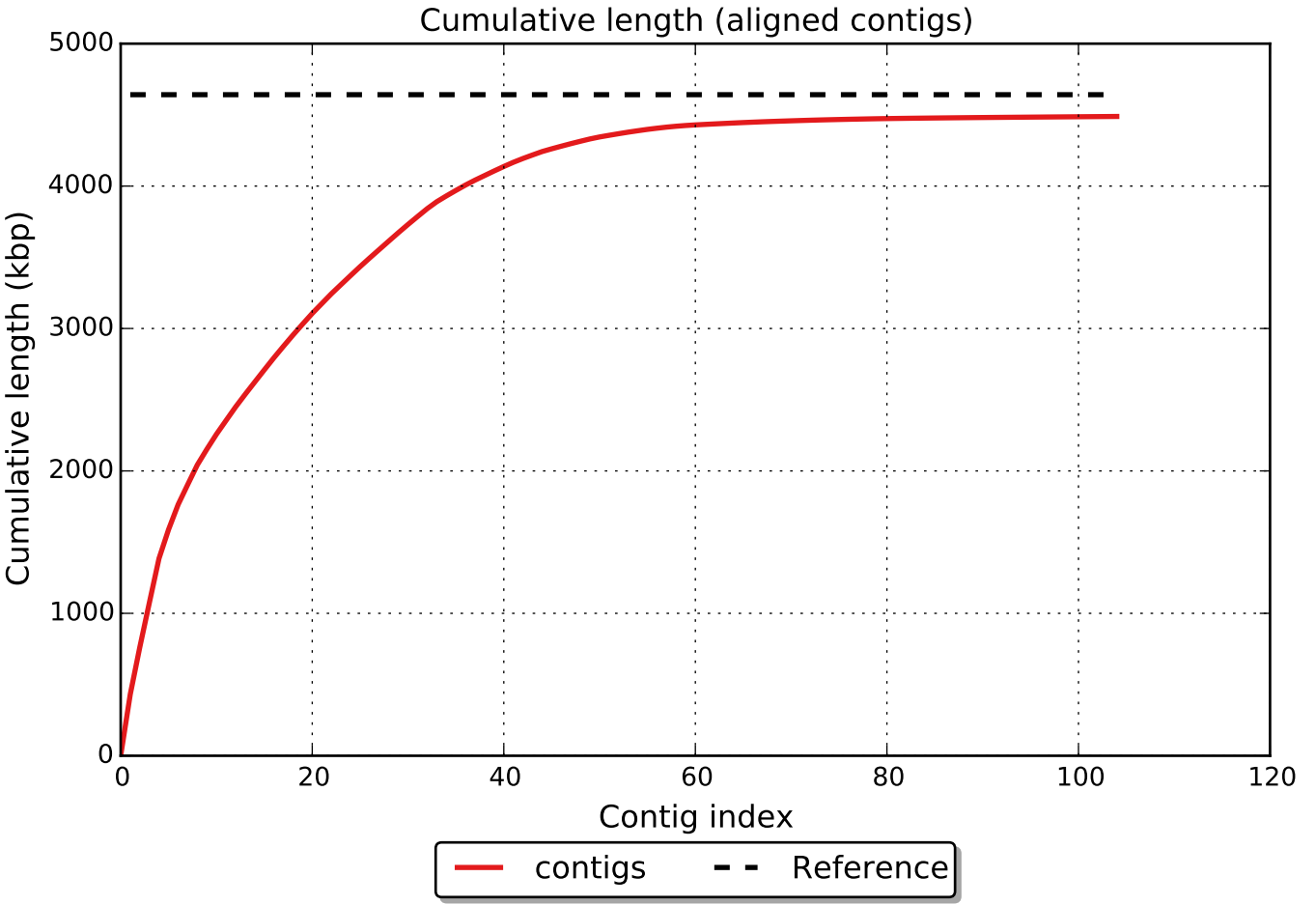

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
contigs

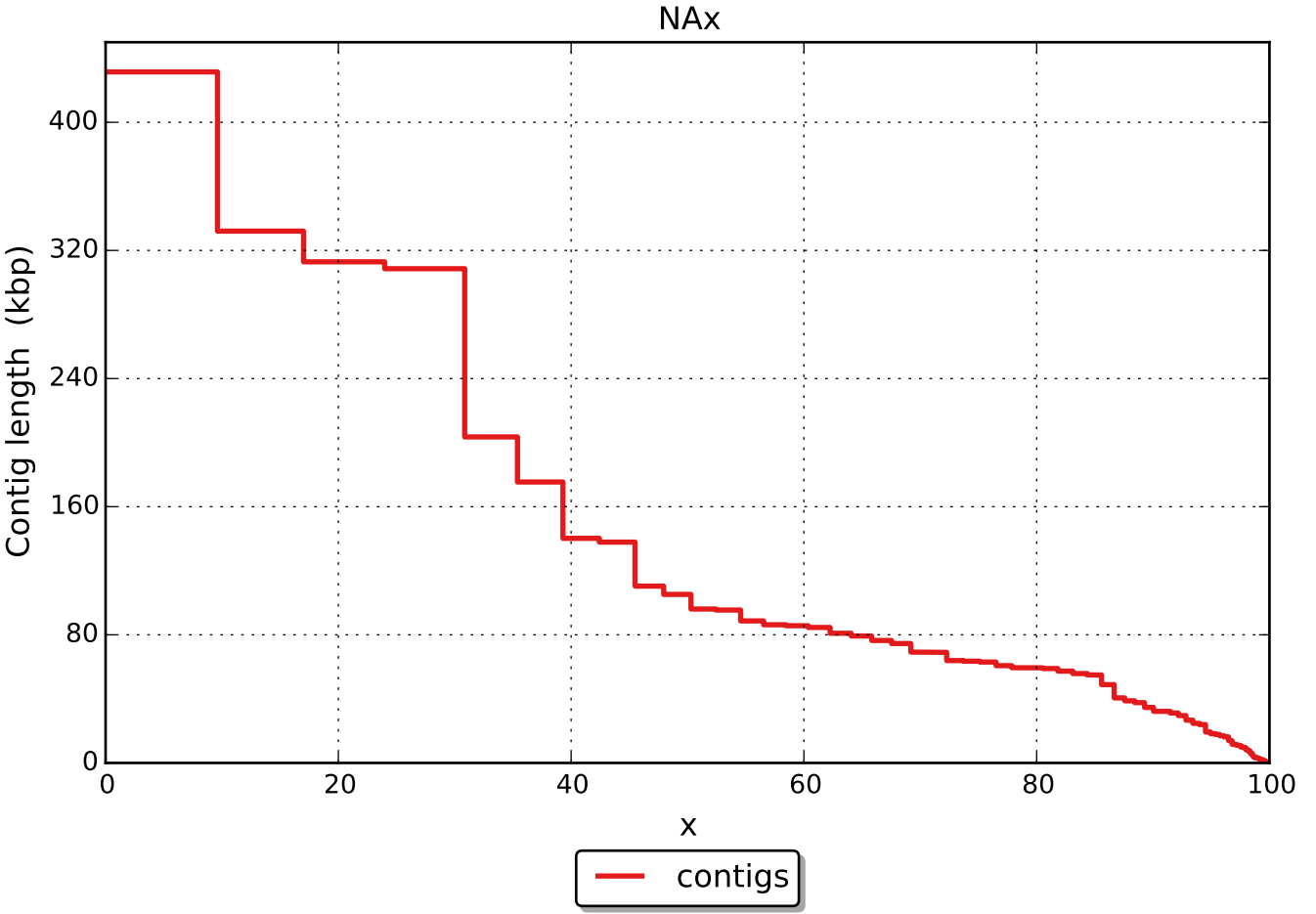

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
contigs

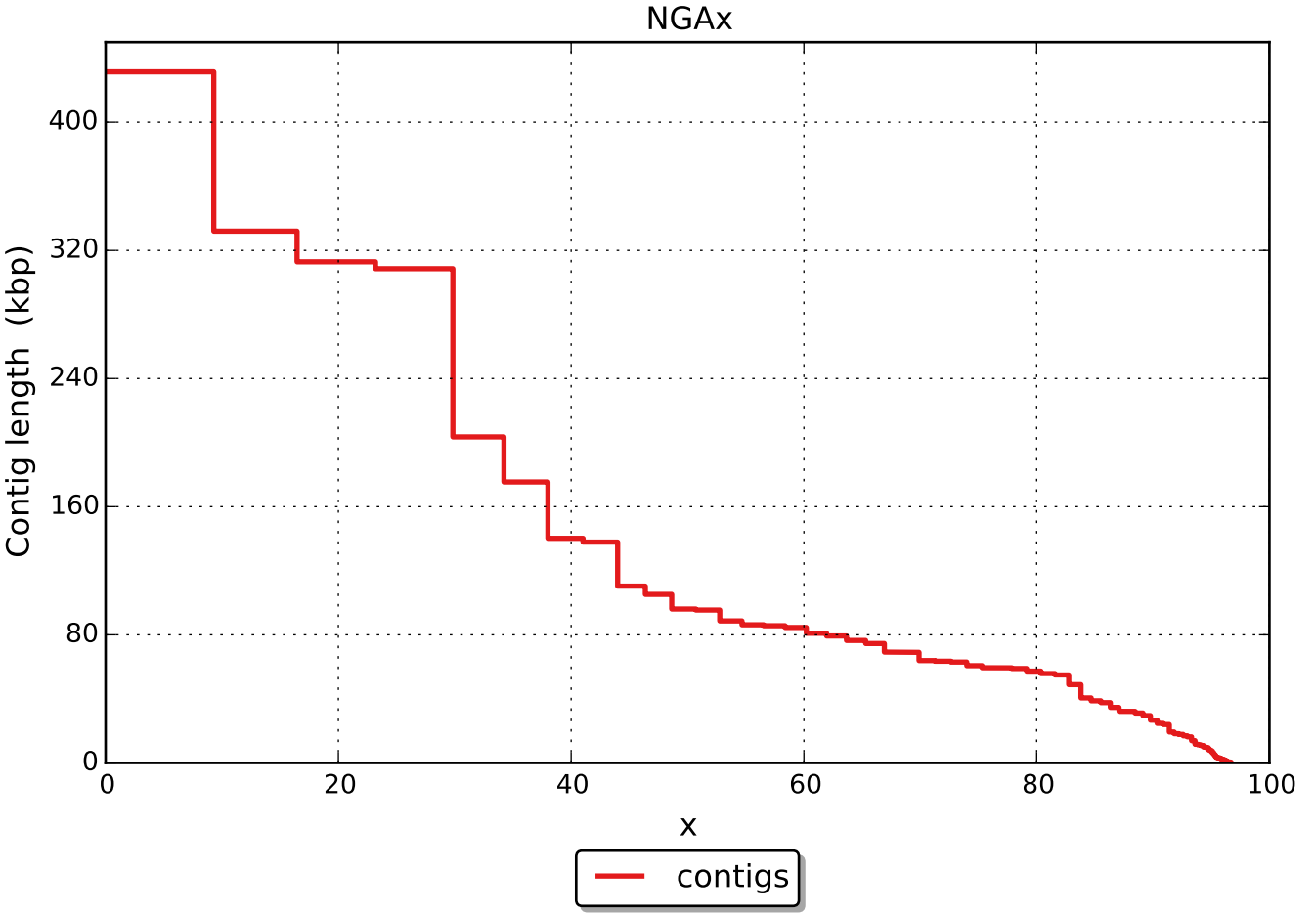

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
Contig index
contigs
Reference


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


Misassemblies
8
7
6
5
4
3
2
1
0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
120
Contig index
contigs
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
contigs