Report

	contigs
# contigs (>= 0 bp)	84
# contigs (>= 1000 bp)	65
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	45
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	27
Total length (>= 0 bp)	4571141
Total length (>= 1000 bp)	4567278
Total length (>= 5000 bp)	4536088
Total length (>= 10000 bp)	4504380
Total length (>= 25000 bp)	4412157
Total length (>= 50000 bp)	3992627
# contigs	66
Largest contig	360895
Total length	4567996
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	175728
NG50	175728
N75	87065
NG75	80764
L50	10
LG50	10
L75	19
LG75	20
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	68375
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.334
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.95
# indels per 100 kbp	0.53
Largest alignment	360895
NA50	175728
NGA50	175728
NA75	87065
NGA75	80764
LA50	10
LGA50	10
LA75	19
LGA75	20

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

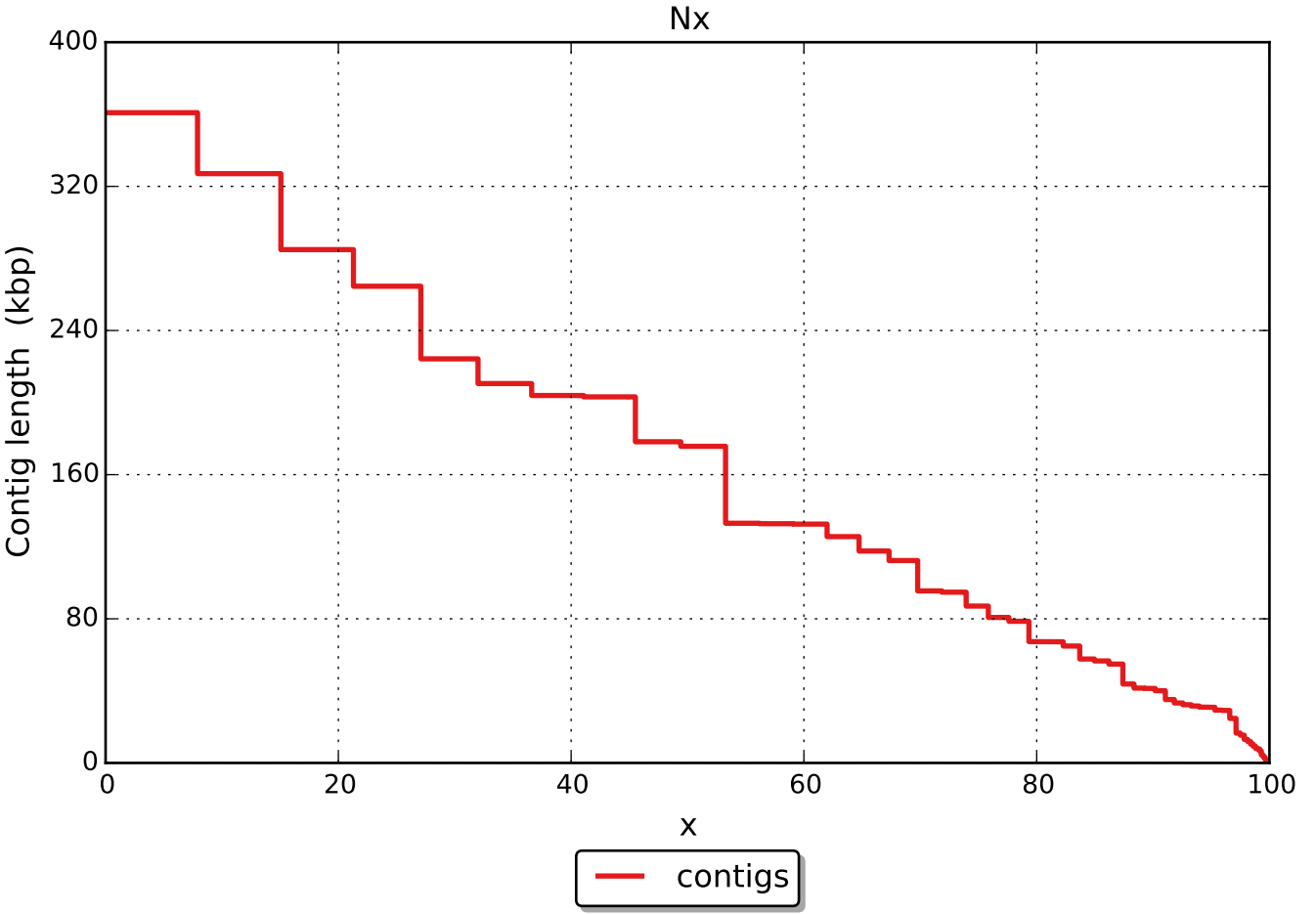
	contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	68375
# local misassemblies	2
# mismatches	454
# indels	24
# short indels	24
# long indels	0
Indels length	31

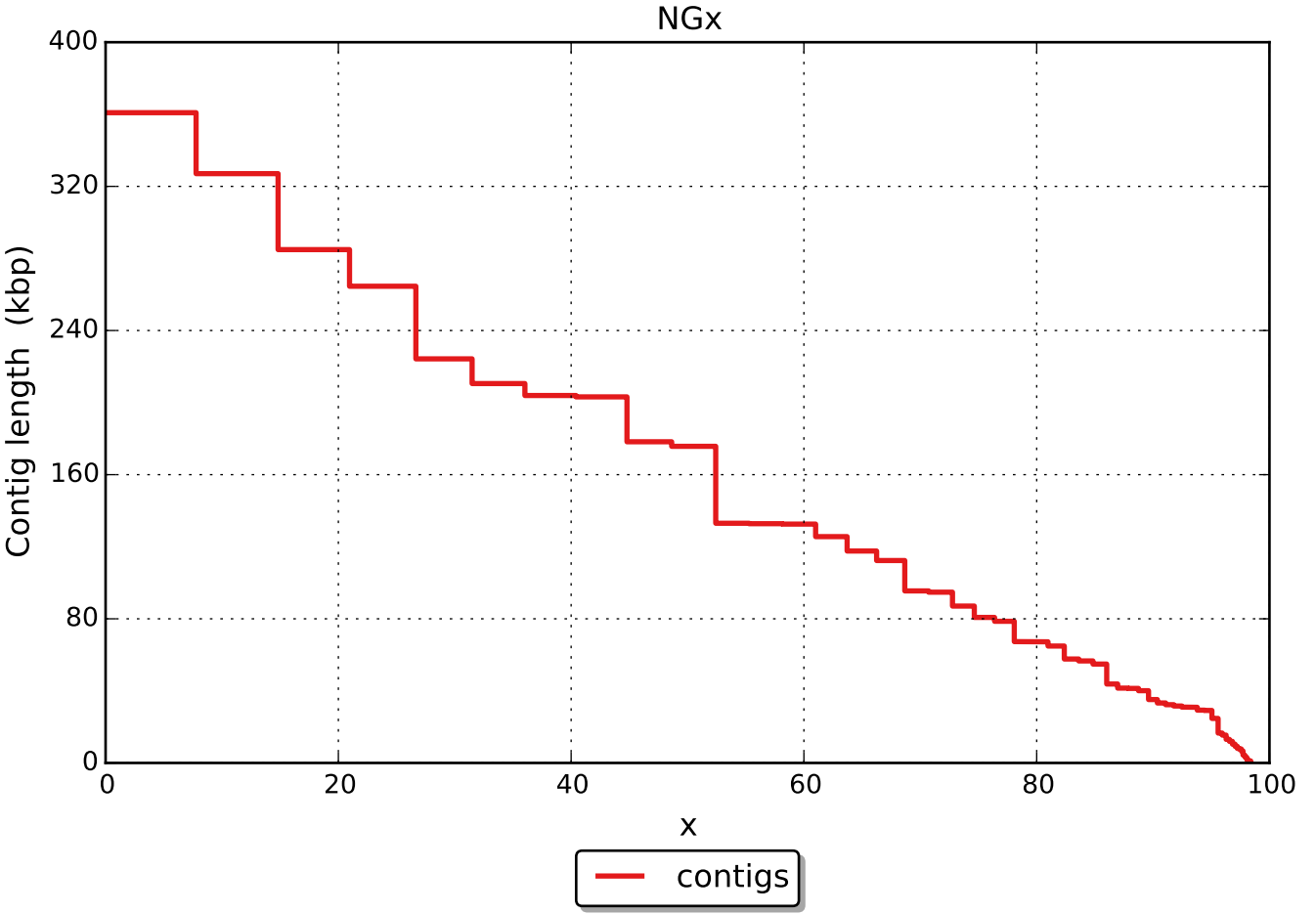
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

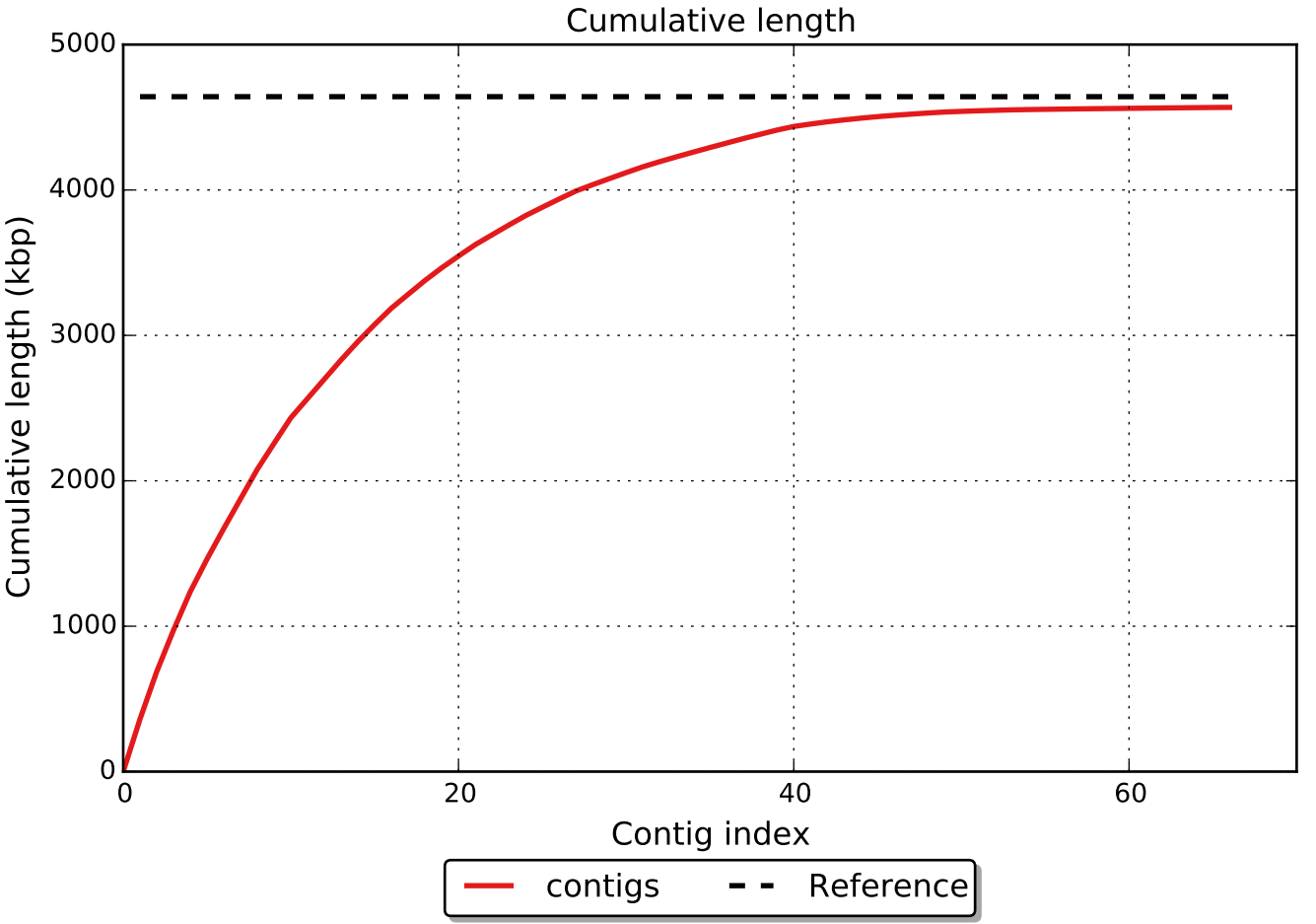
Unaligned report

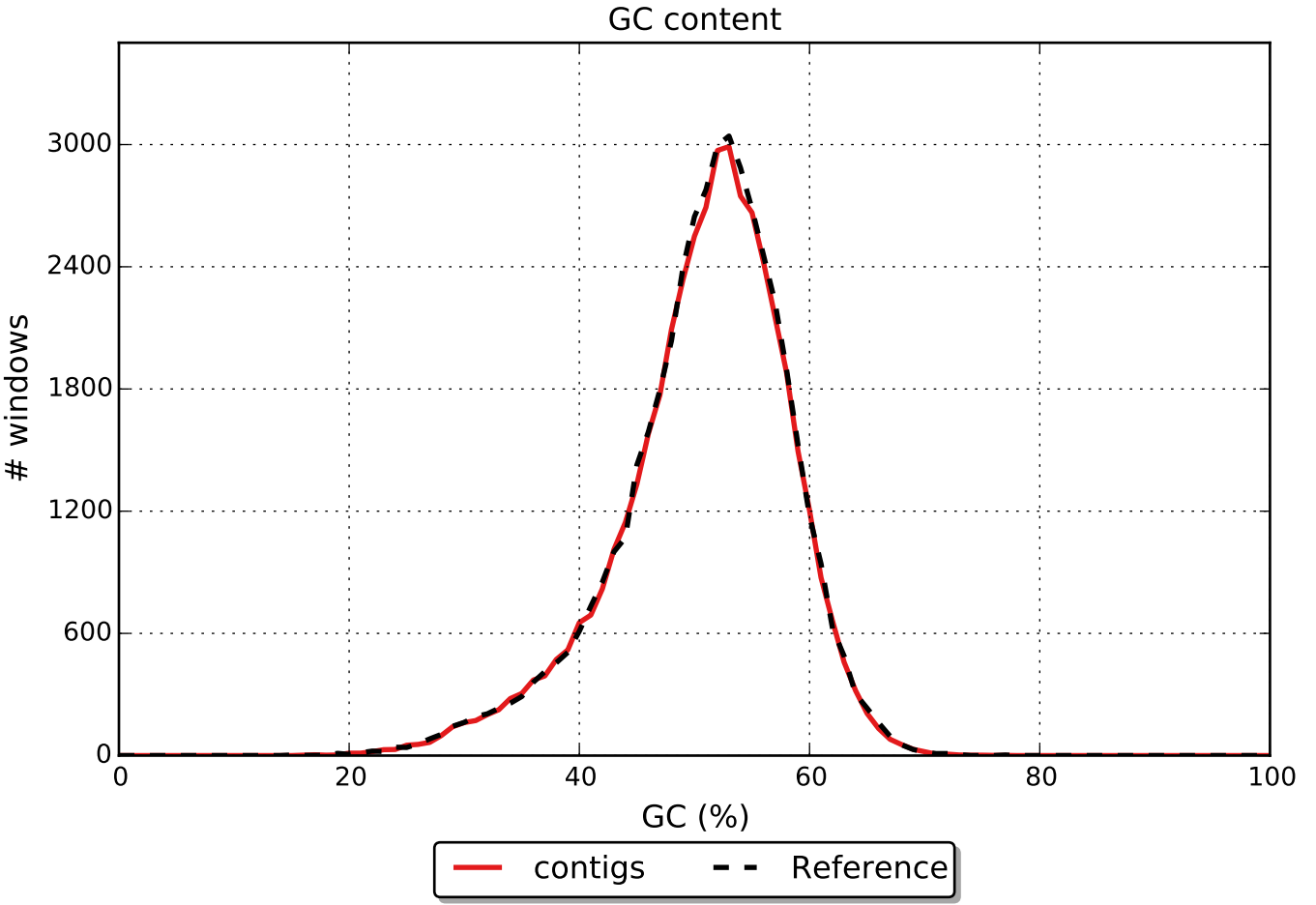
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

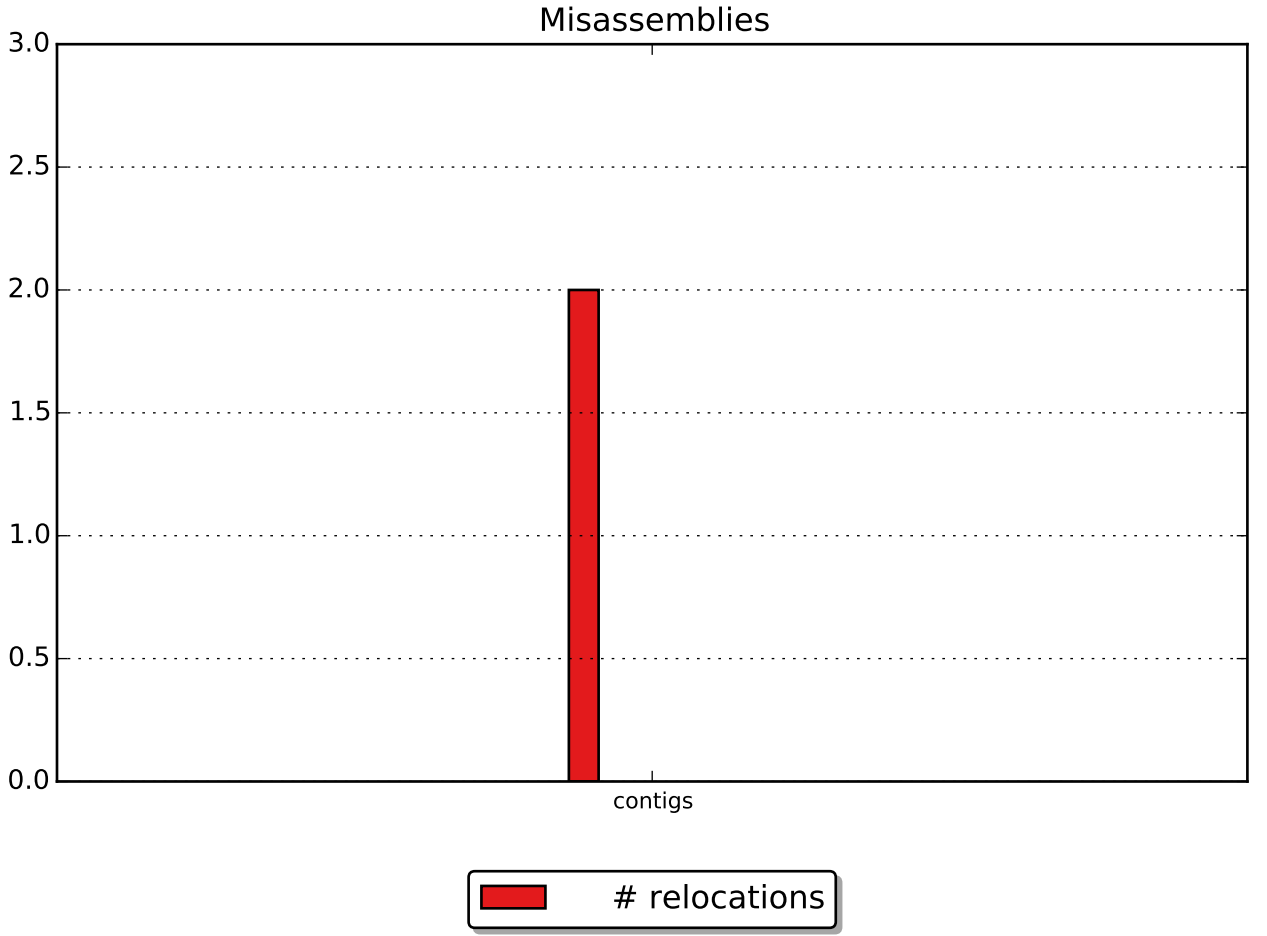
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

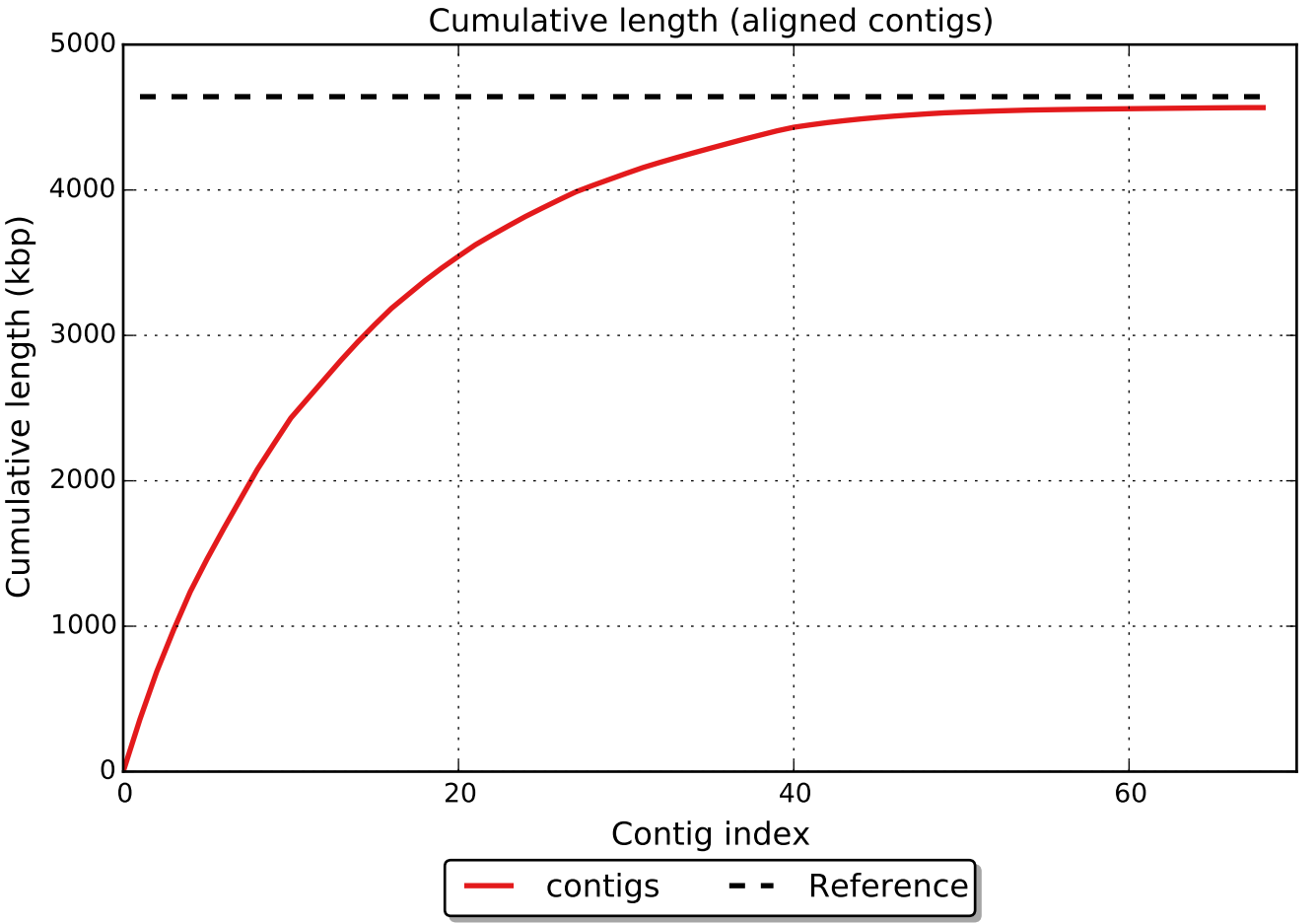

Nx
400
320
240
160
80
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

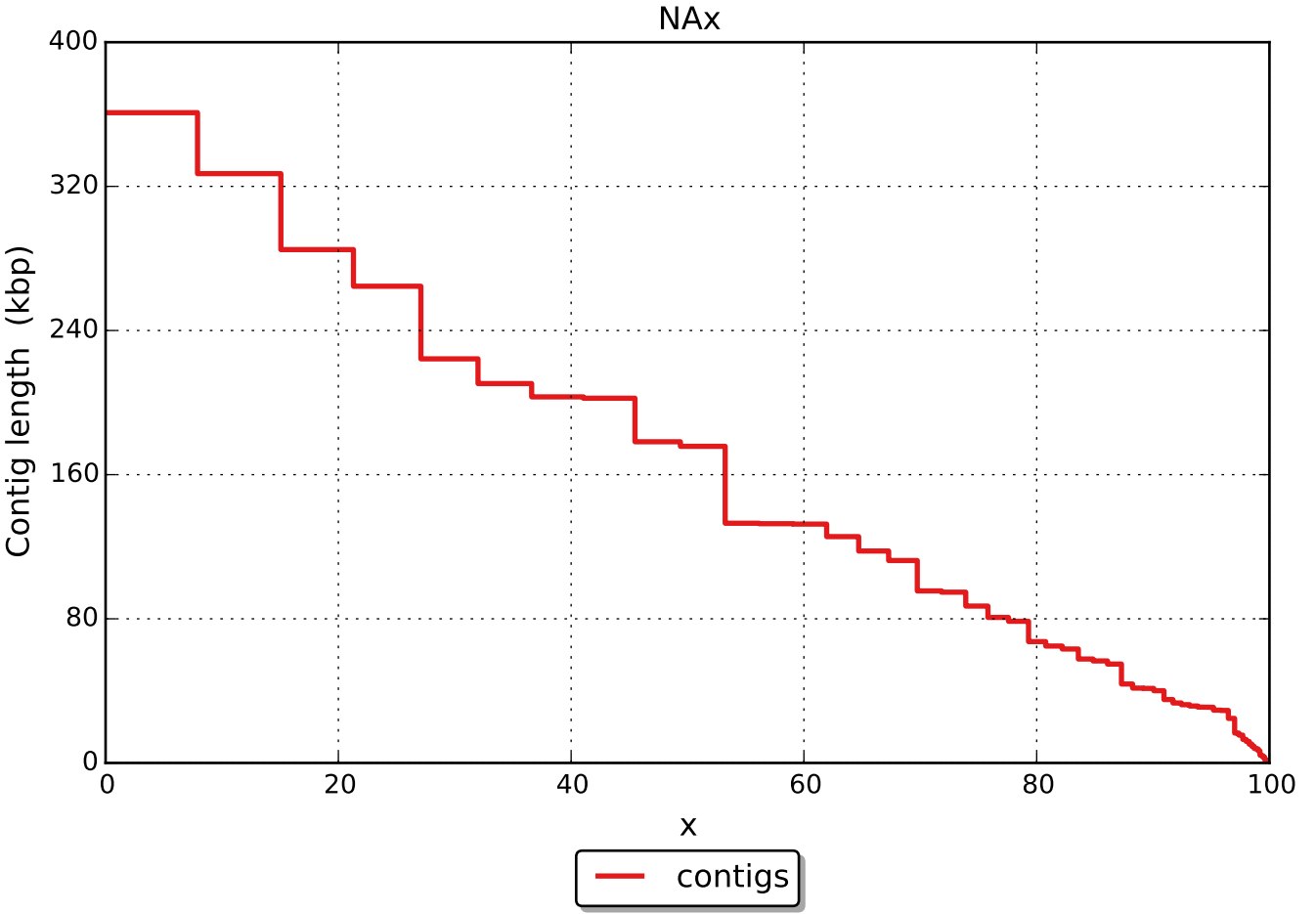

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
contigs

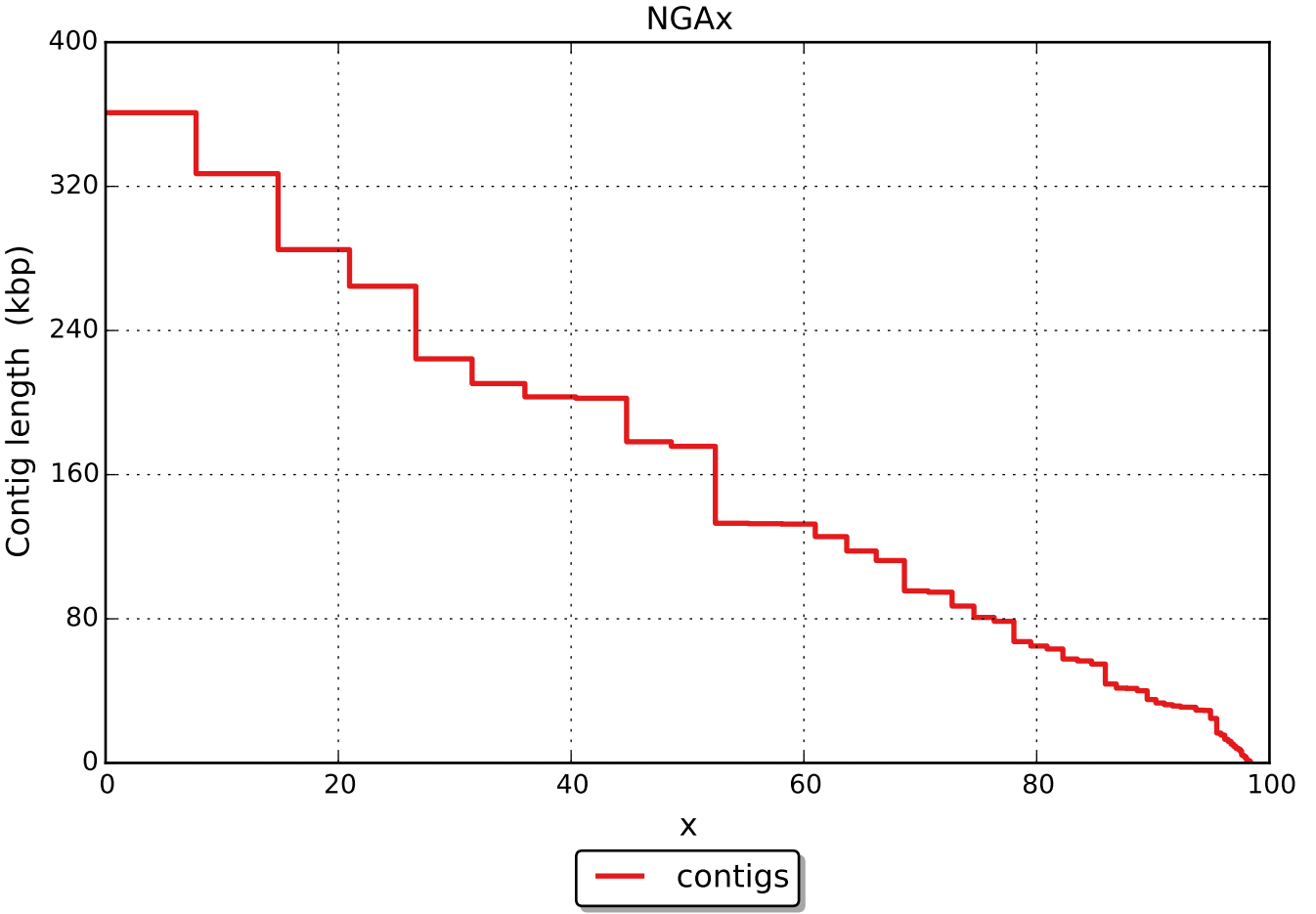

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
Contig index
contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs
Reference


Misassemblies
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
20
40
60
Contig index
contigs
Reference


NAx
400
320
240
160
80
0
Contig length (kbp)
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