Report

	contigs
# contigs (>= 1000 bp)	54
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	42
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	26
Total length (>= 1000 bp)	4708714
Total length (>= 5000 bp)	4691082
Total length (>= 10000 bp)	4668137
Total length (>= 25000 bp)	4620809
Total length (>= 50000 bp)	4177287
# contigs	65
Largest contig	349059
Total length	4717232
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	177303
NG50	177303
N75	99302
NG75	99302
L50	9
LG50	9
L75	18
LG75	18
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.684
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	247.32
# indels per 100 kbp	0.44
Largest alignment	333124
NA50	173841
NGA50	173841
NA75	87711
NGA75	94467
LA50	10
LGA50	10
LA75	20
LGA75	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).

Misassemblies report

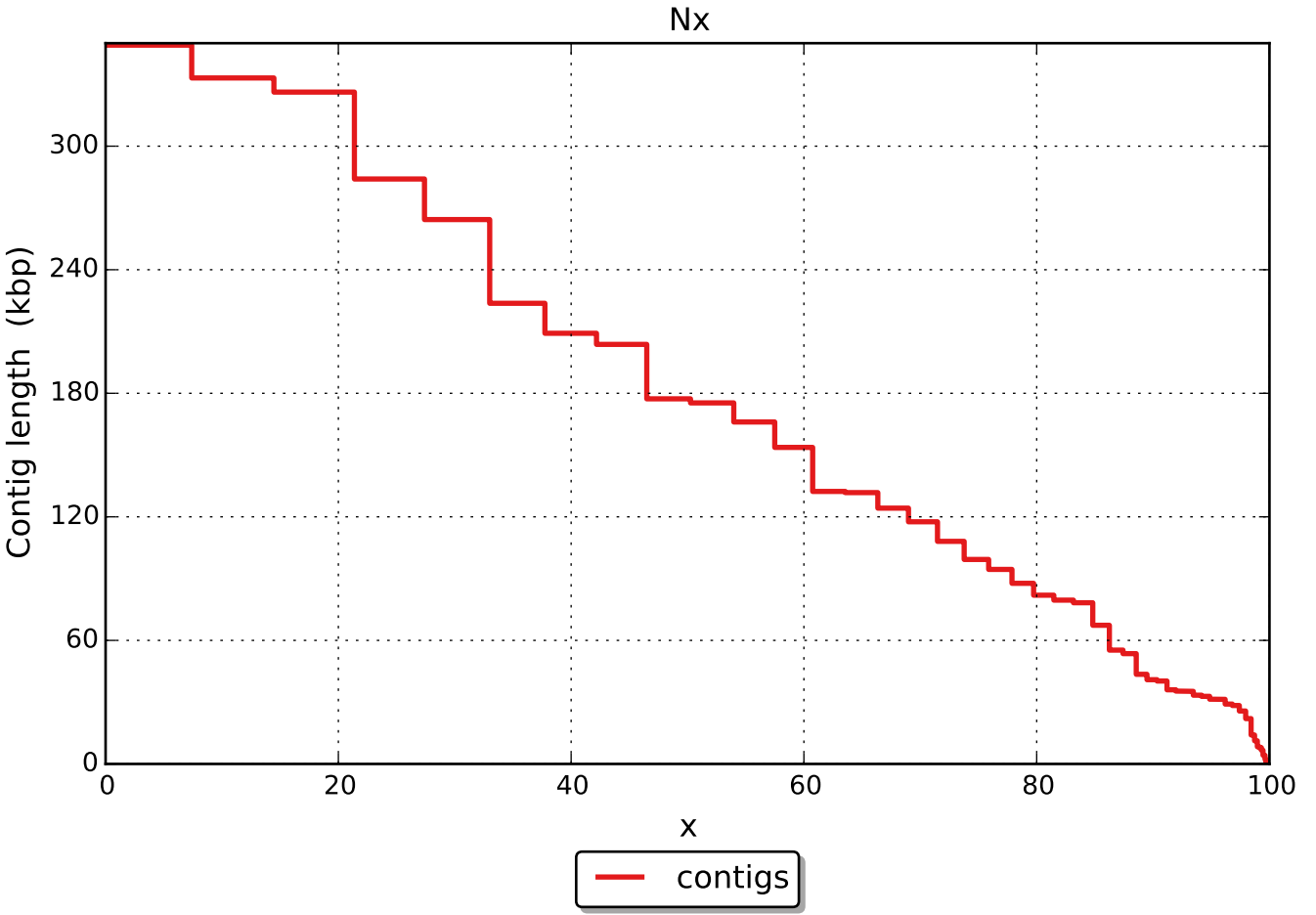
	contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	3
Misassembled contigs length	711322
# local misassemblies	1
# mismatches	11214
# indels	20
# short indels	20
# long indels	0
Indels length	20

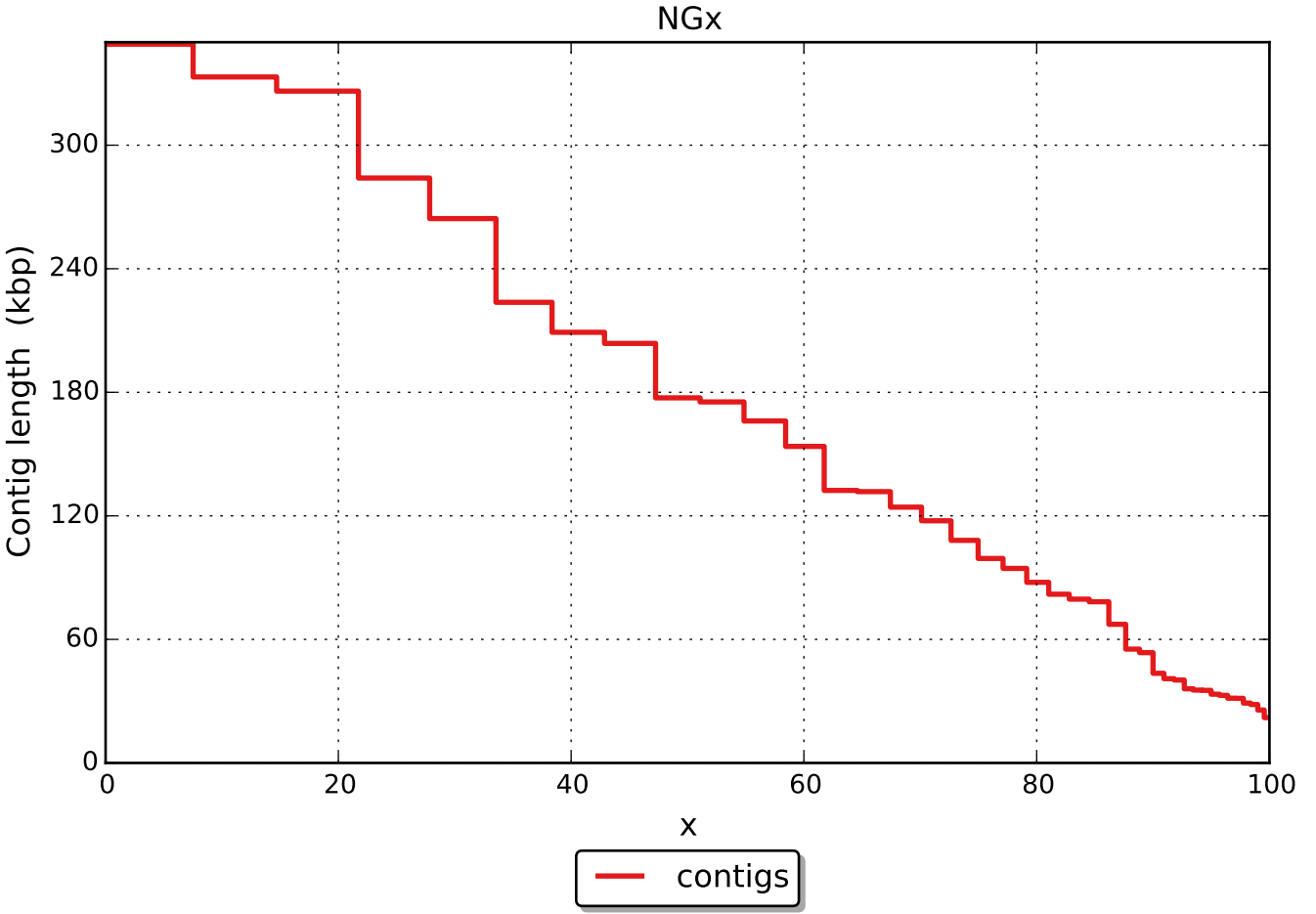
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

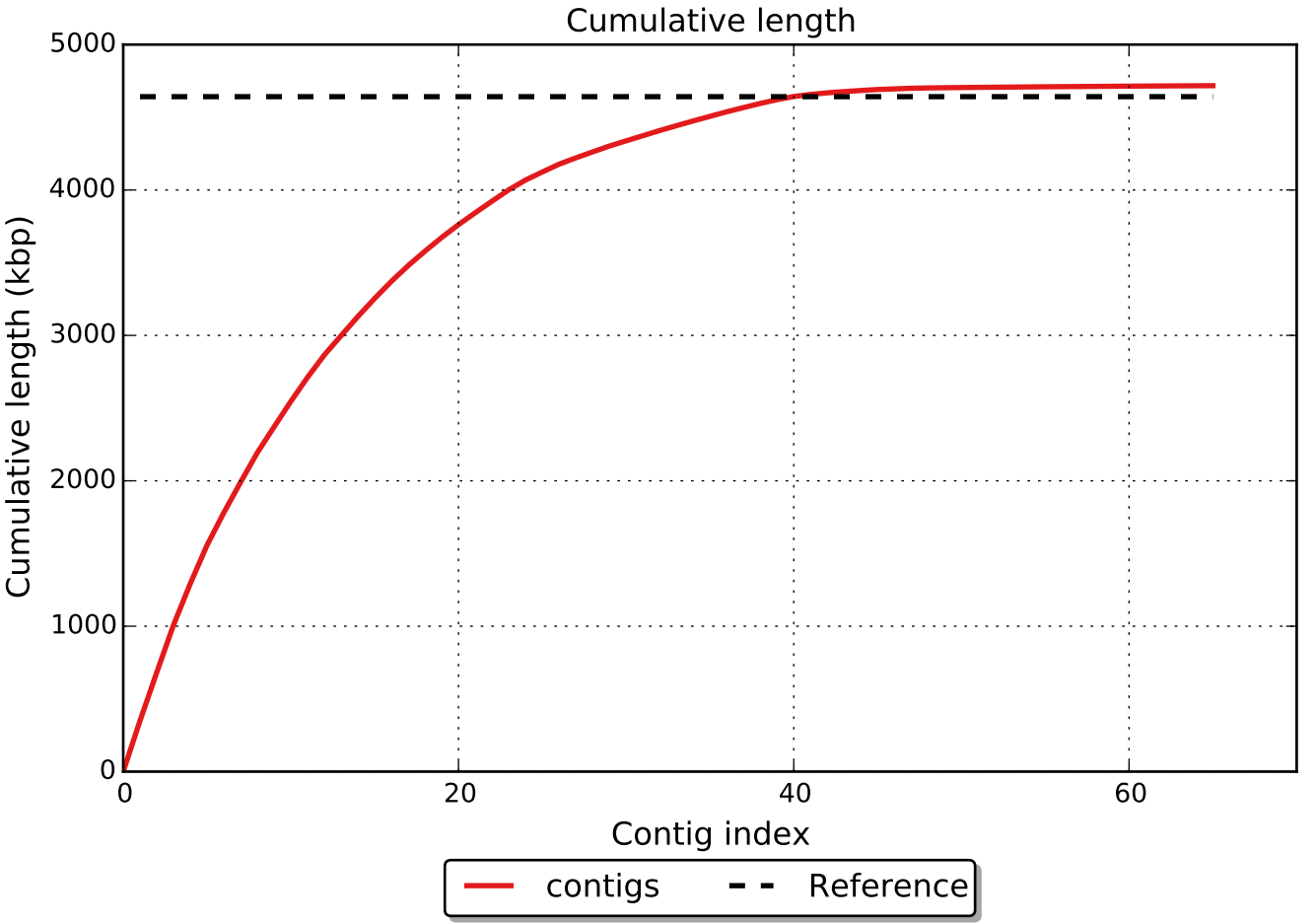
Unaligned report

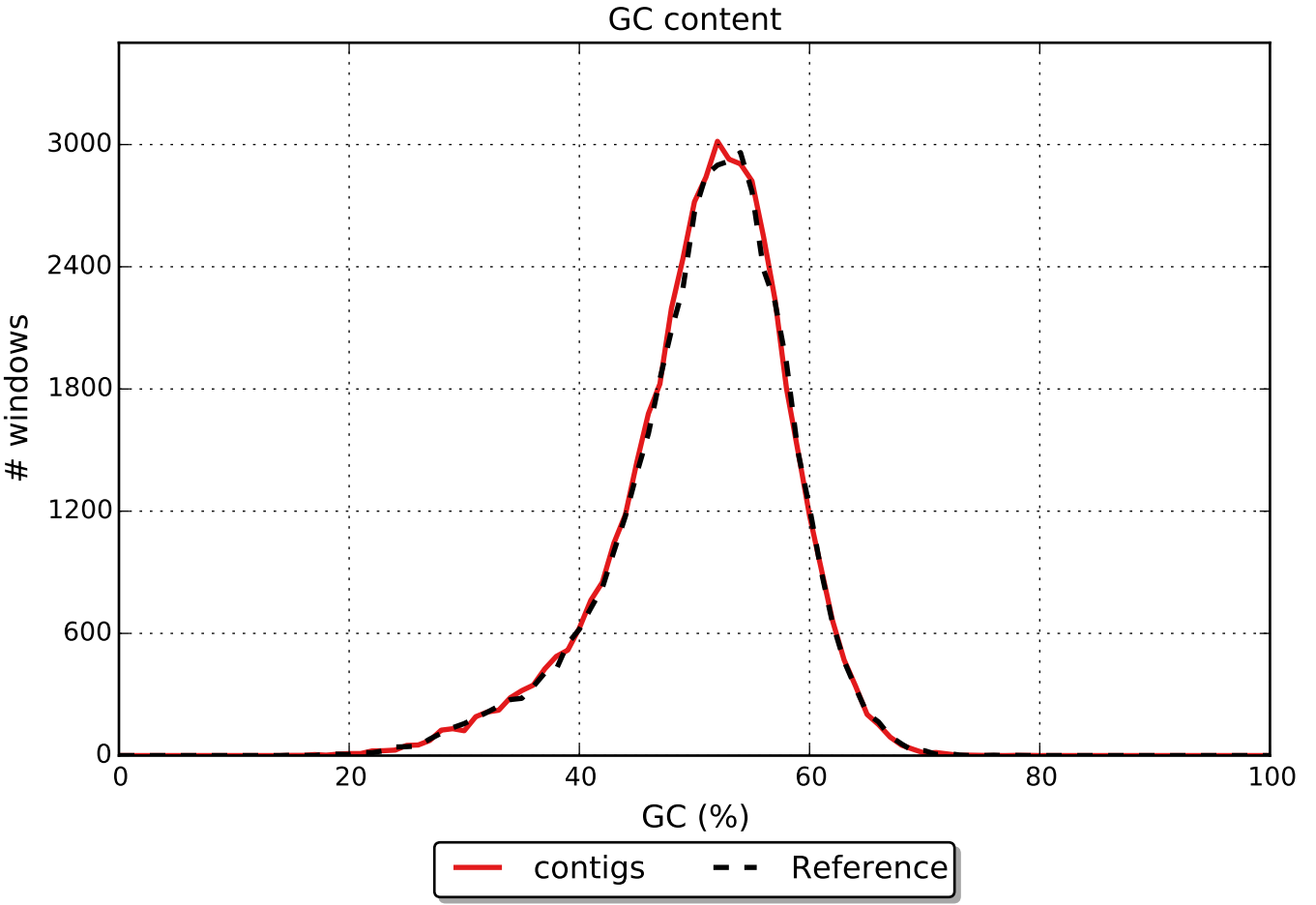
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

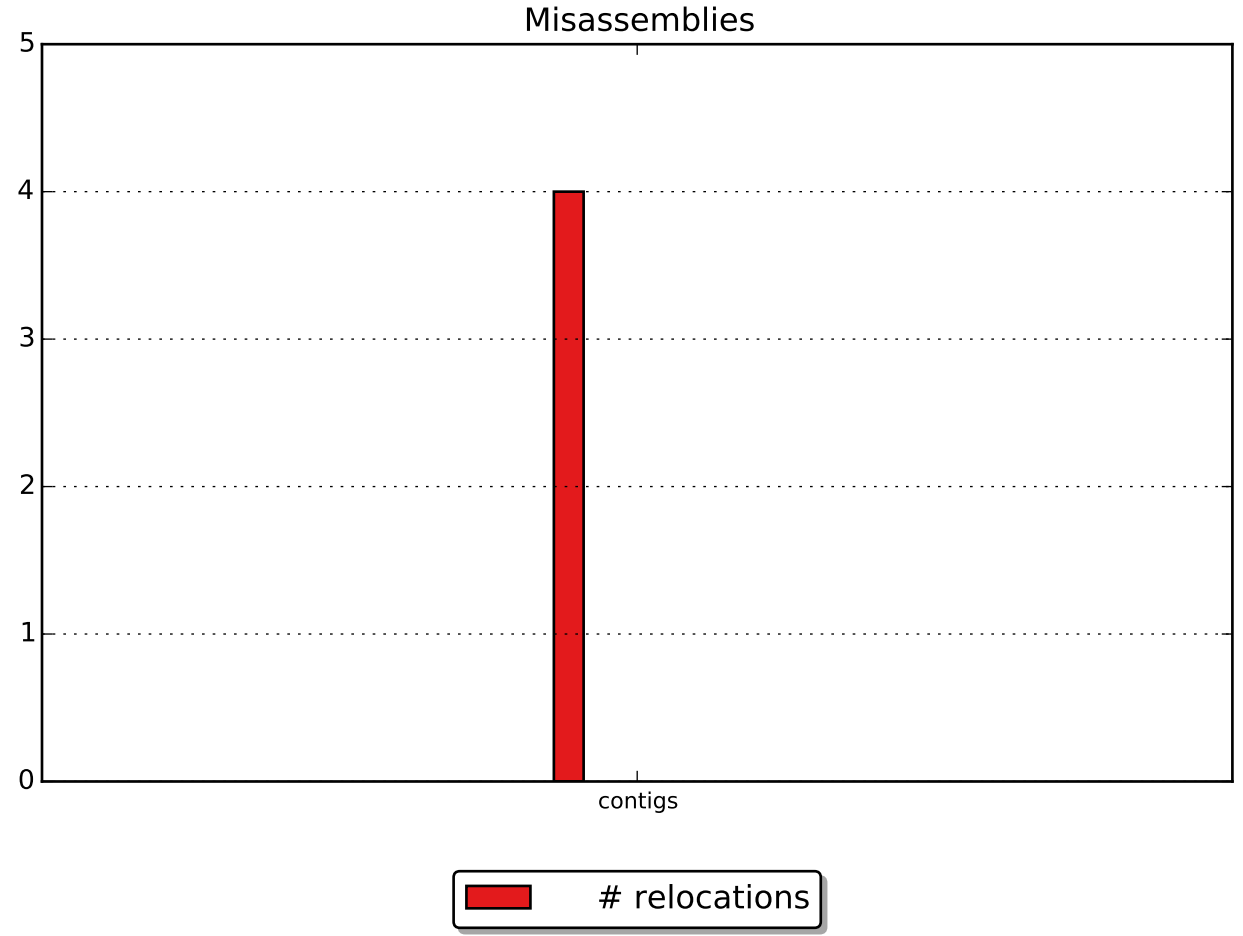
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

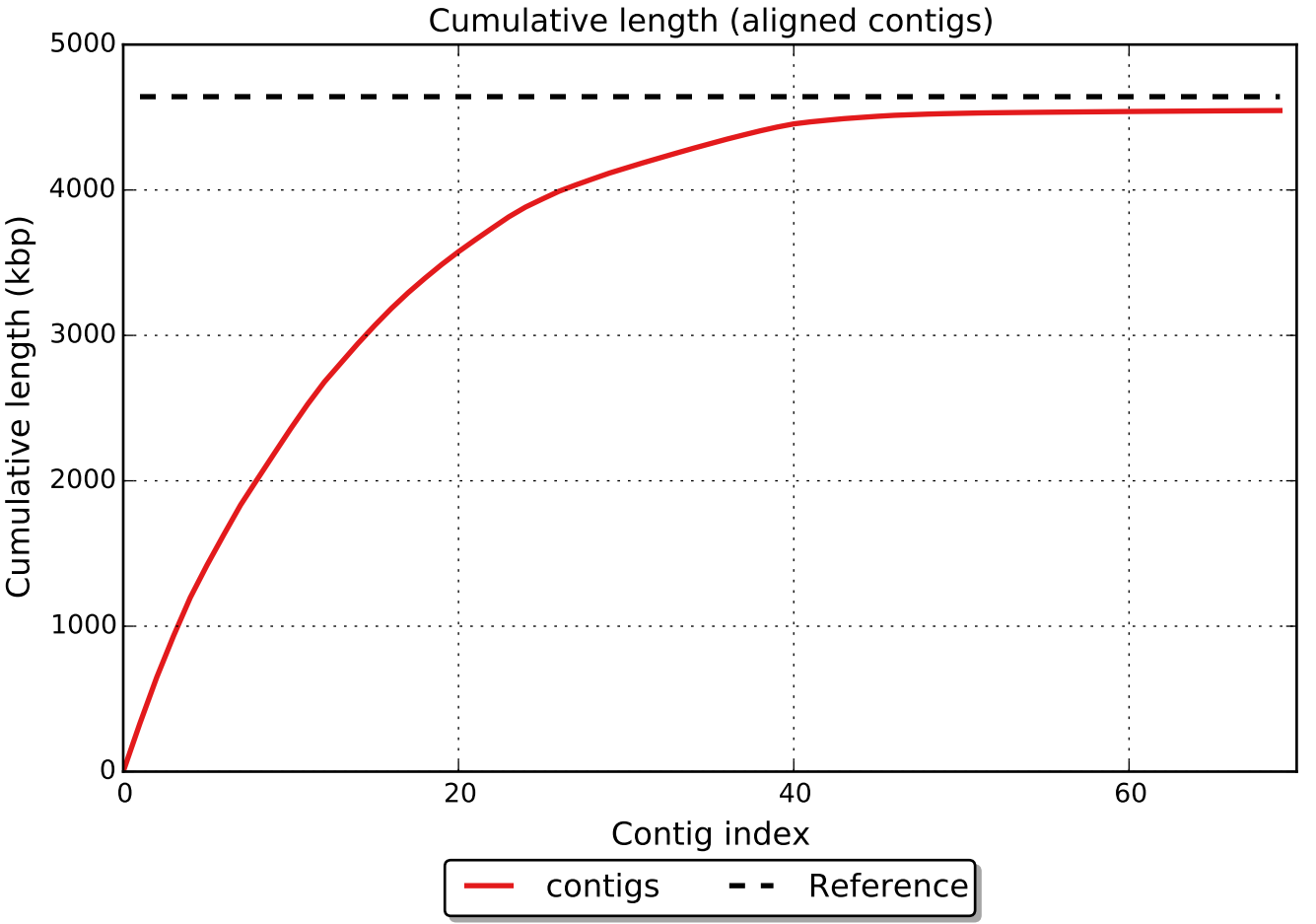

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

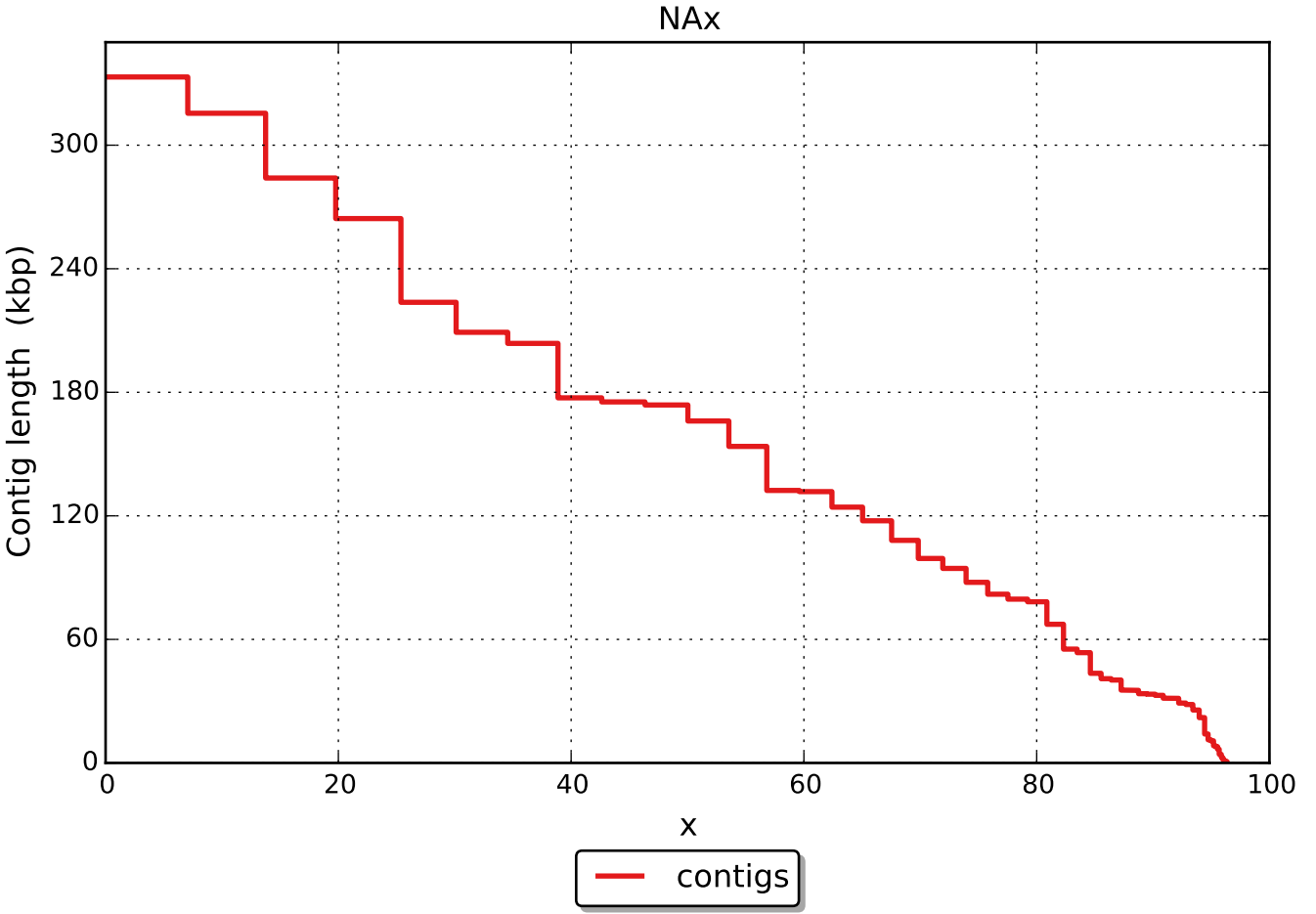

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs

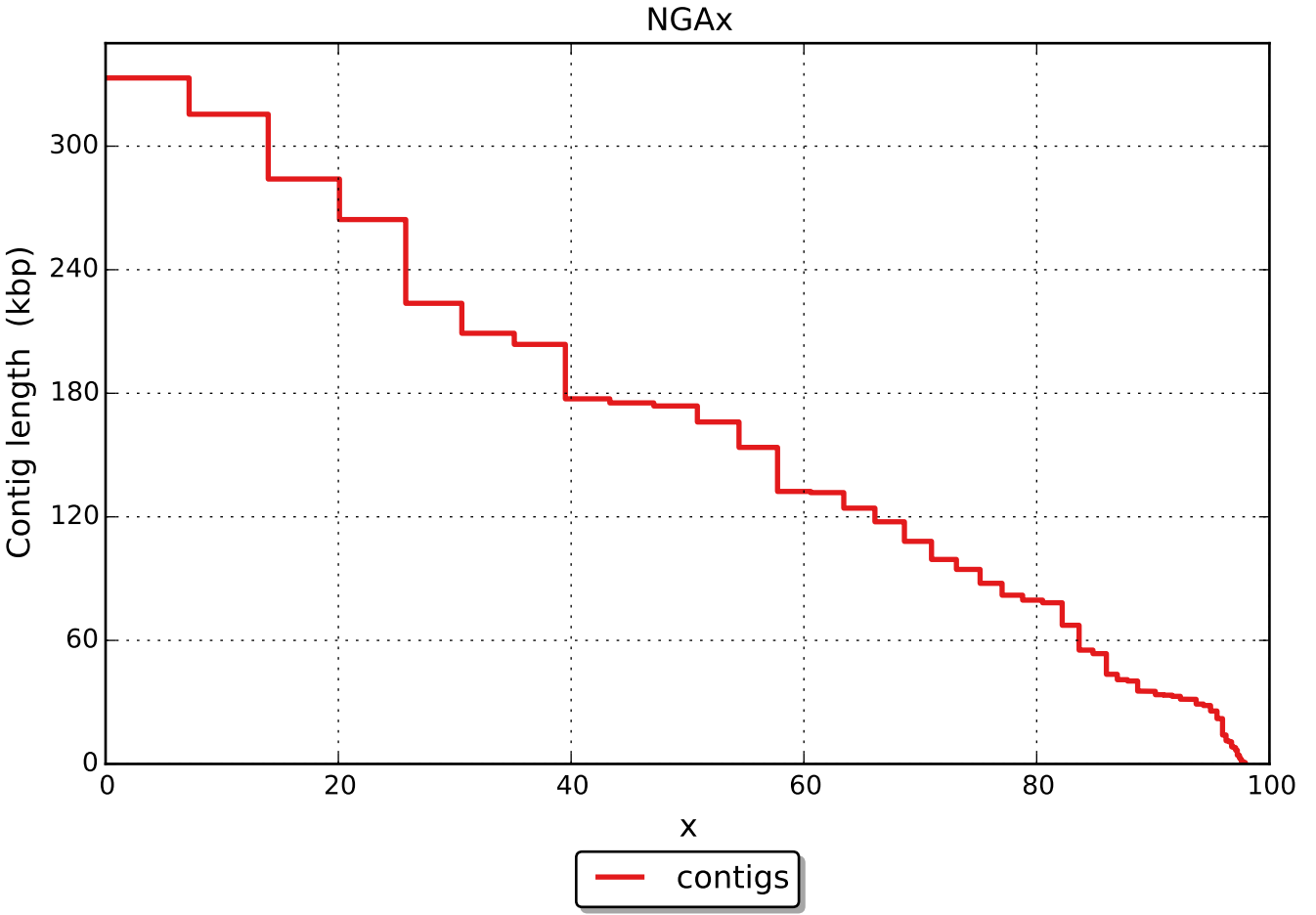

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
20
40
60
Contig index
contigs
Reference


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


Misassemblies
5
4
3
2
1
0
contigs
relocations


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


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
contigs