Report

	contigs
# contigs (>= 1000 bp)	128
# contigs (>= 5000 bp)	98
# contigs (>= 10000 bp)	75
# contigs (>= 25000 bp)	47
# contigs (>= 50000 bp)	31
Total length (>= 1000 bp)	3857165
Total length (>= 5000 bp)	3779813
Total length (>= 10000 bp)	3613214
Total length (>= 25000 bp)	3184093
Total length (>= 50000 bp)	2652022
# contigs	136
Largest contig	161420
Total length	3863039
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.78
N50	67824
NG50	59359
N75	33561
NG75	12988
L50	19
LG50	25
L75	38
LG75	64
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.042
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	556.31
# indels per 100 kbp	0.34
Largest alignment	142244
NA50	64886
NGA50	54883
NA75	32212
NGA75	12988
LA50	20
LGA50	26
LA75	40
LGA75	67

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

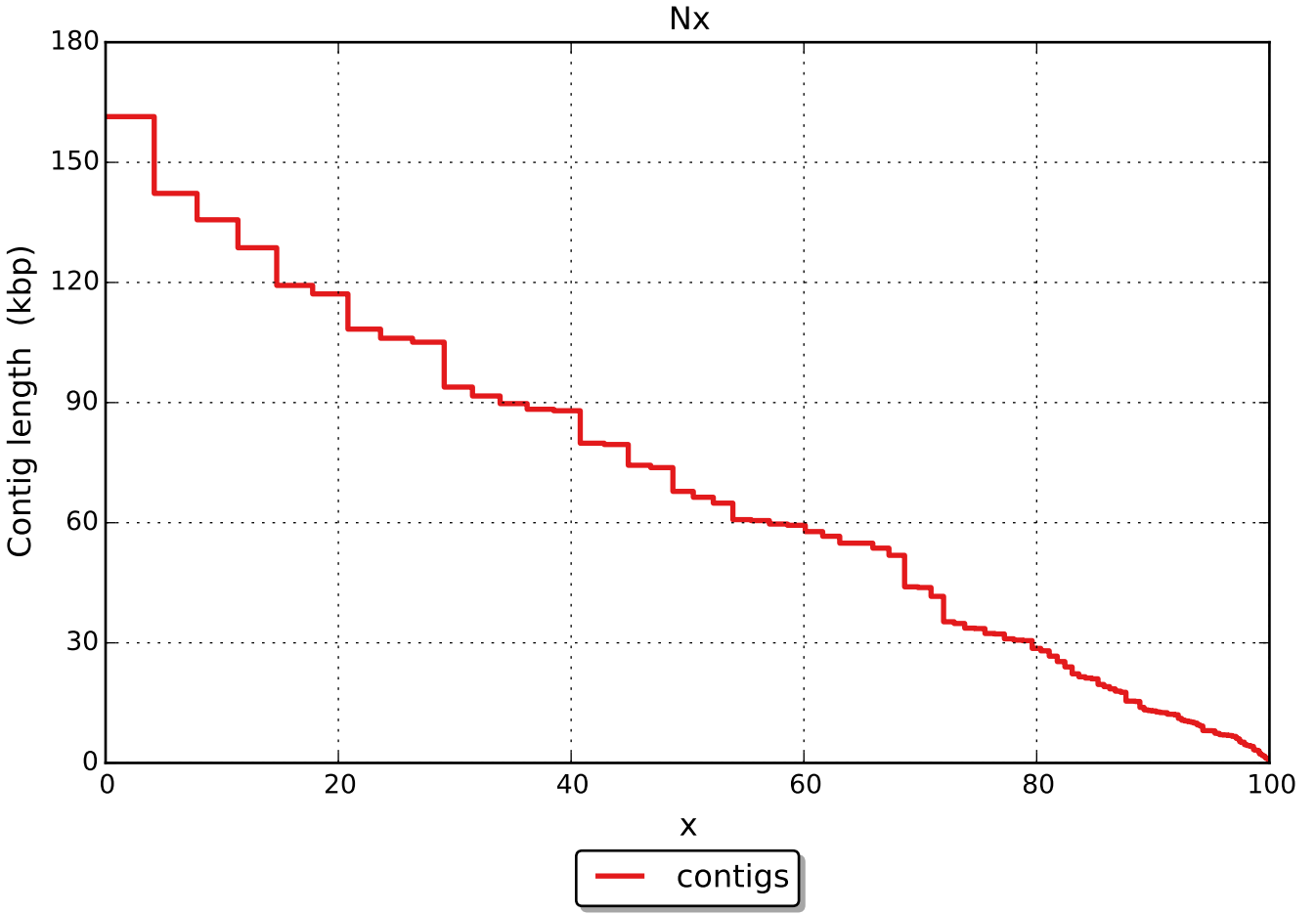
	contigs
# misassemblies	5
# relocations	4
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	310368
# local misassemblies	2
# mismatches	21443
# indels	13
# short indels	13
# long indels	0
Indels length	19

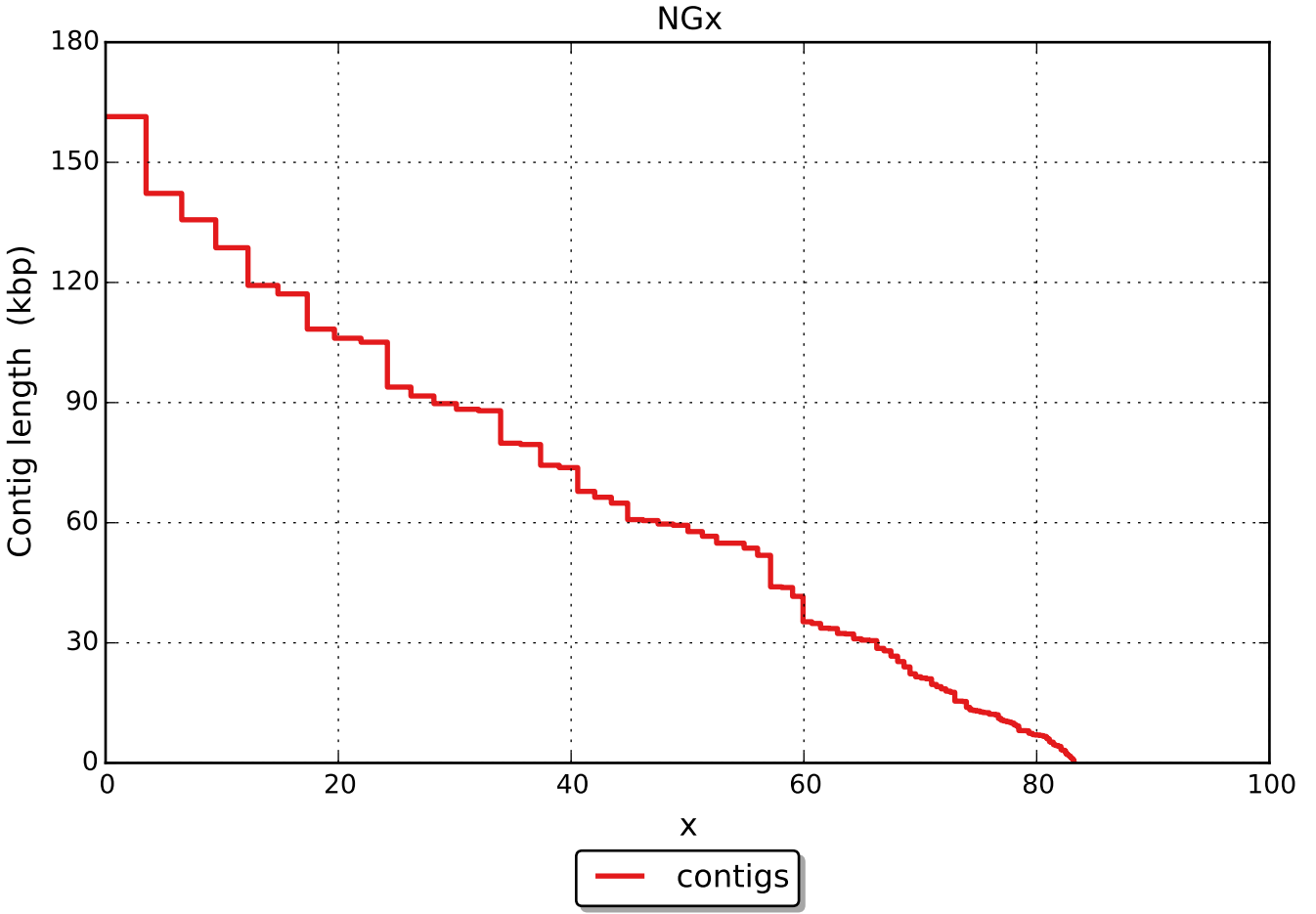
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

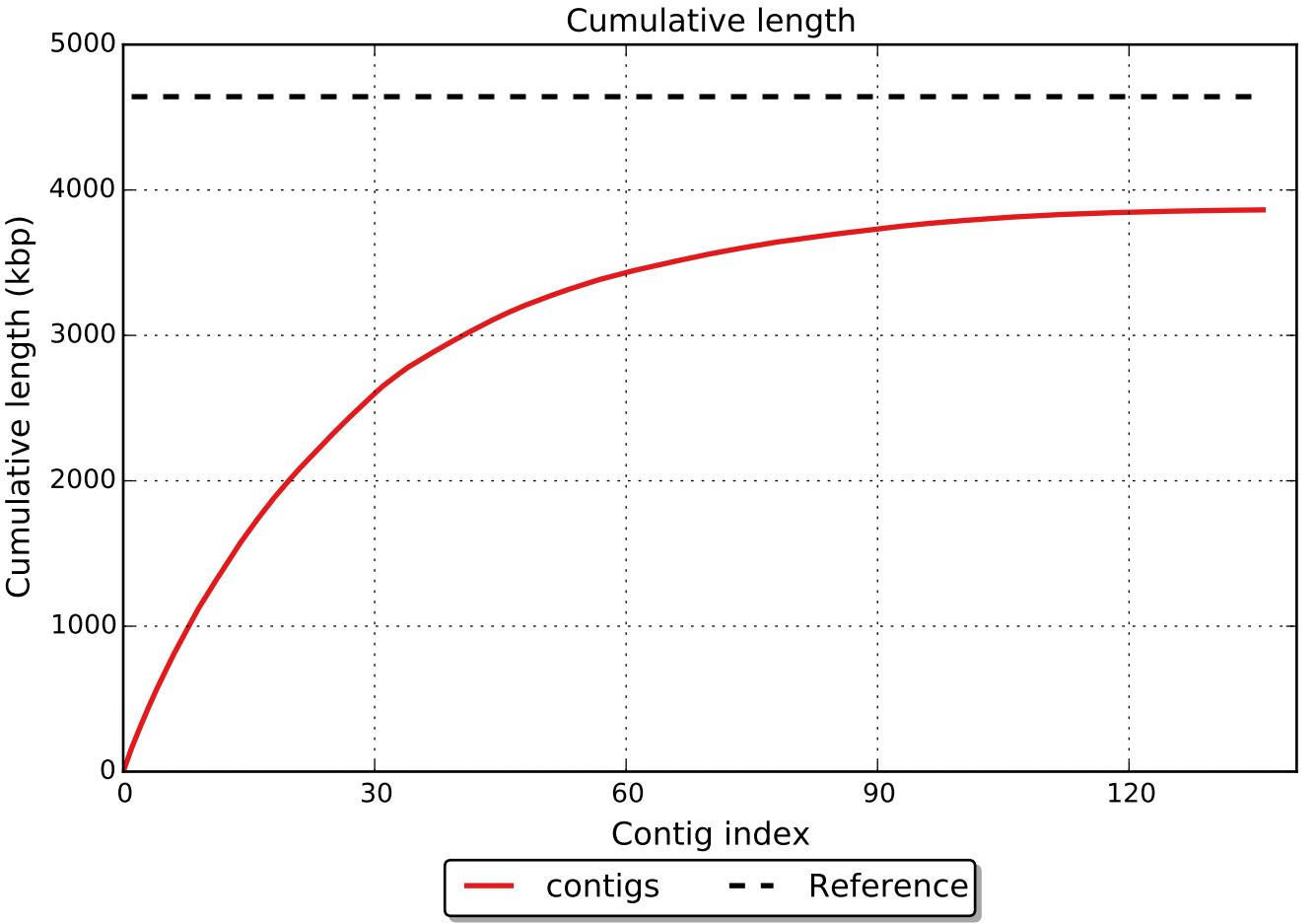
Unaligned report

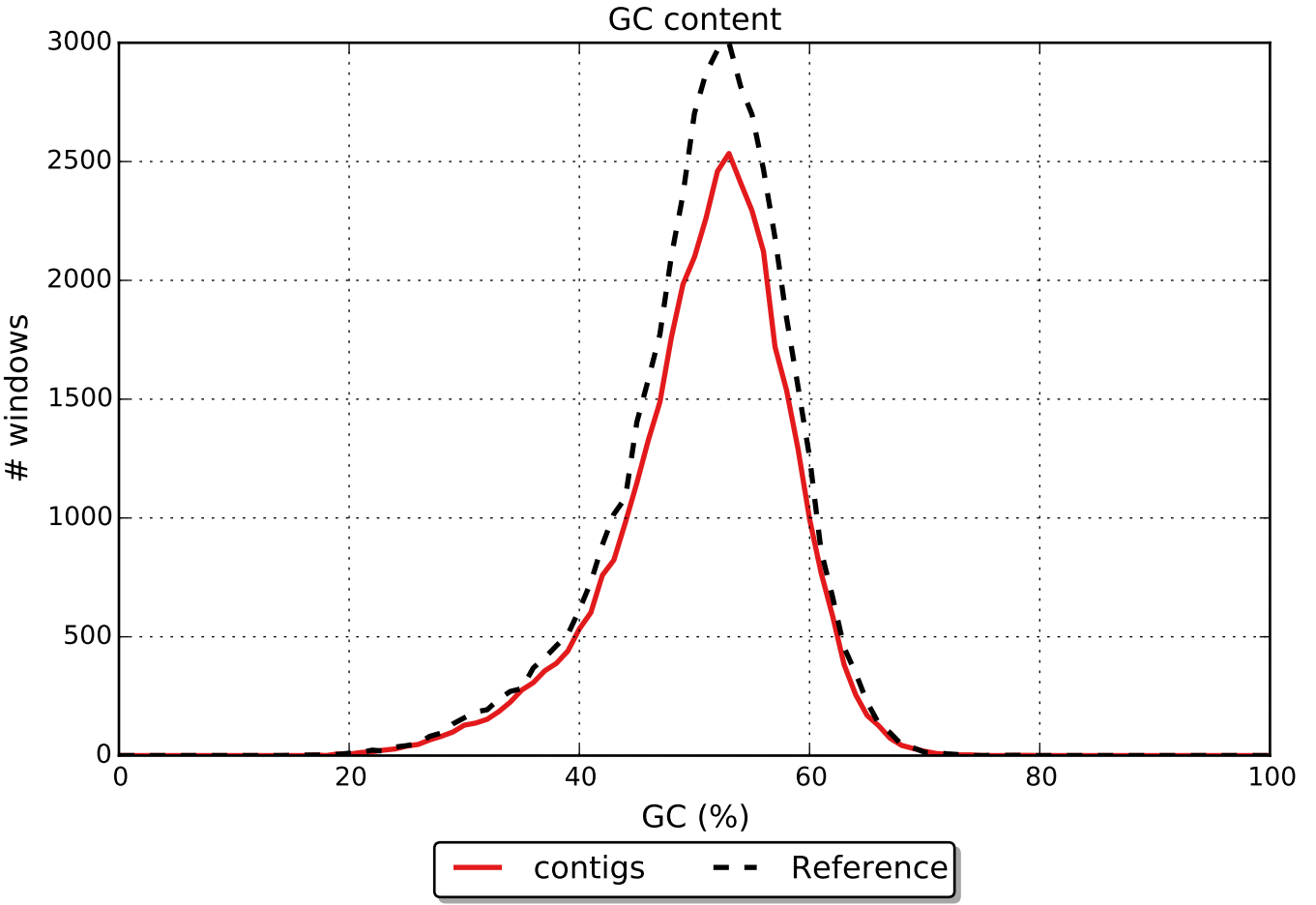
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

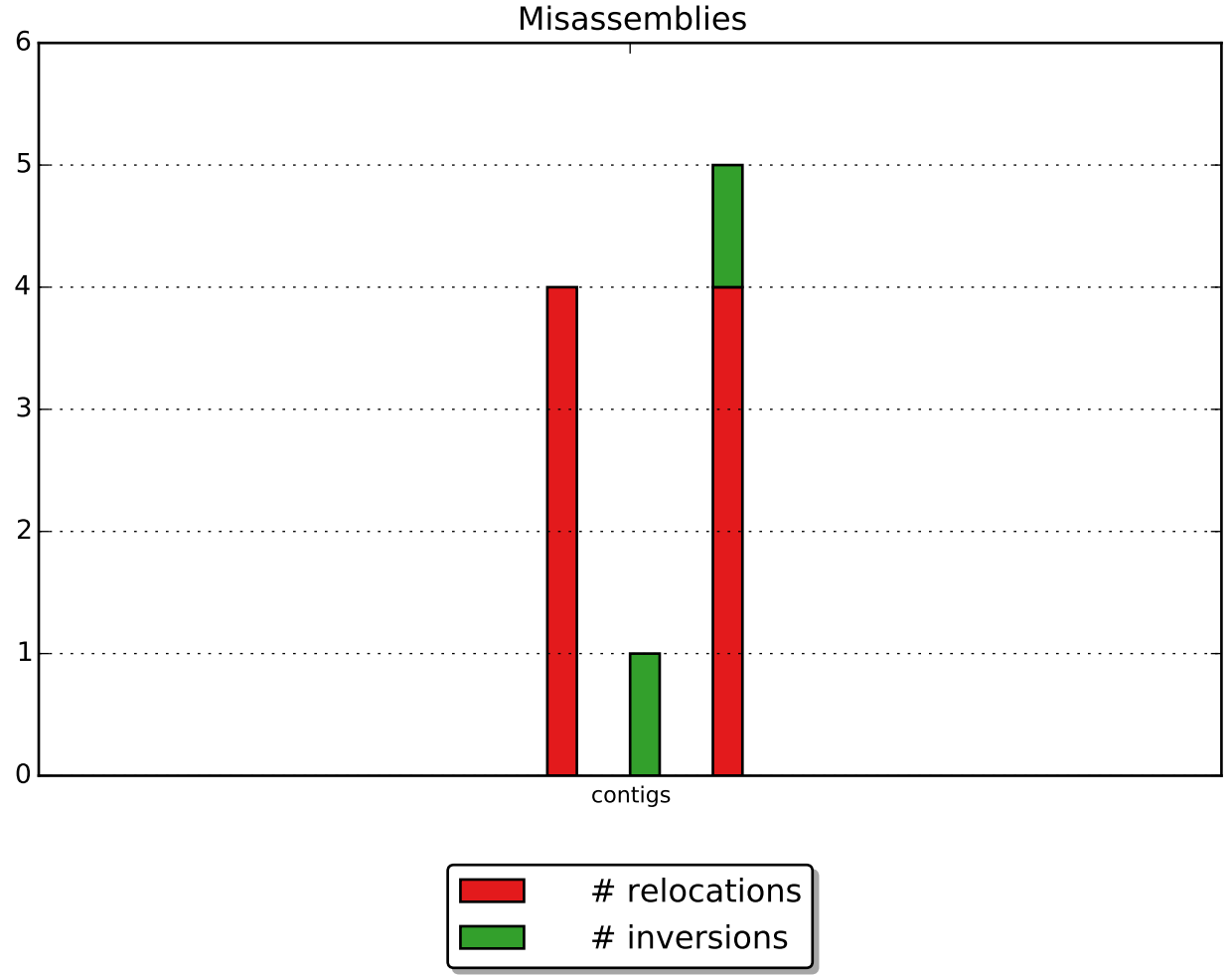
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

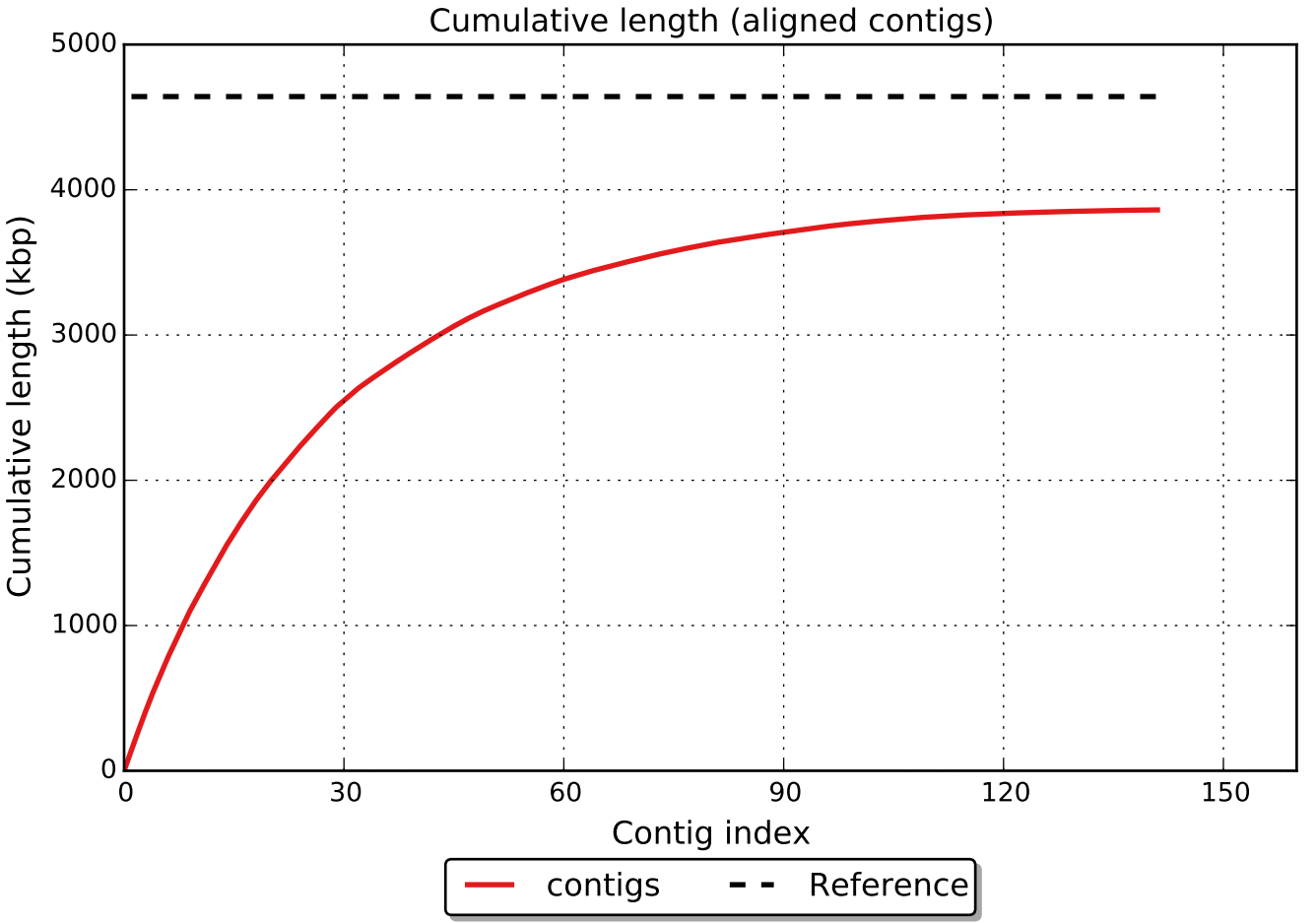

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs

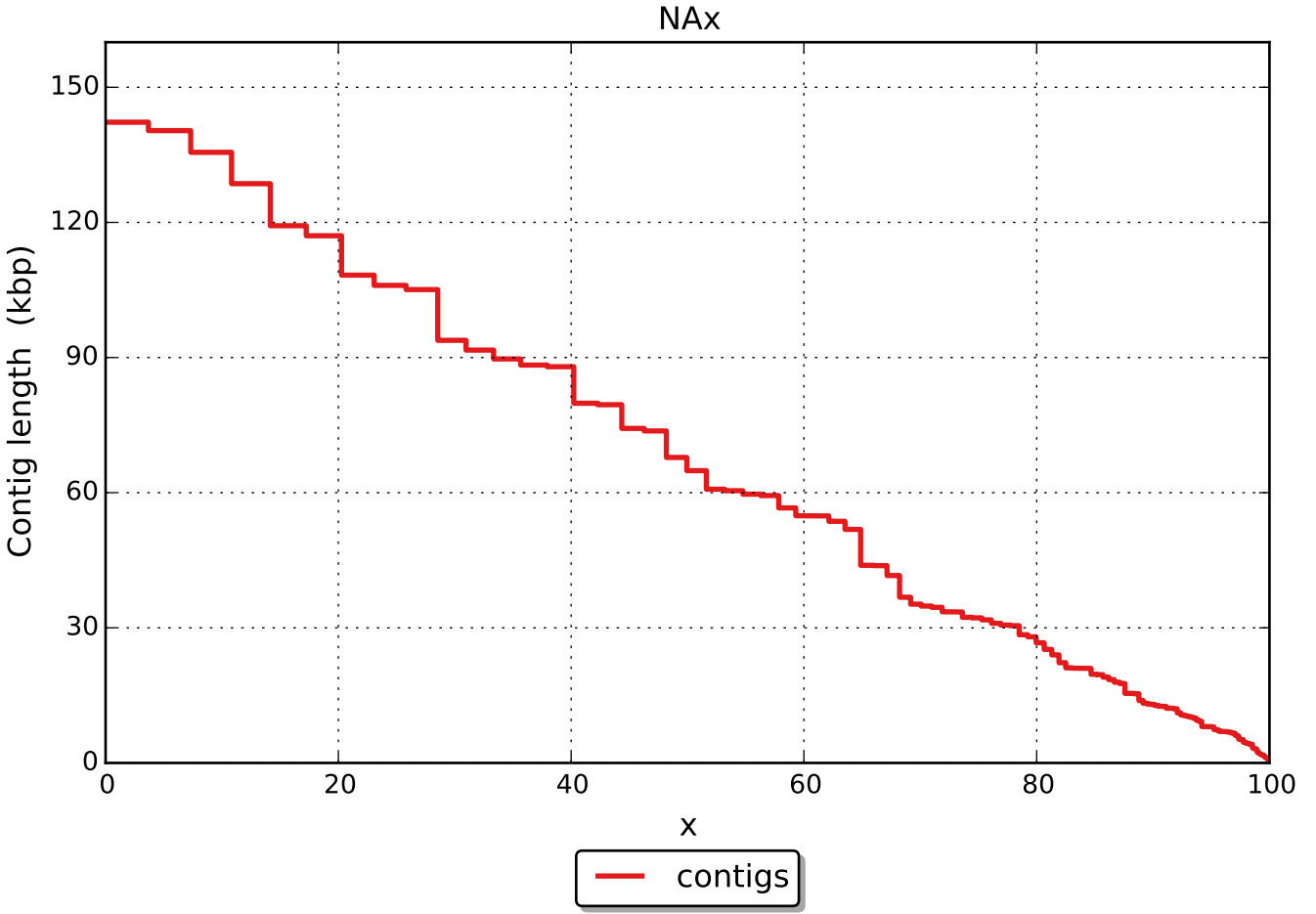

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs

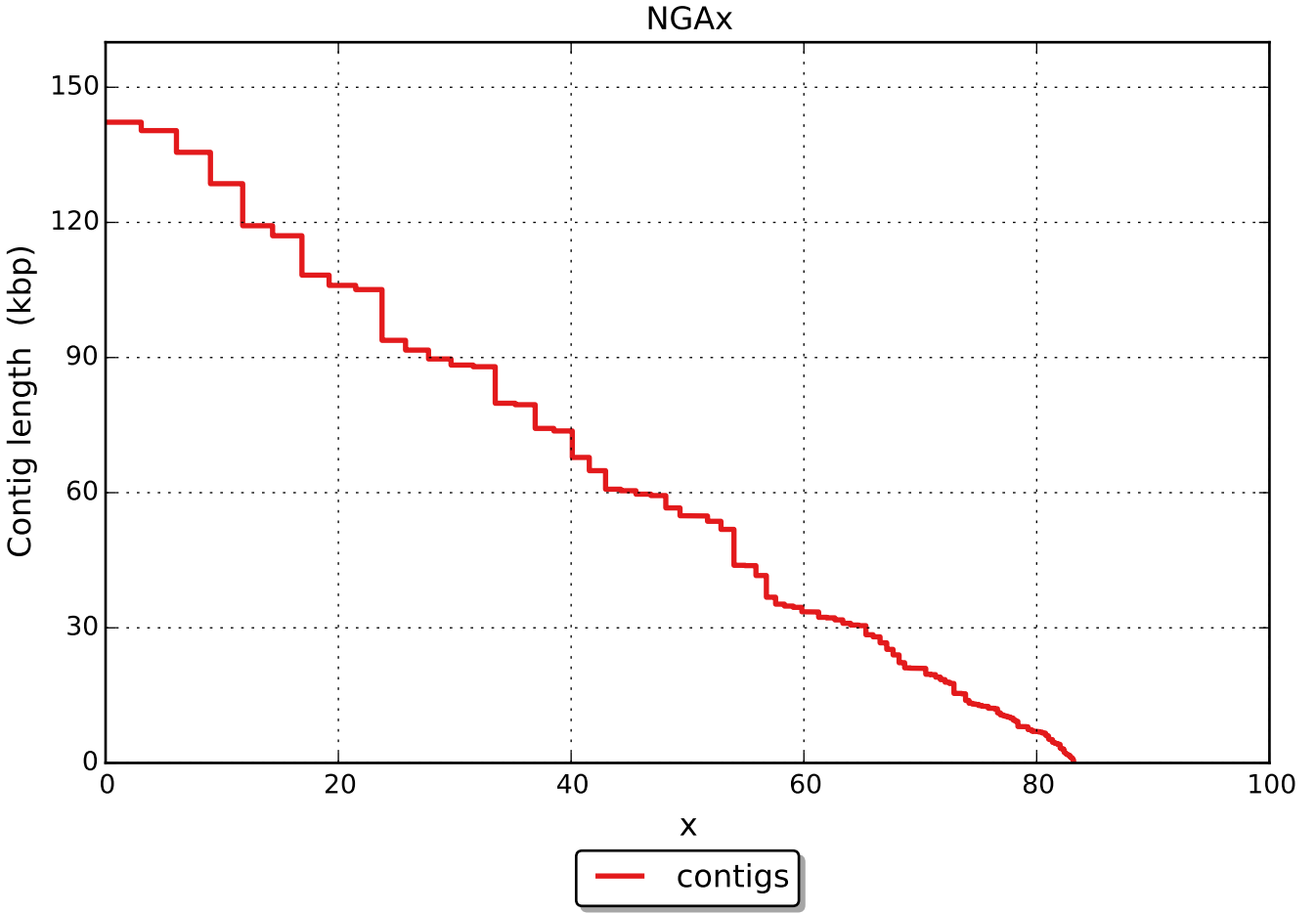

Cumulative length
5000
4000
3000
2000
1000
0
Cumulative length (kbp)
0
30
60
90
120
Contig index
contigs
Reference


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


Misassemblies
6
5
4
3
2
1
0
contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
Contig index
contigs
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
contigs