Report

	contigs
# contigs (>= 0 bp)	466
# contigs (>= 1000 bp)	312
# contigs (>= 5000 bp)	214
# contigs (>= 10000 bp)	158
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	4598127
Total length (>= 1000 bp)	4566781
Total length (>= 5000 bp)	4293829
Total length (>= 10000 bp)	3874768
Total length (>= 25000 bp)	2261811
Total length (>= 50000 bp)	596627
# contigs	329
Largest contig	93001
Total length	4580023
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	24538
NG50	24528
N75	13897
NG75	13351
L50	59
LG50	60
L75	121
LG75	125
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	49828
# local misassemblies	8
# unaligned contigs	0 + 2 part
Unaligned length	51
Genome fraction (%)	98.066
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.59
# indels per 100 kbp	0.94
Largest alignment	93001
NA50	24538
NGA50	24528
NA75	13617
NGA75	13351
LA50	59
LGA50	60
LA75	122
LGA75	125

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

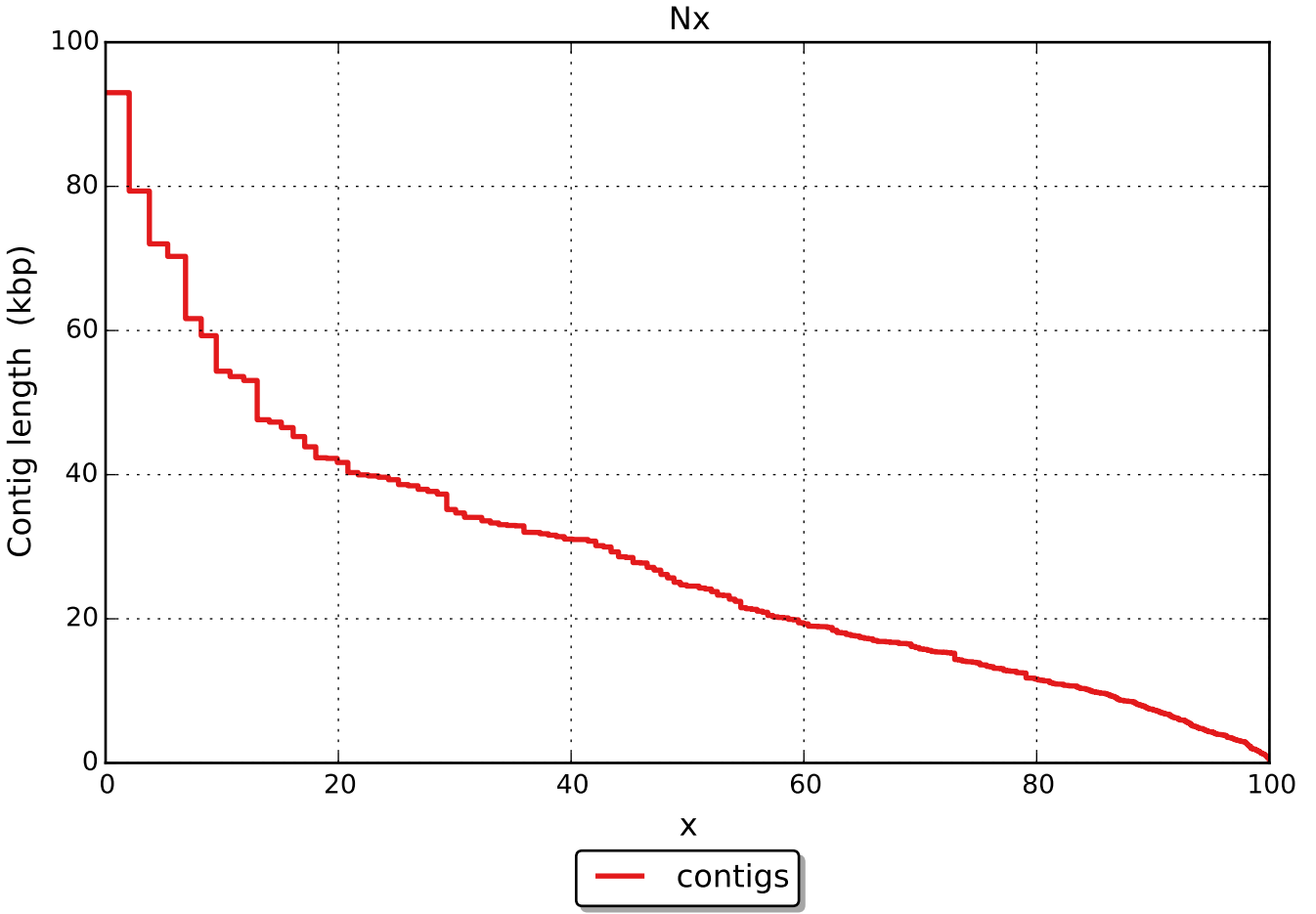
	contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	49828
# local misassemblies	8
# mismatches	1438
# indels	43
# short indels	42
# long indels	1
Indels length	138

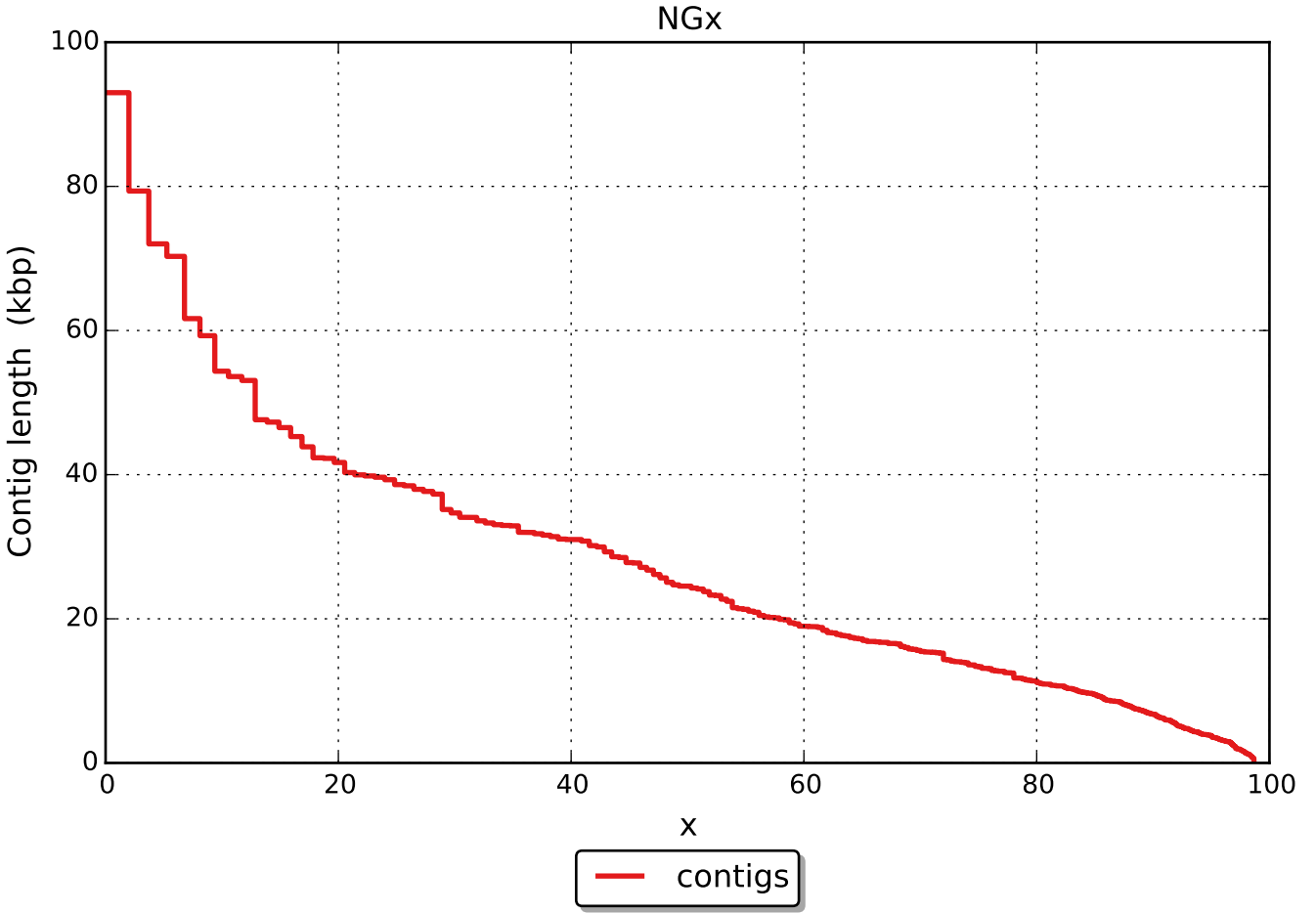
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

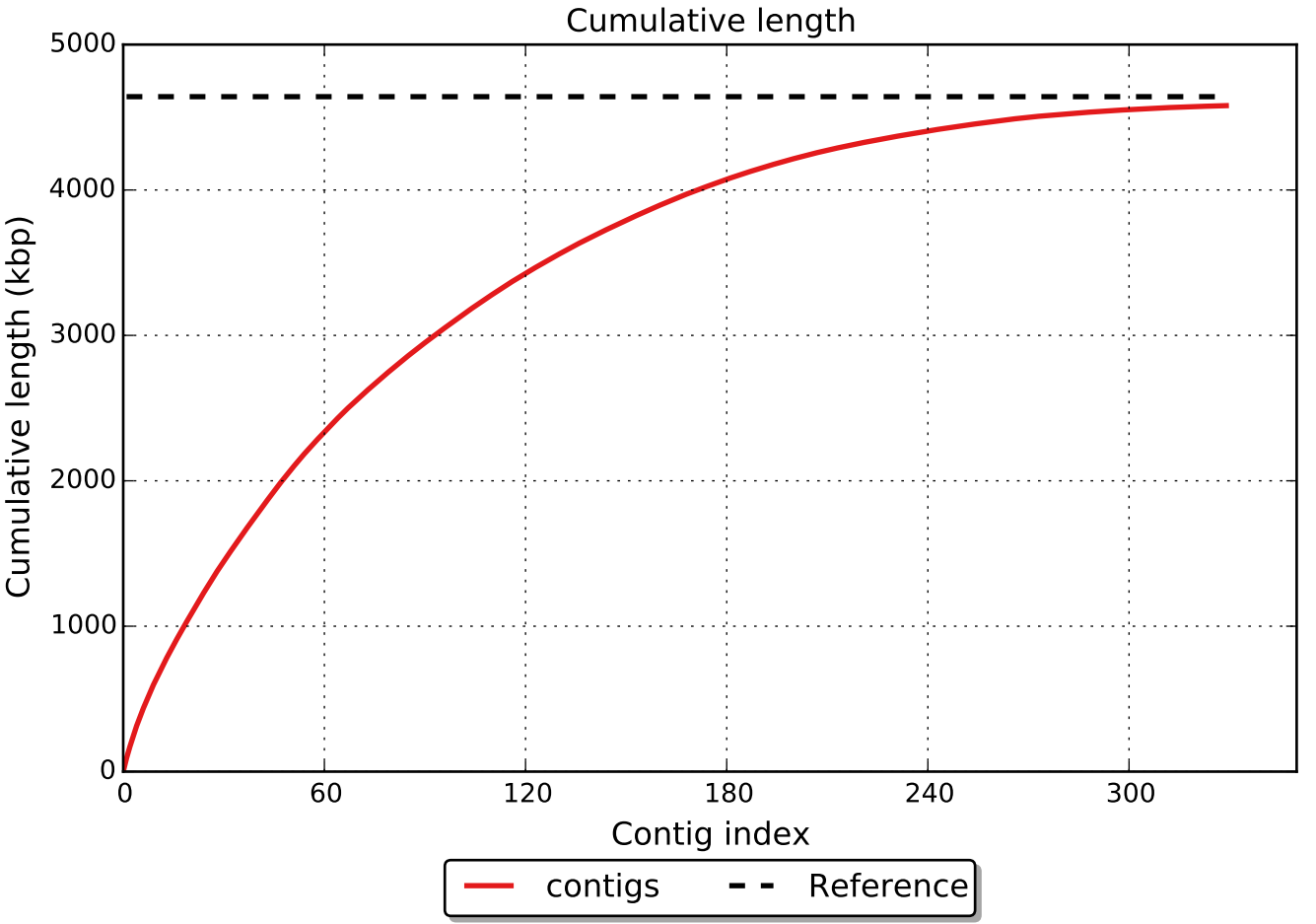
Unaligned report

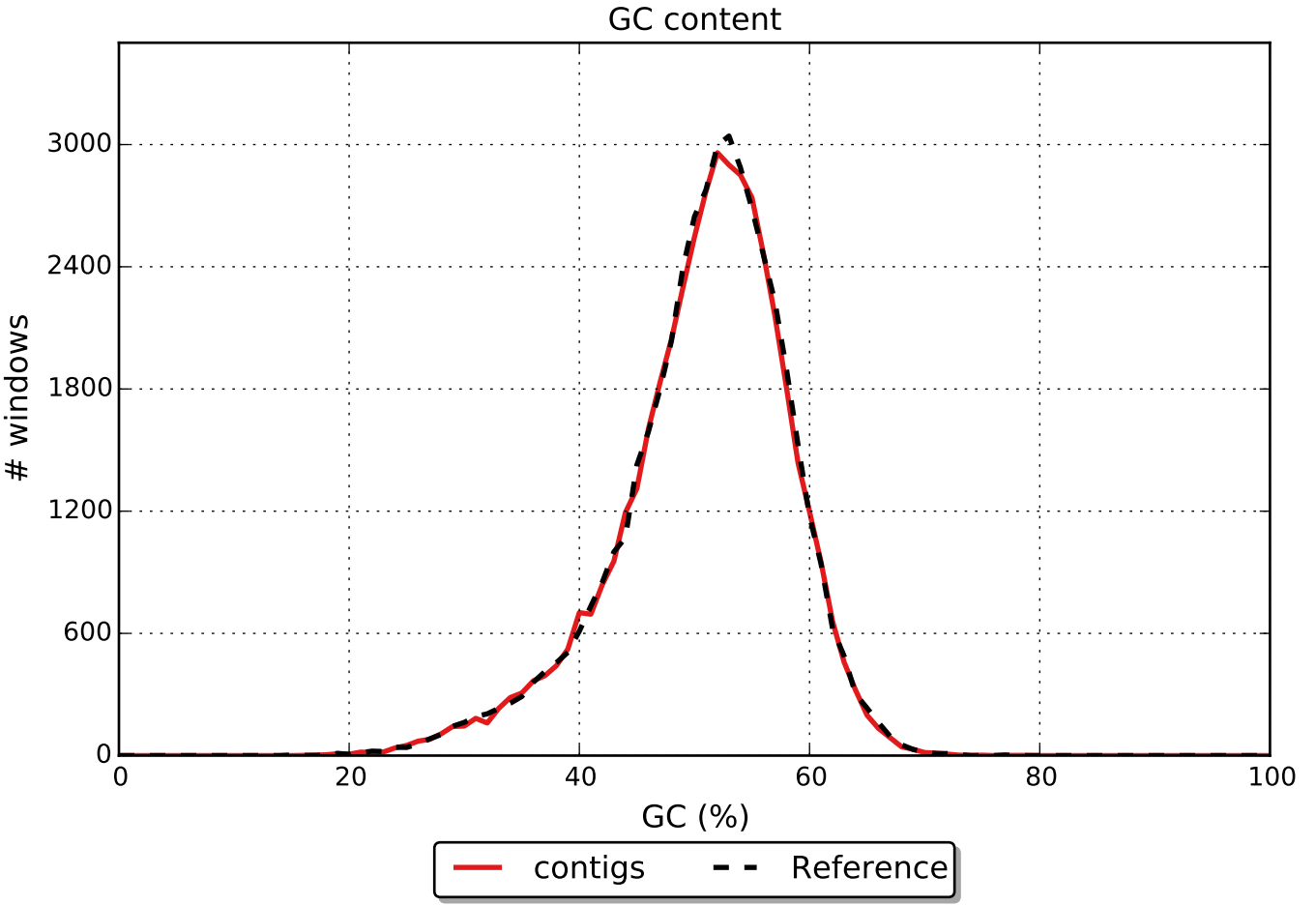
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	51
# N's	0

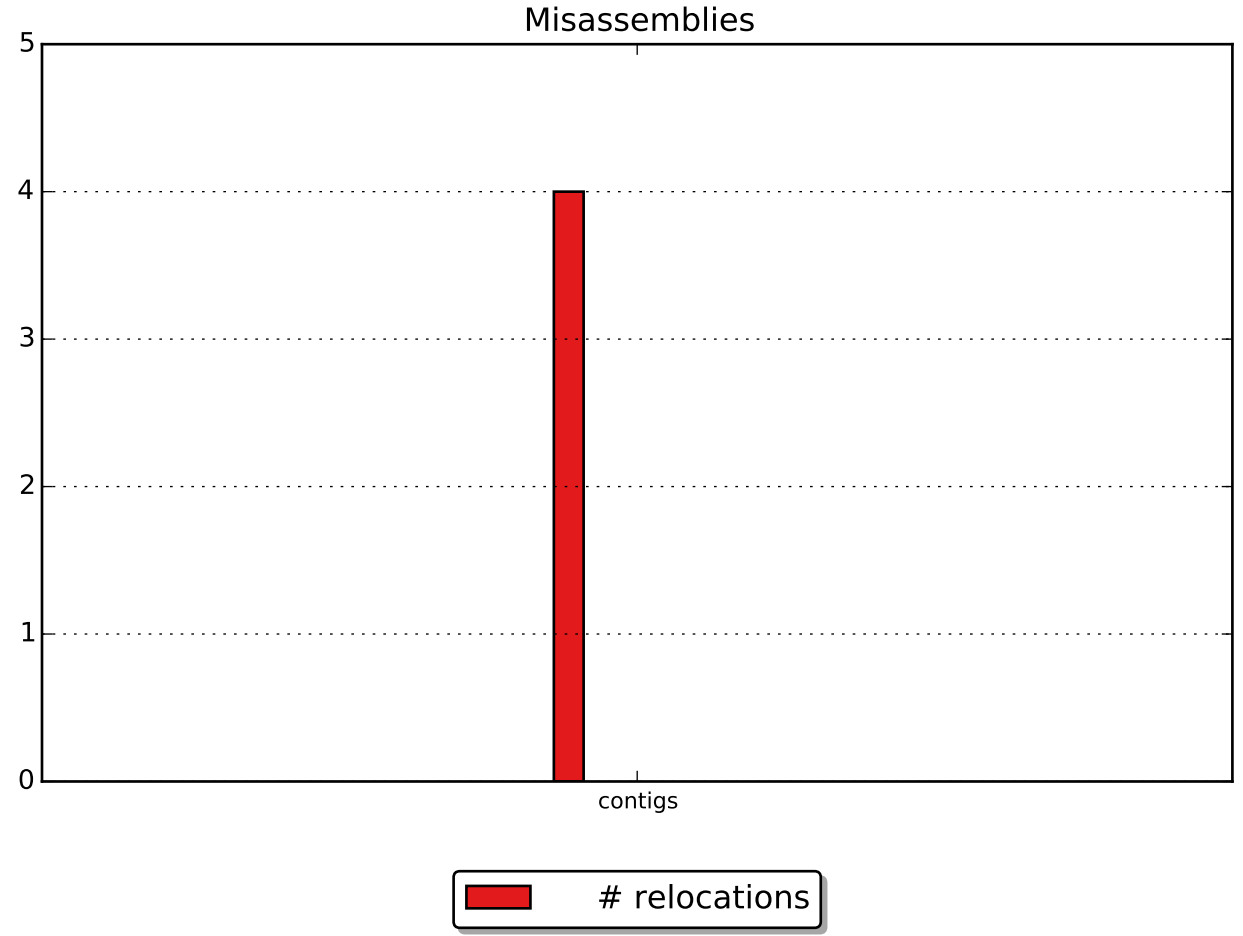
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

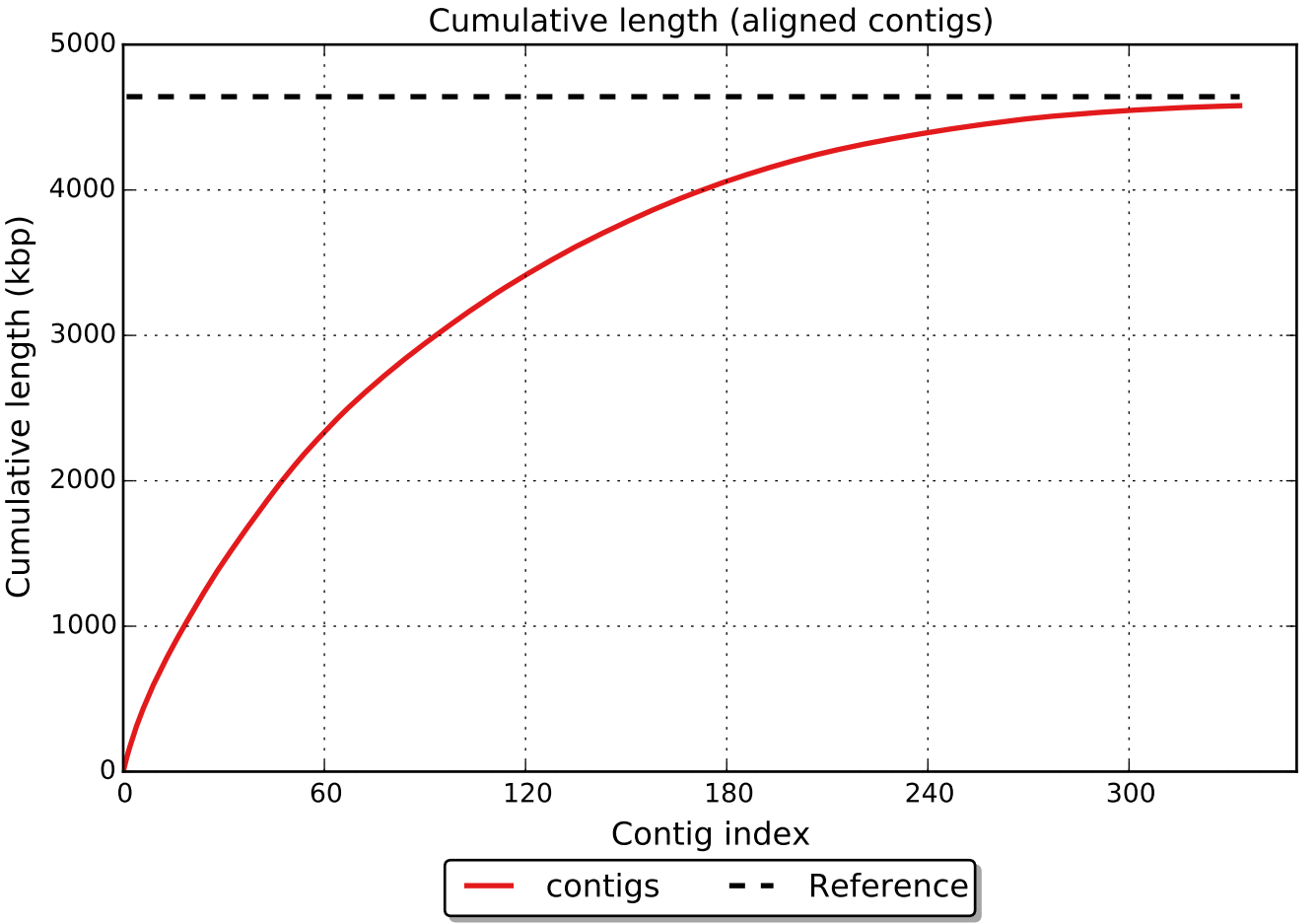

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
contigs

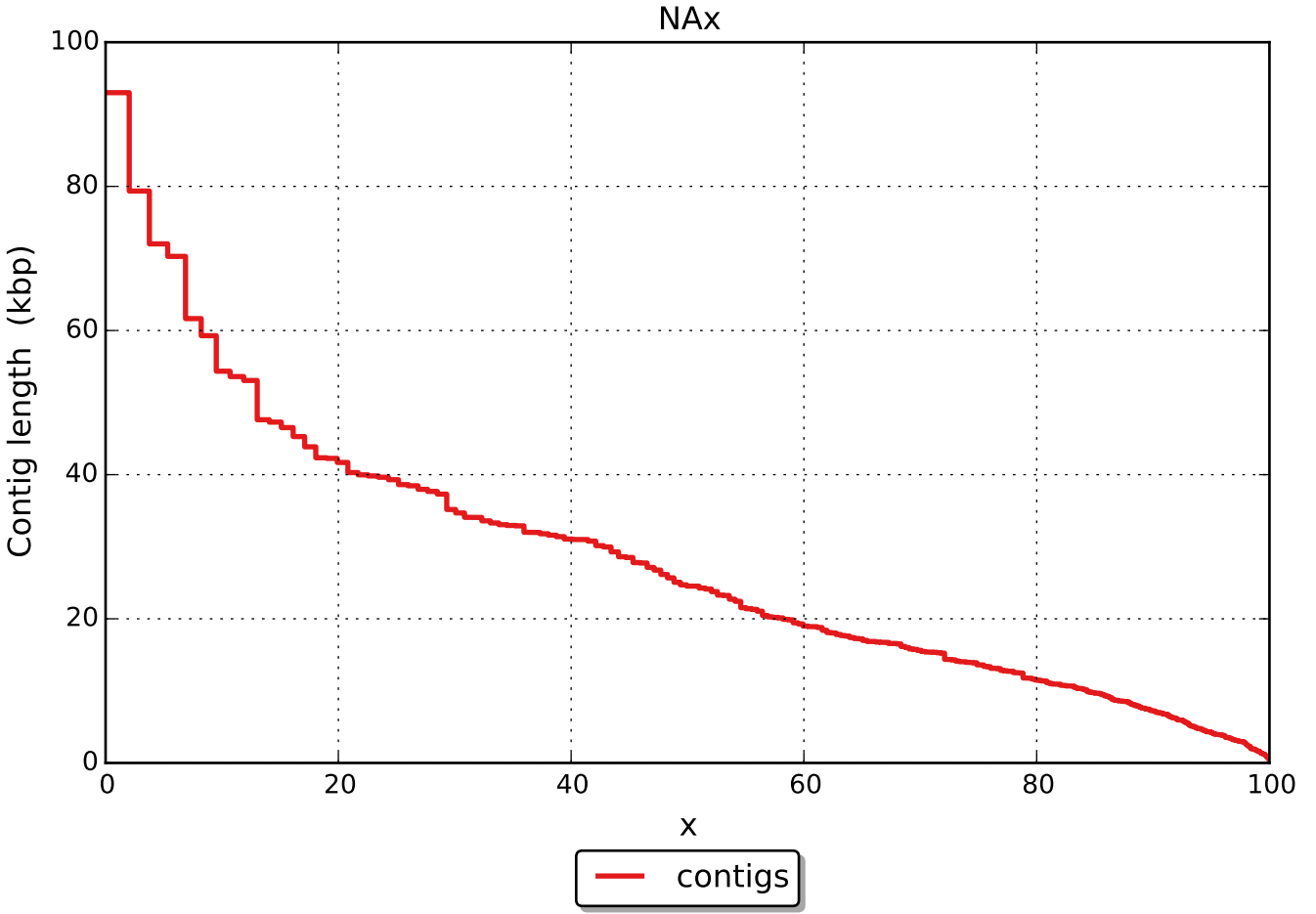

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
contigs

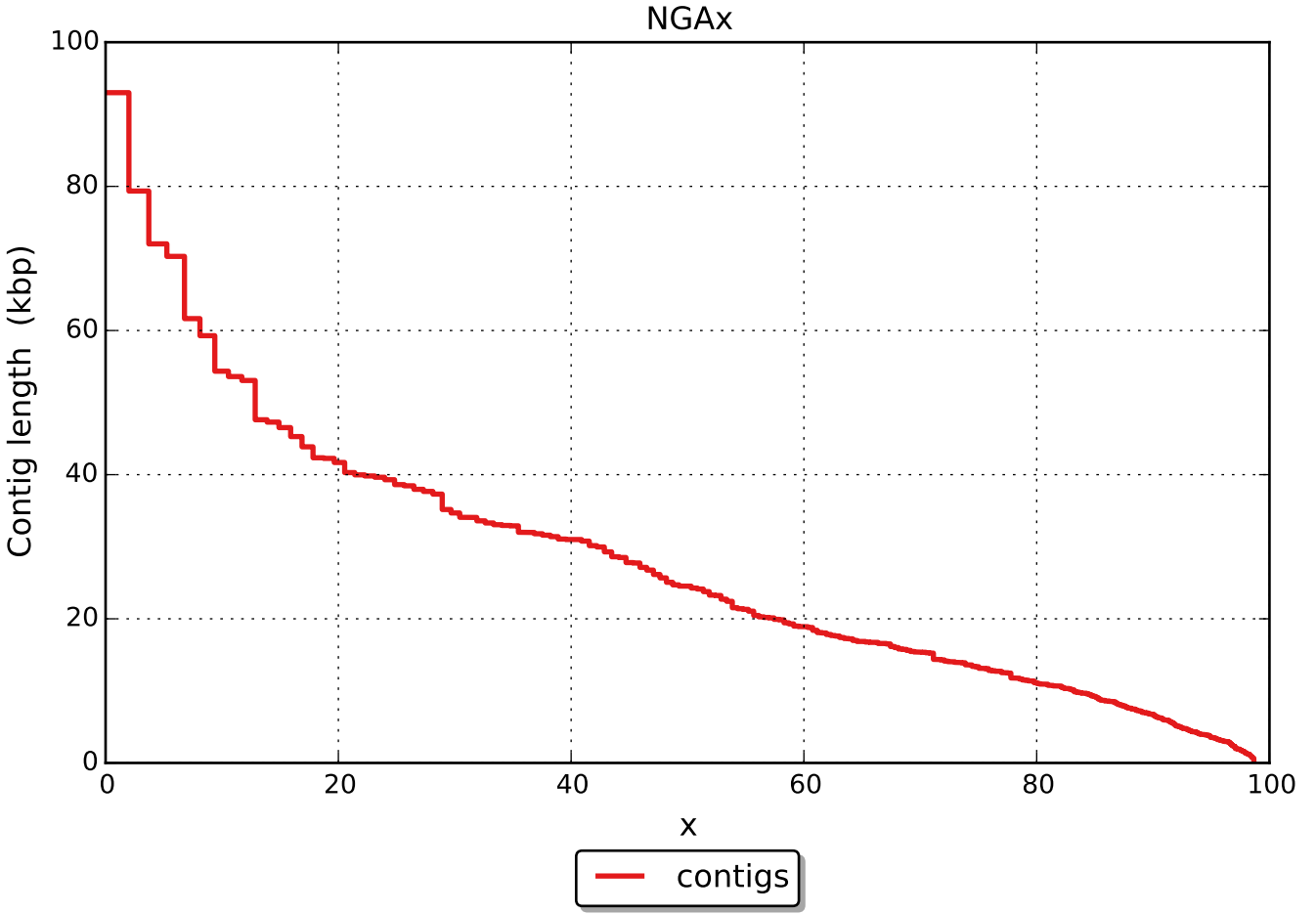

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
contigs
Reference


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


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


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