Report

	contigs
# contigs (>= 1000 bp)	306
# contigs (>= 5000 bp)	217
# contigs (>= 10000 bp)	140
# contigs (>= 25000 bp)	44
# contigs (>= 50000 bp)	10
Total length (>= 1000 bp)	4053805
Total length (>= 5000 bp)	3803326
Total length (>= 10000 bp)	3243086
Total length (>= 25000 bp)	1810803
Total length (>= 50000 bp)	648317
# contigs	324
Largest contig	108881
Total length	4065644
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	21370
NG50	17466
N75	11412
NG75	7929
L50	54
LG50	69
L75	123
LG75	167
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.642
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	906.44
# indels per 100 kbp	0.46
Largest alignment	108881
NA50	20324
NGA50	17103
NA75	11412
NGA75	7899
LA50	56
LGA50	71
LA75	125
LGA75	170

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

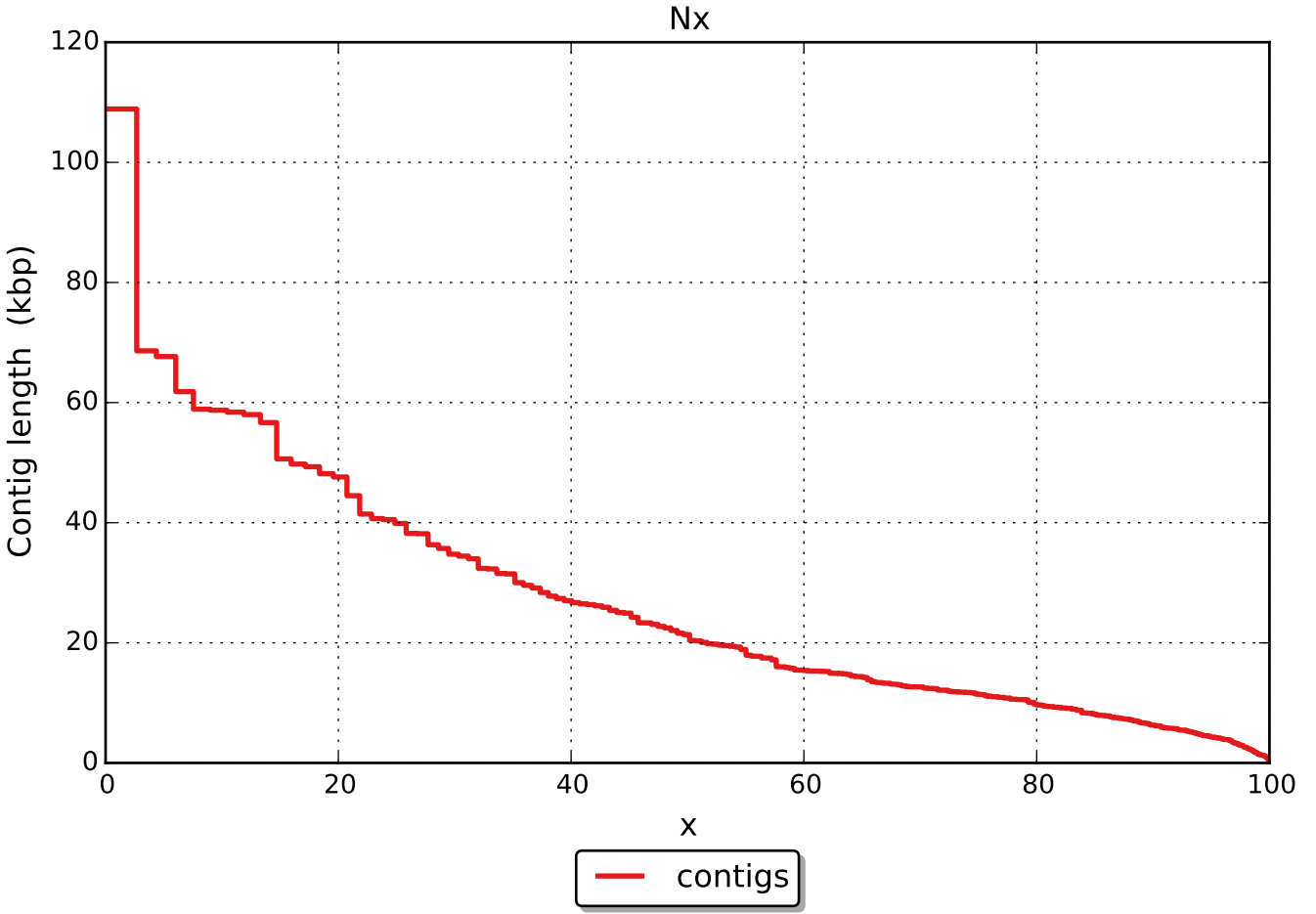
	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	122783
# local misassemblies	2
# mismatches	35612
# indels	18
# short indels	18
# long indels	0
Indels length	24

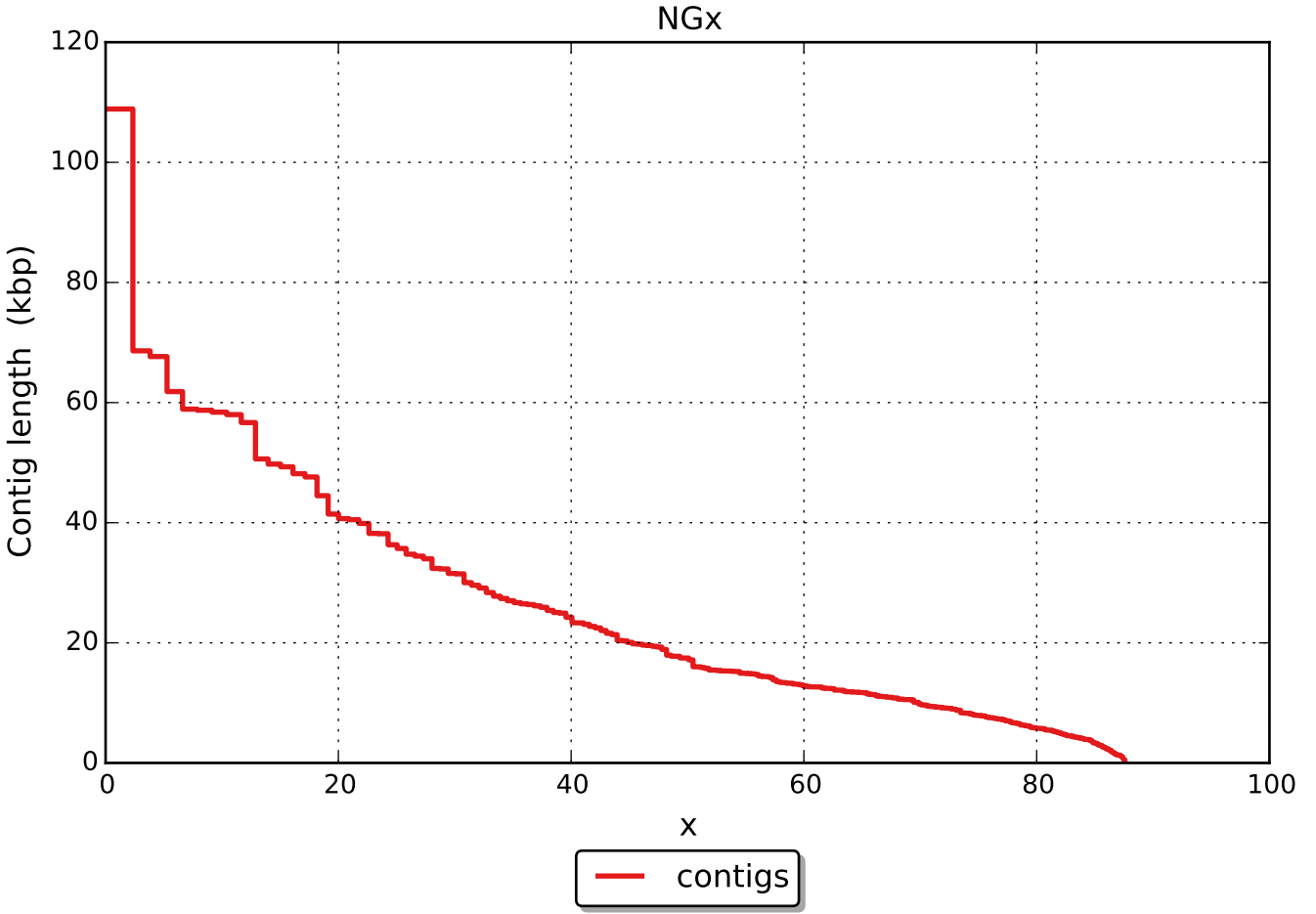
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

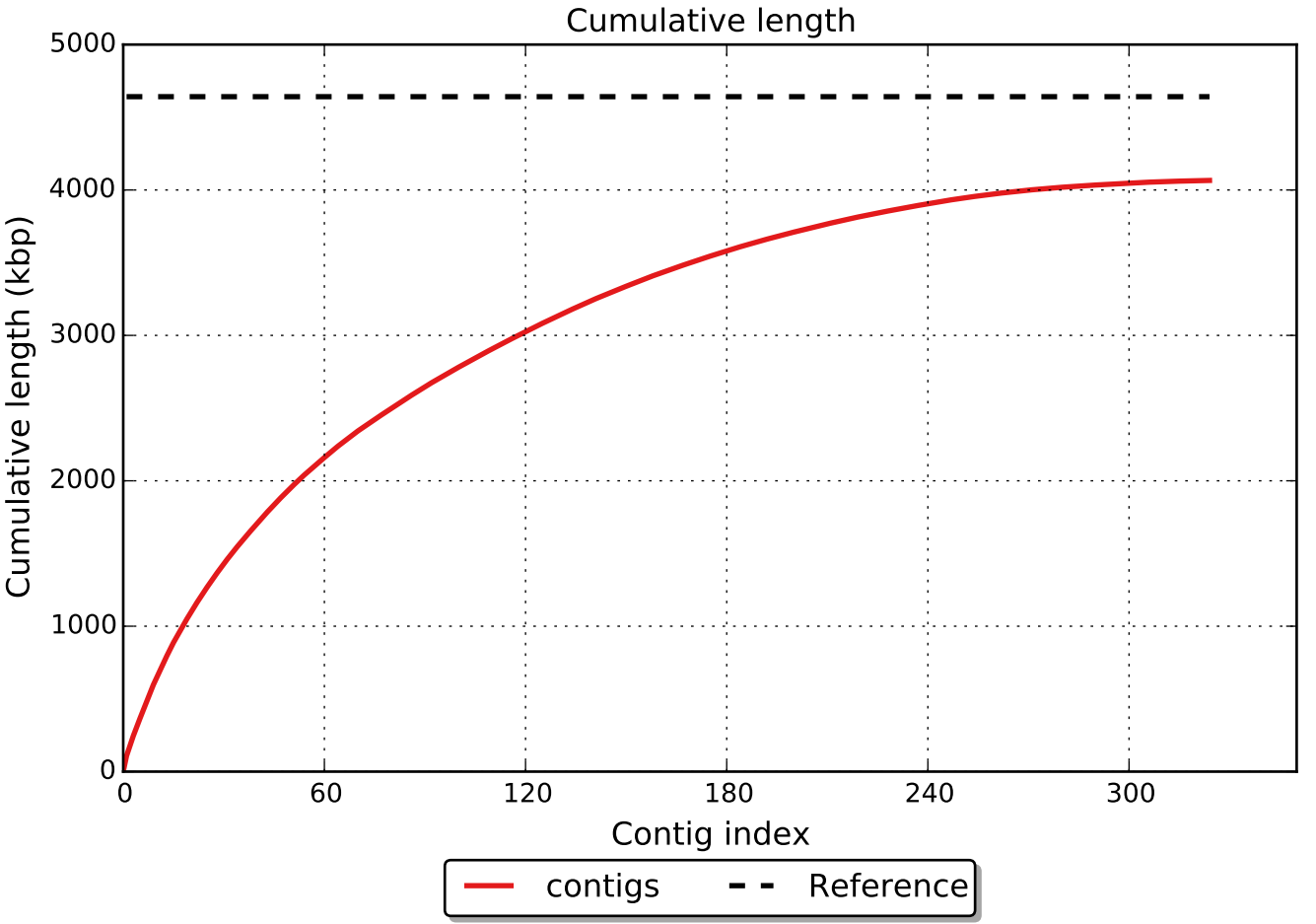
Unaligned report

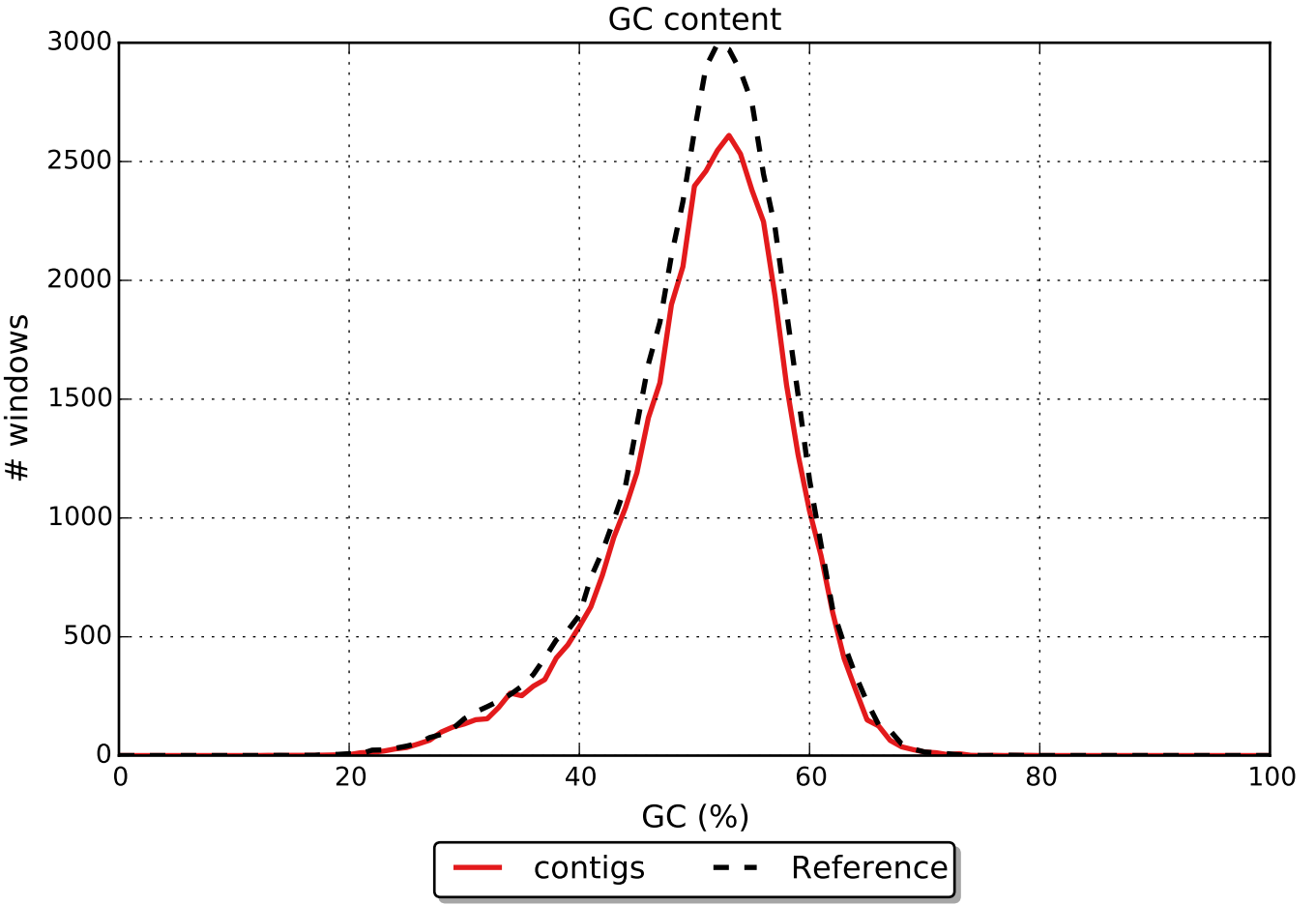
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

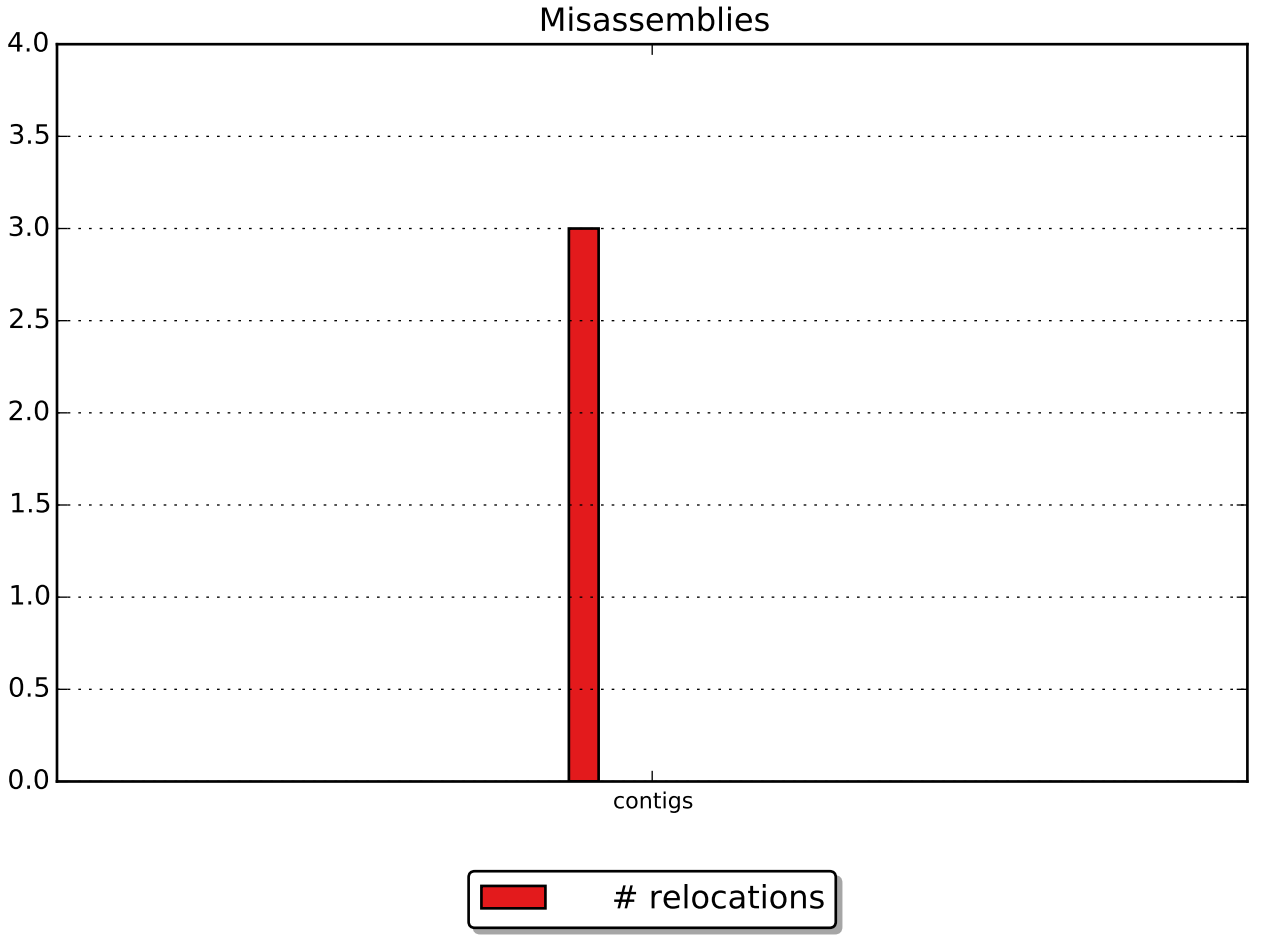
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

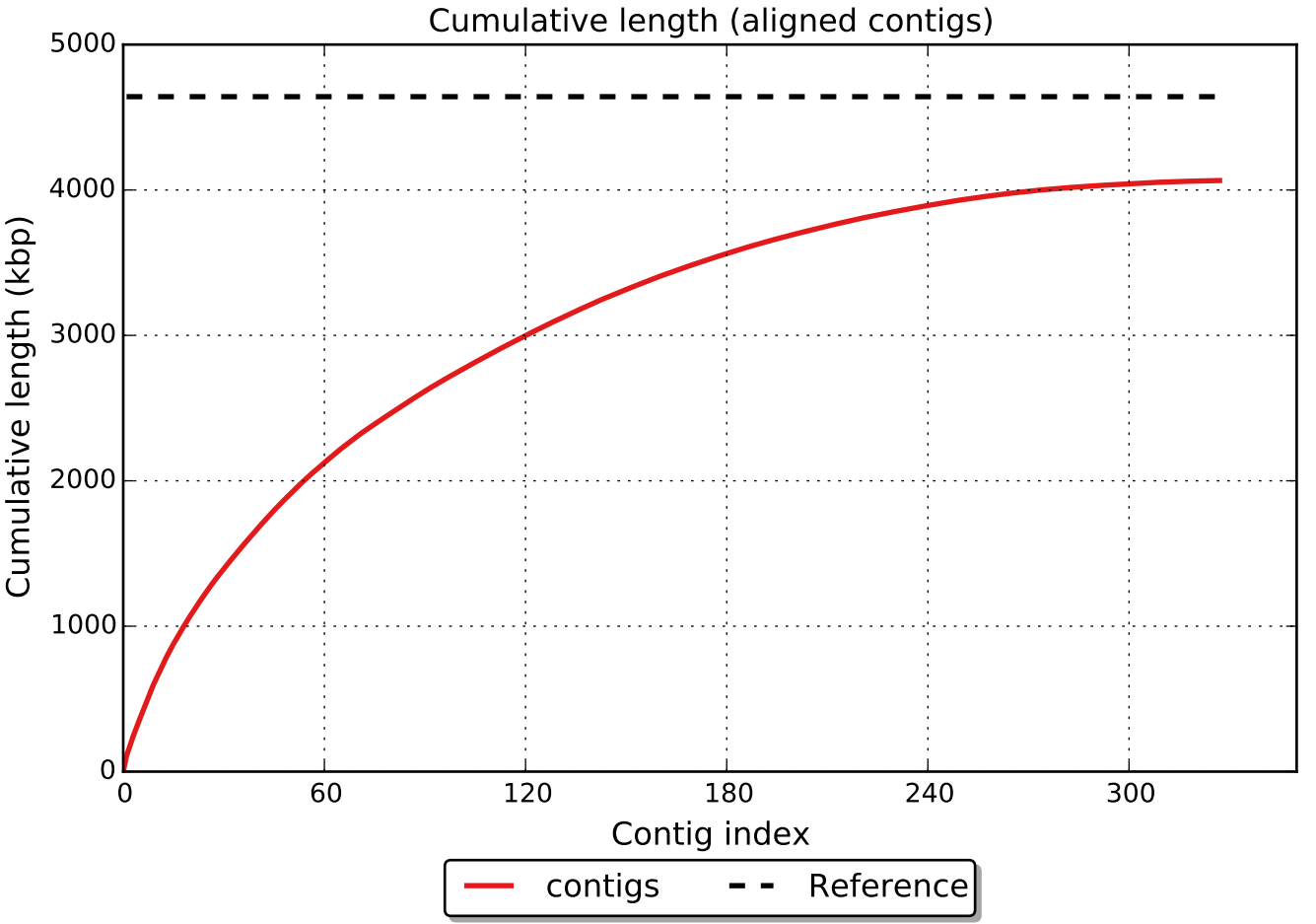

Nx
120
100
80
60
40
20
0
Contig length (kbp)
0
20
40
60
80
100
x
contigs

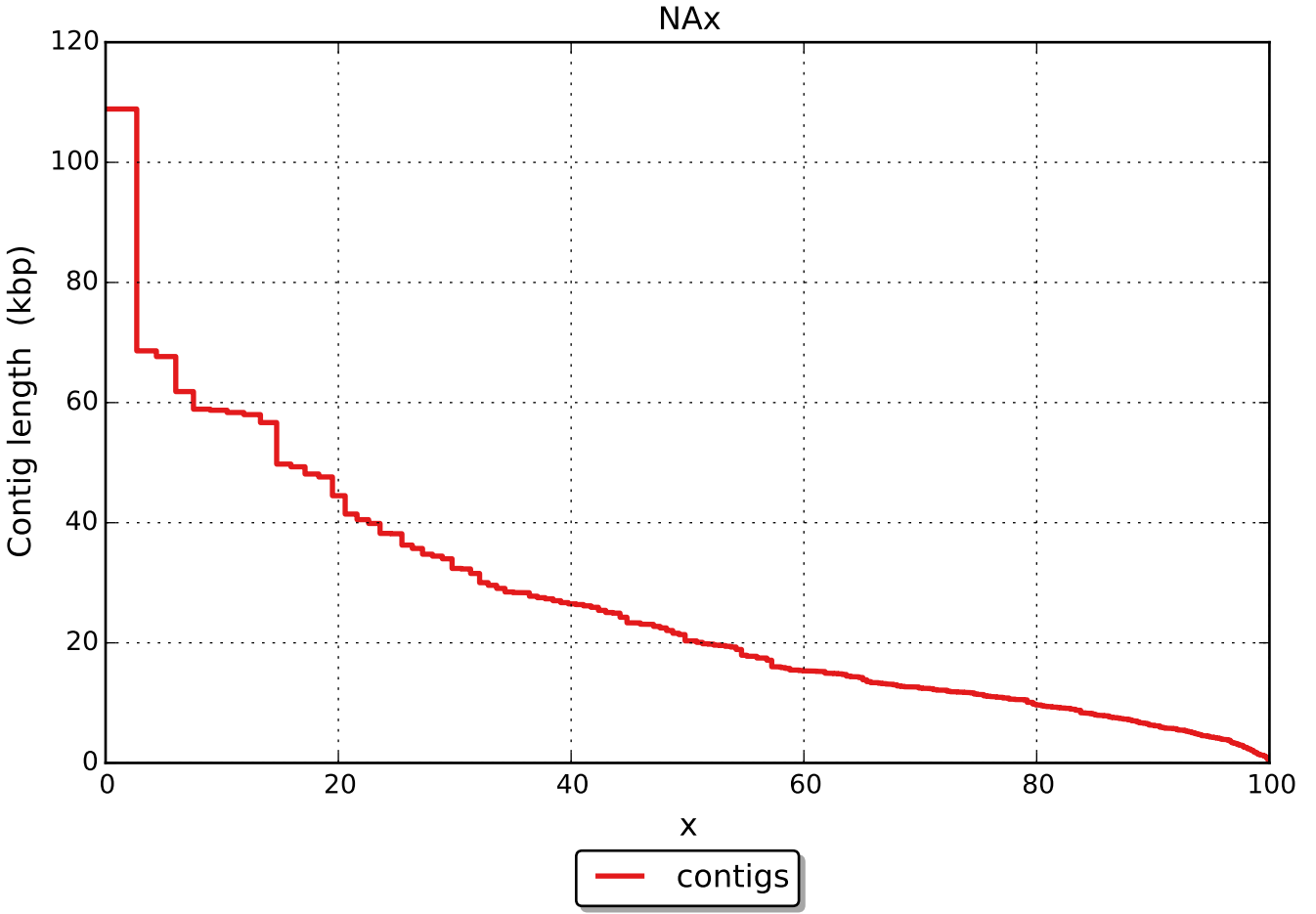

NGx
Contig length (kbp)
120
100
80
60
40
20
0
0
20
40
60
80
100
x
contigs

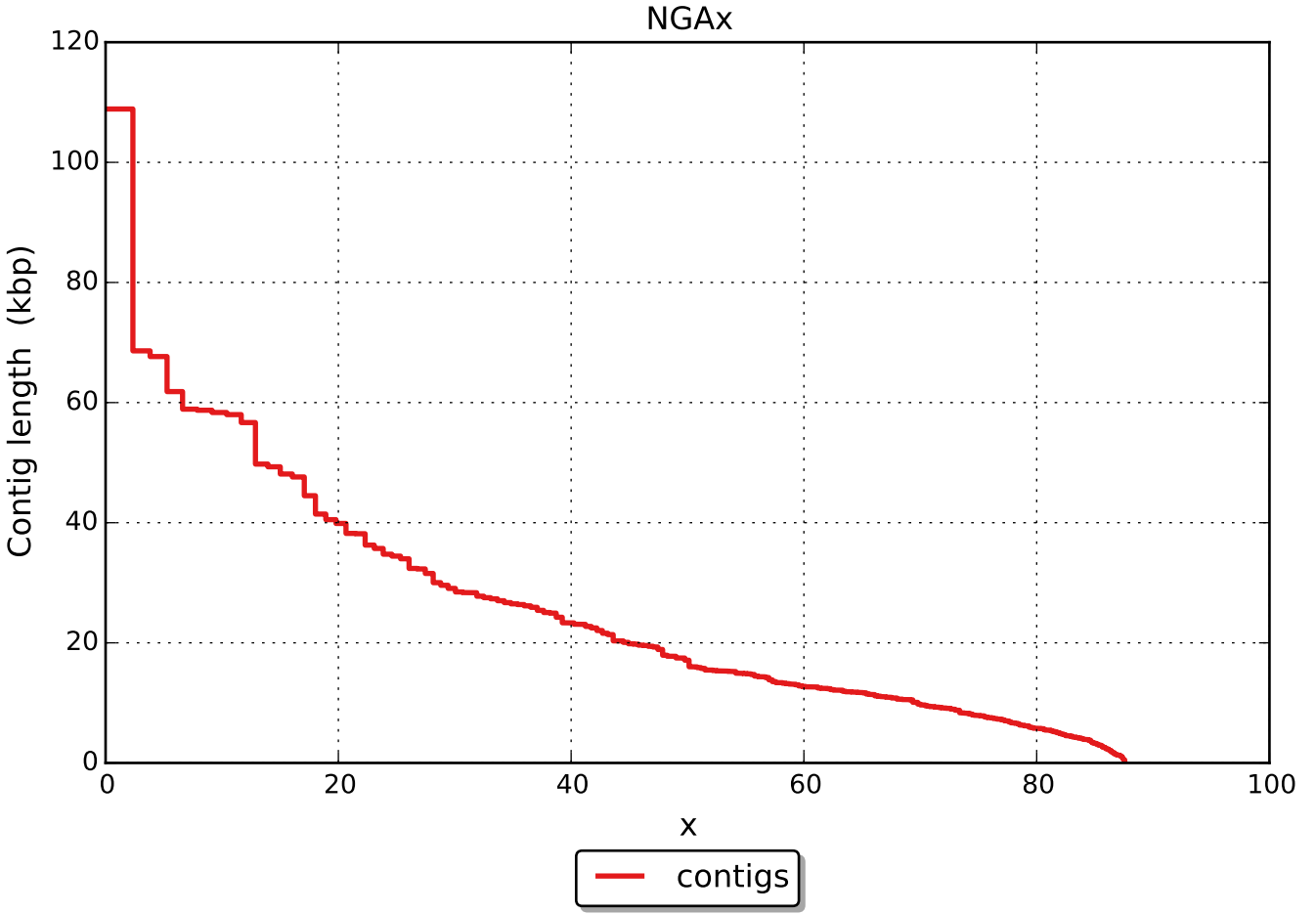

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
contigs
Reference


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


Misassemblies
4.0
3.5
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
60
120
180
240
300
Contig index
contigs
Reference


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


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