Report

	contigs
# contigs (>= 0 bp)	5756
# contigs (>= 1000 bp)	814
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3588841
Total length (>= 1000 bp)	1169703
Total length (>= 5000 bp)	5900
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2825
Largest contig	5900
Total length	2576835
Reference length	4641652
GC (%)	50.86
Reference GC (%)	50.79
N50	947
NG50	574
N75	697
L50	937
LG50	2347
L75	1733
# misassemblies	54
# misassembled contigs	53
Misassembled contigs length	82247
# local misassemblies	6
# unaligned contigs	4 + 7 part
Unaligned length	5952
Genome fraction (%)	55.326
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.25
# indels per 100 kbp	1.75
Largest alignment	5583
NA50	932
NGA50	568
NA75	685
LA50	957
LGA50	2387
LA75	1764

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

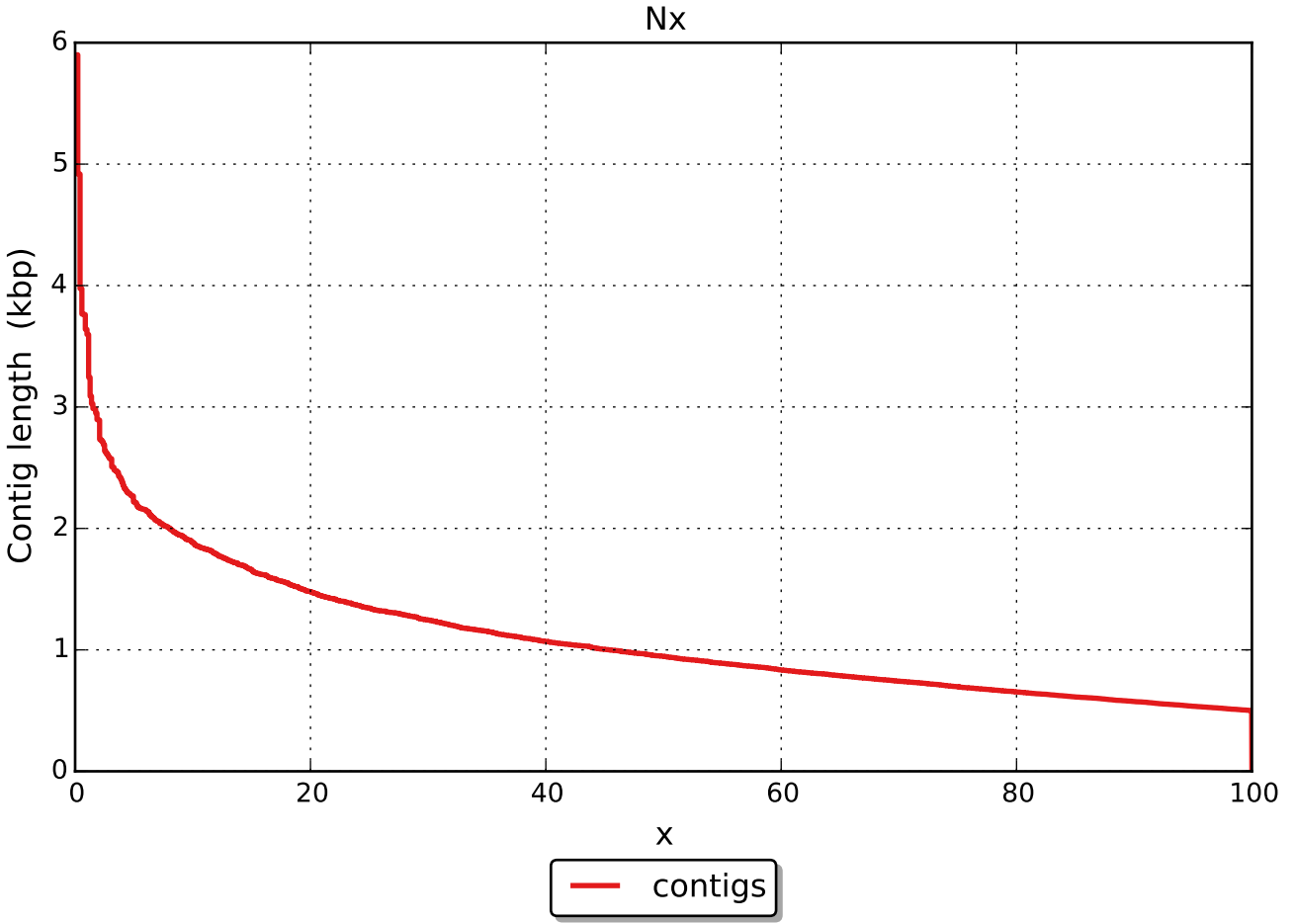
	contigs
# misassemblies	54
# relocations	54
# translocations	0
# inversions	0
# misassembled contigs	53
Misassembled contigs length	82247
# local misassemblies	6
# mismatches	597
# indels	45
# short indels	45
# long indels	0
Indels length	60

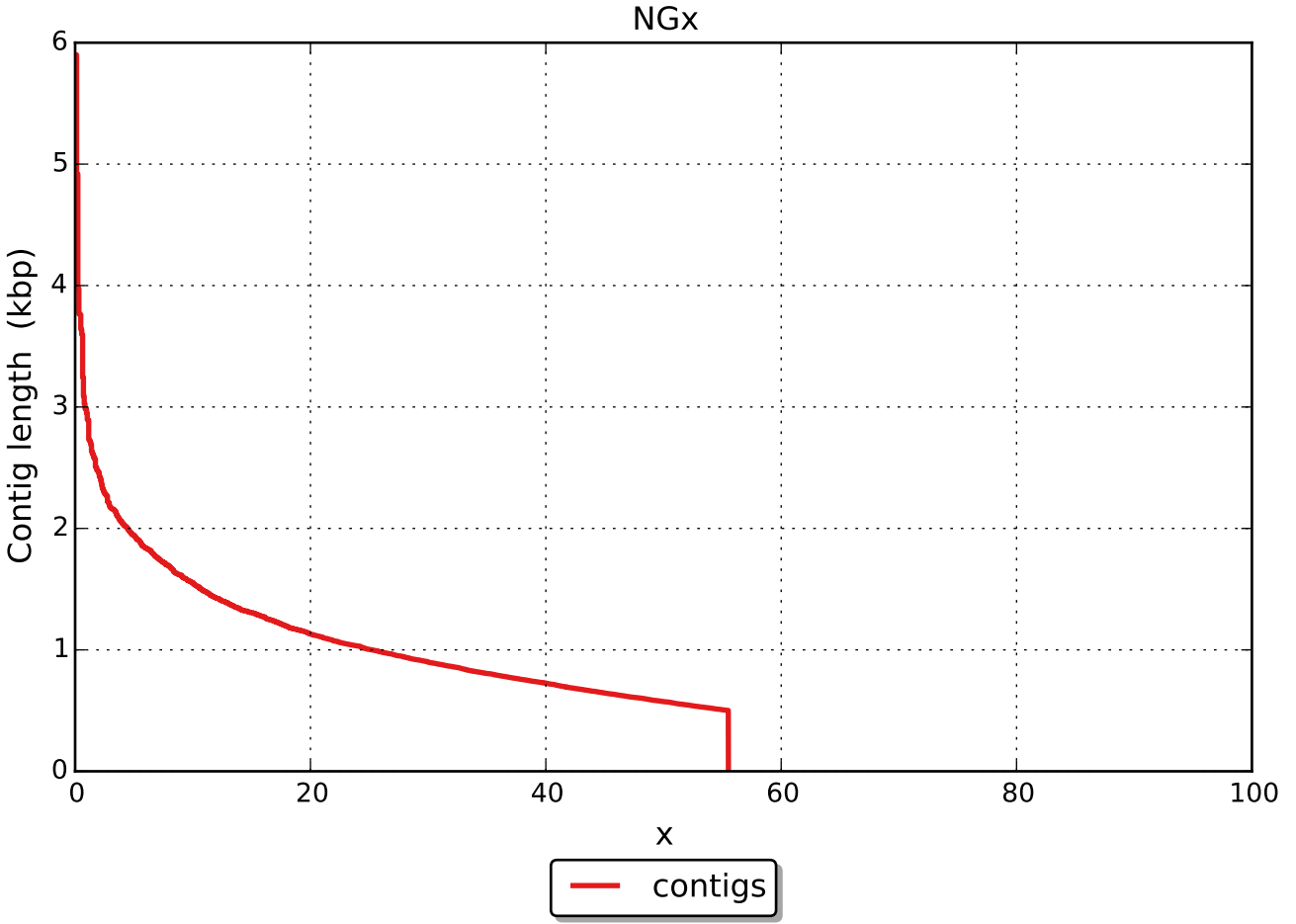
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

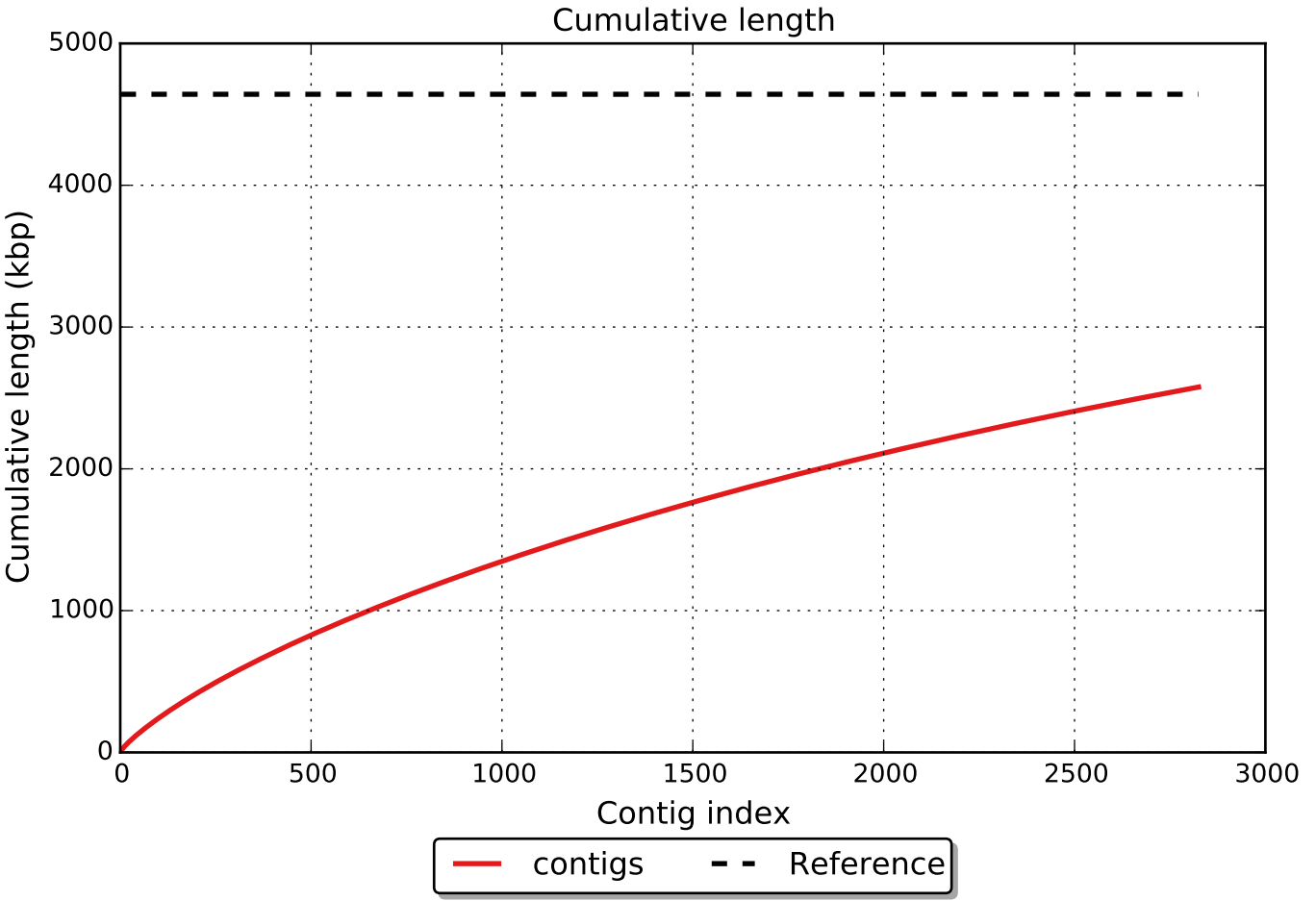
Unaligned report

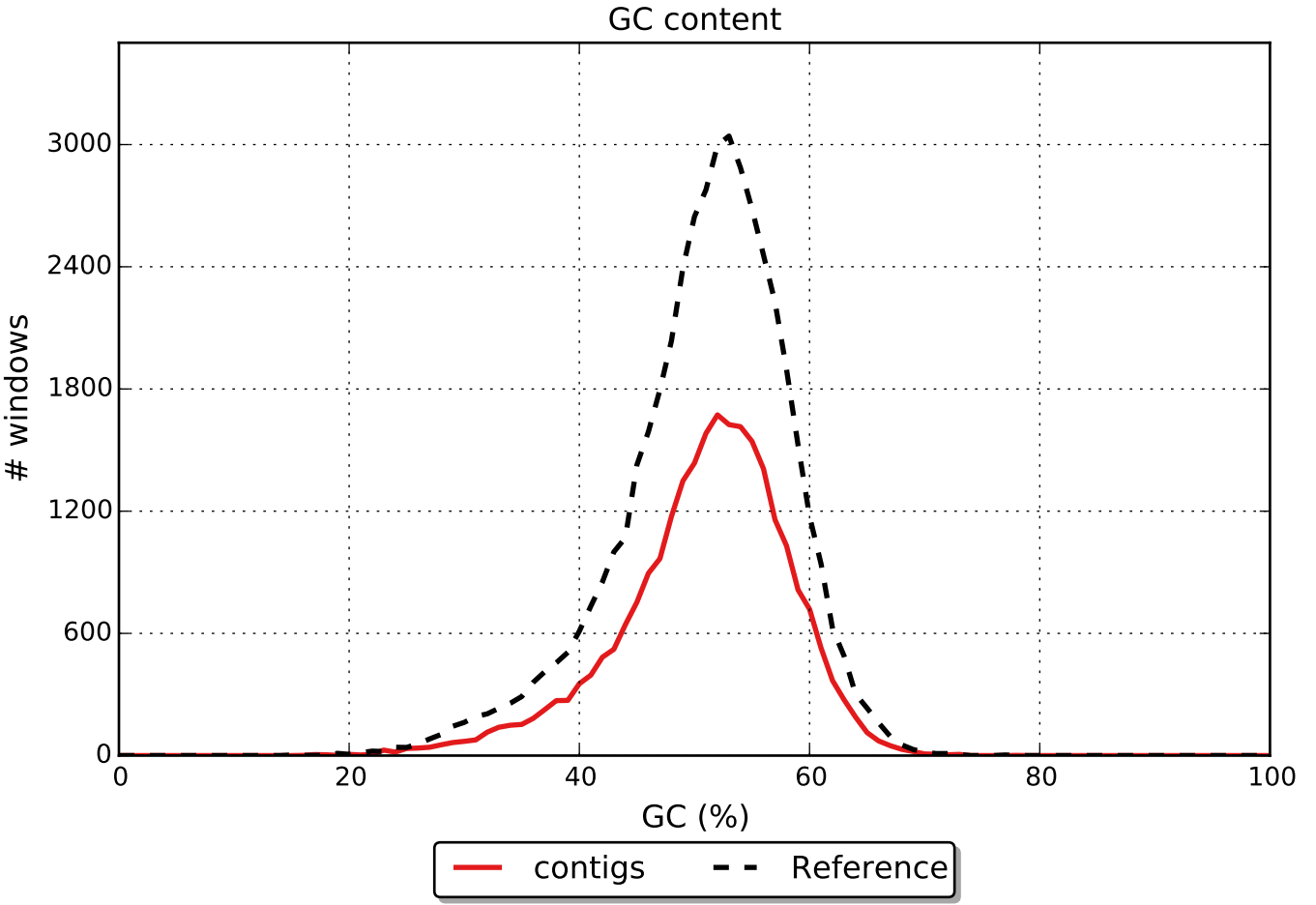
	contigs
# fully unaligned contigs	4
Fully unaligned length	4225
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1727
# N's	0

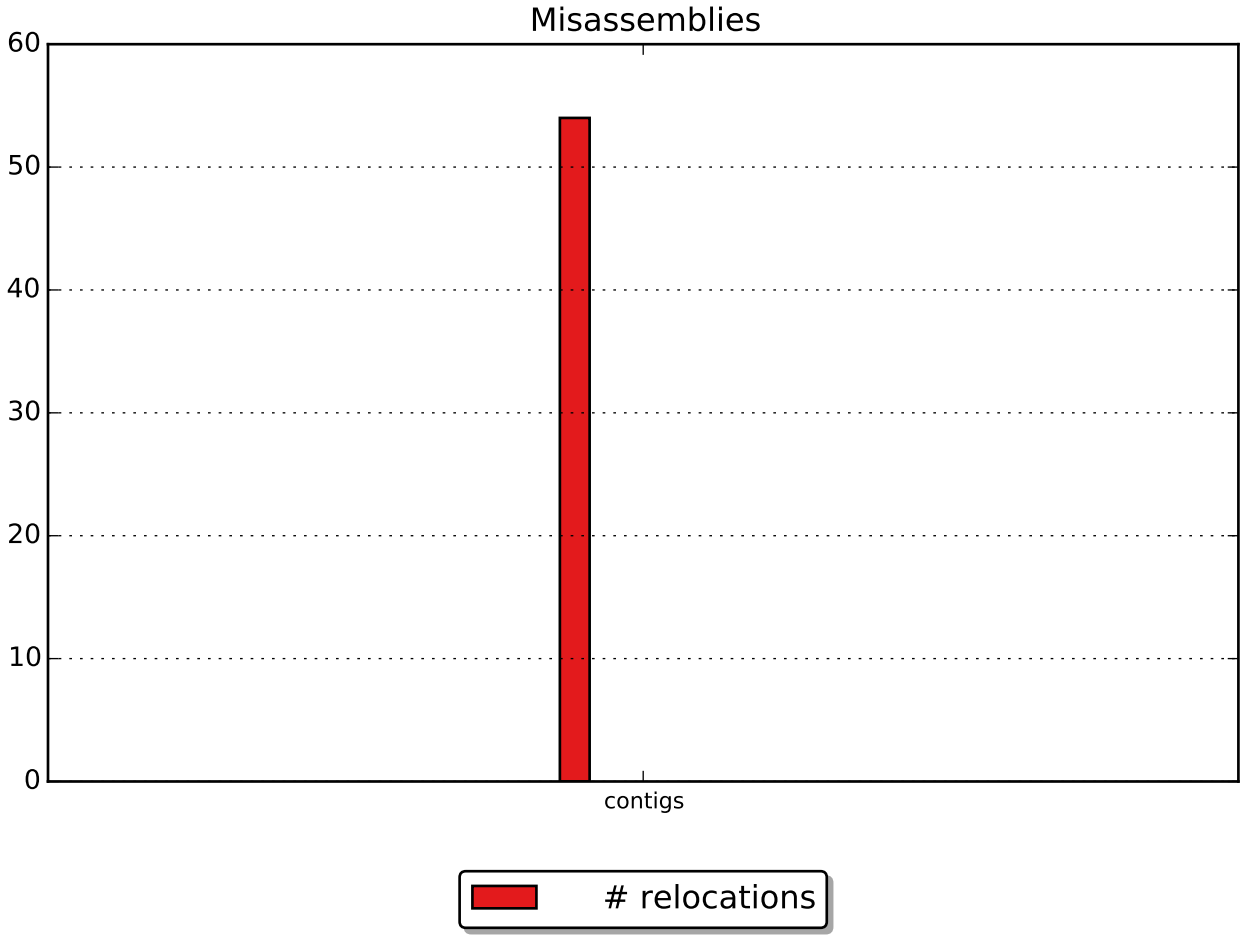
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

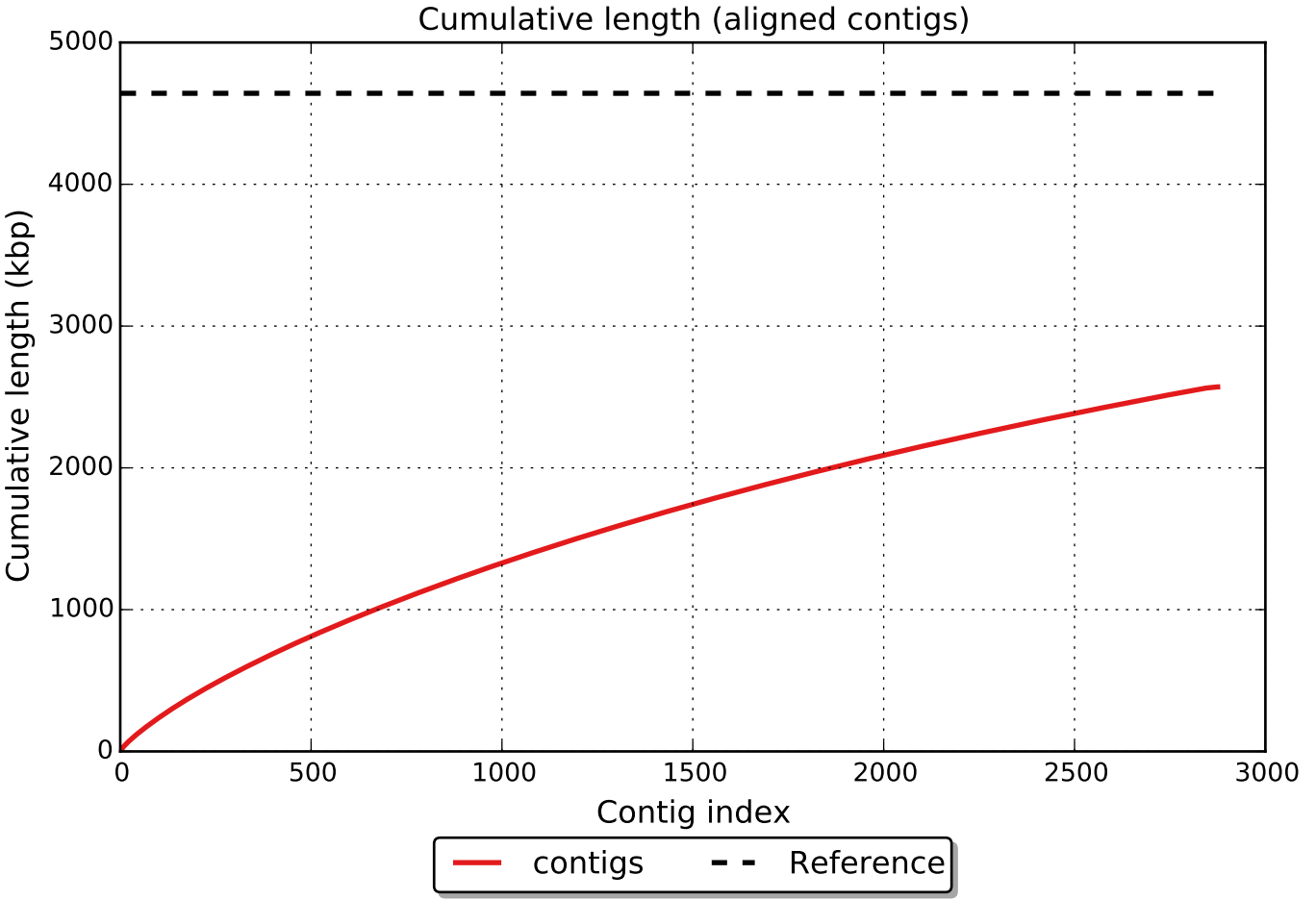

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs

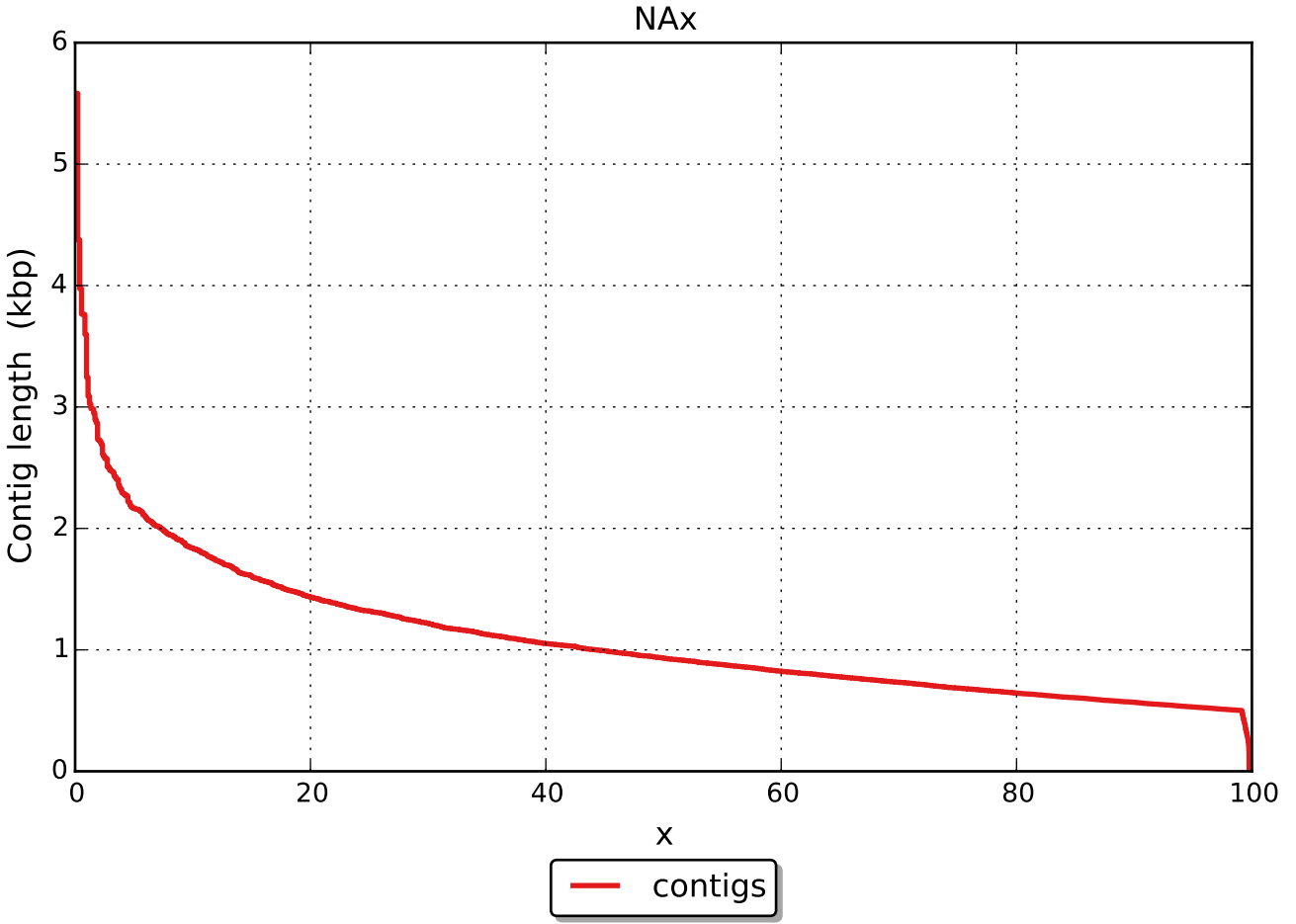

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs

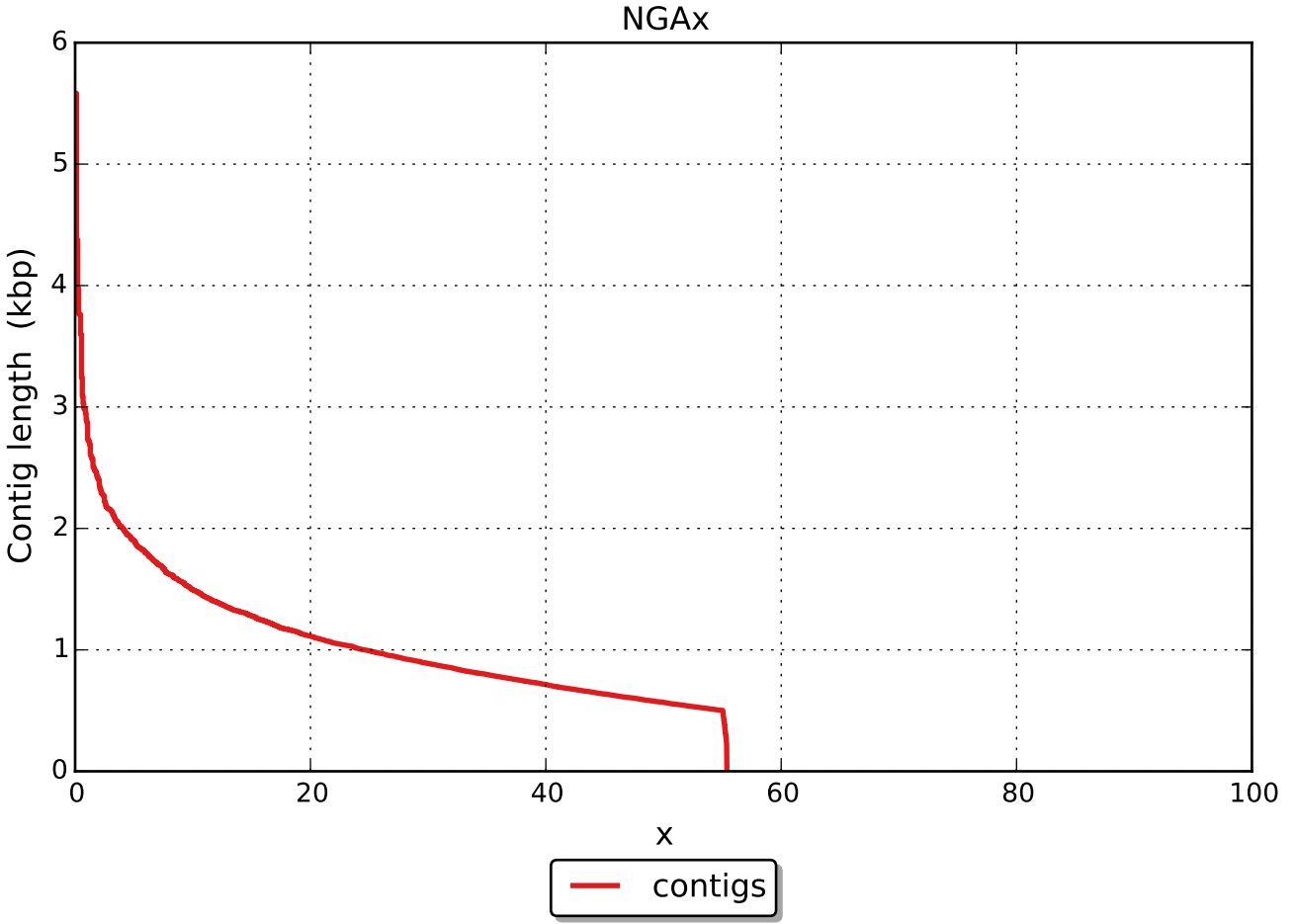

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
contigs
Reference


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


Misassemblies
60
50
40
30
20
10
0
contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
contigs