Report

	final.contigs
# contigs (>= 1000 bp)	1125
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1592403
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4025
Largest contig	4336
Total length	3617036
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	929
NG50	787
N75	688
NG75	529
L50	1350
LG50	1952
L75	2485
LG75	3762
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 7 part
Unaligned length	750
Genome fraction (%)	73.718
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	184.88
# indels per 100 kbp	0.06
Largest alignment	4336
NA50	929
NGA50	786
NA75	687
NGA75	529
LA50	1350
LGA50	1952
LA75	2486
LGA75	3763

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

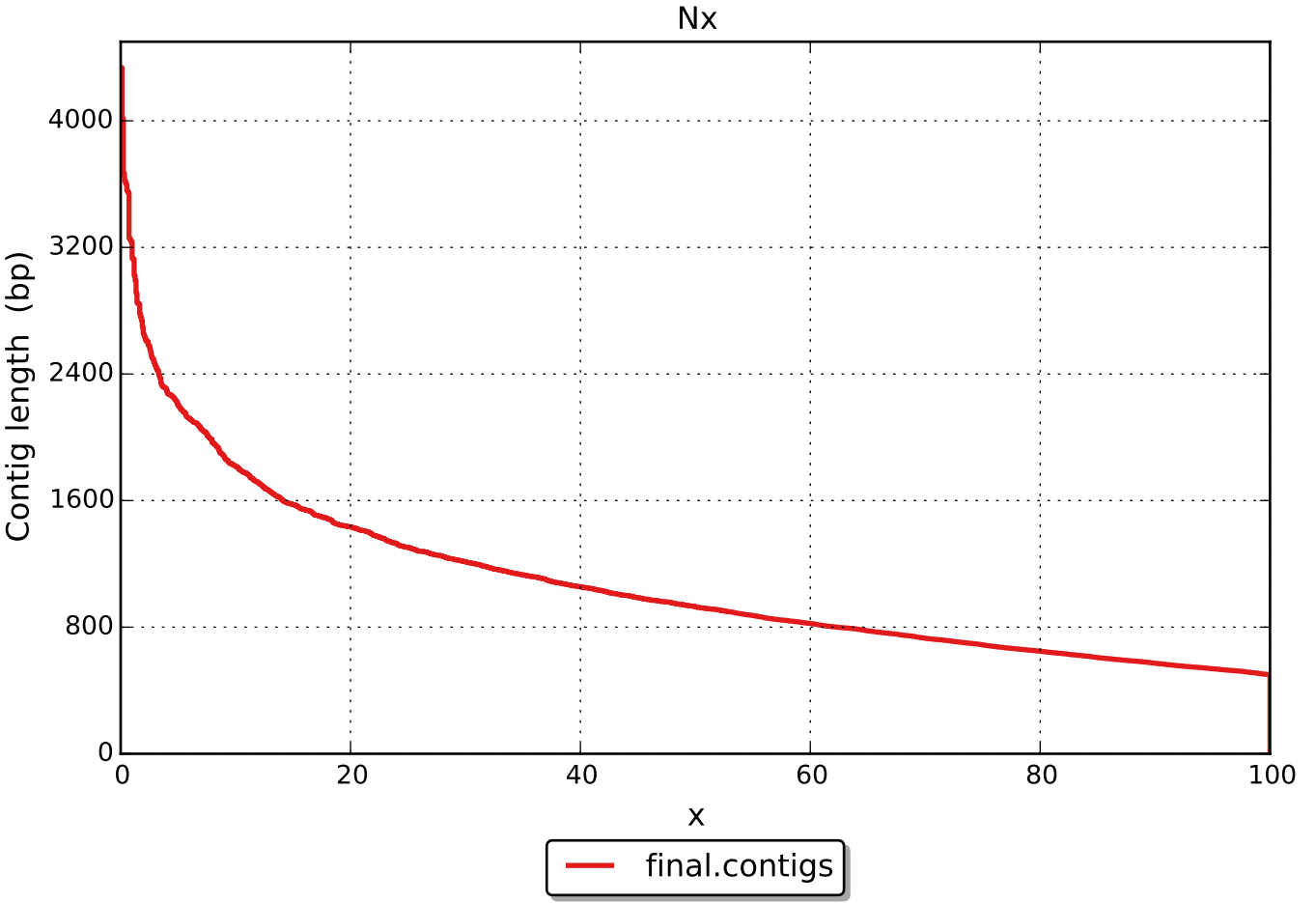
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	6326
# indels	2
# short indels	2
# long indels	0
Indels length	2

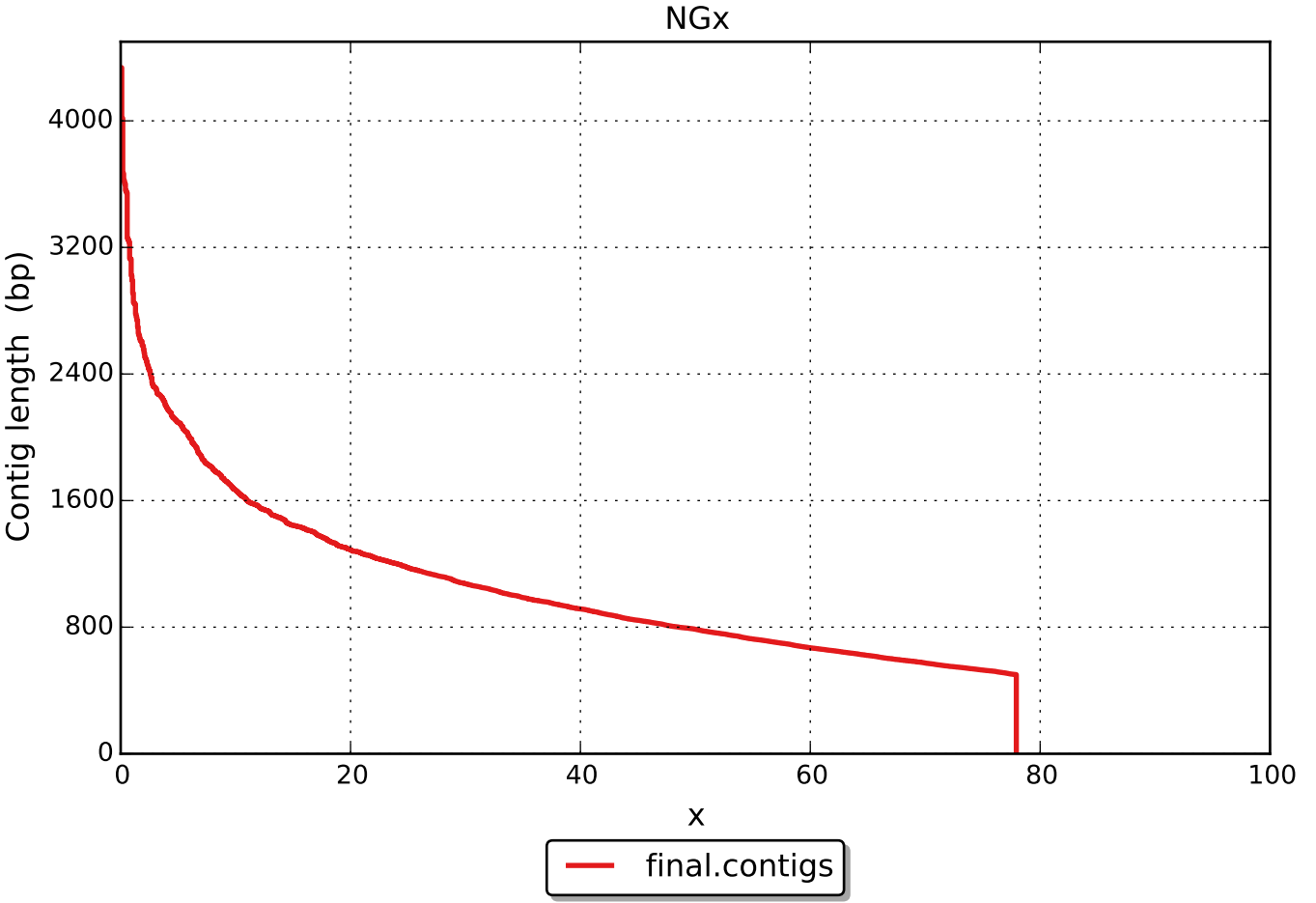
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

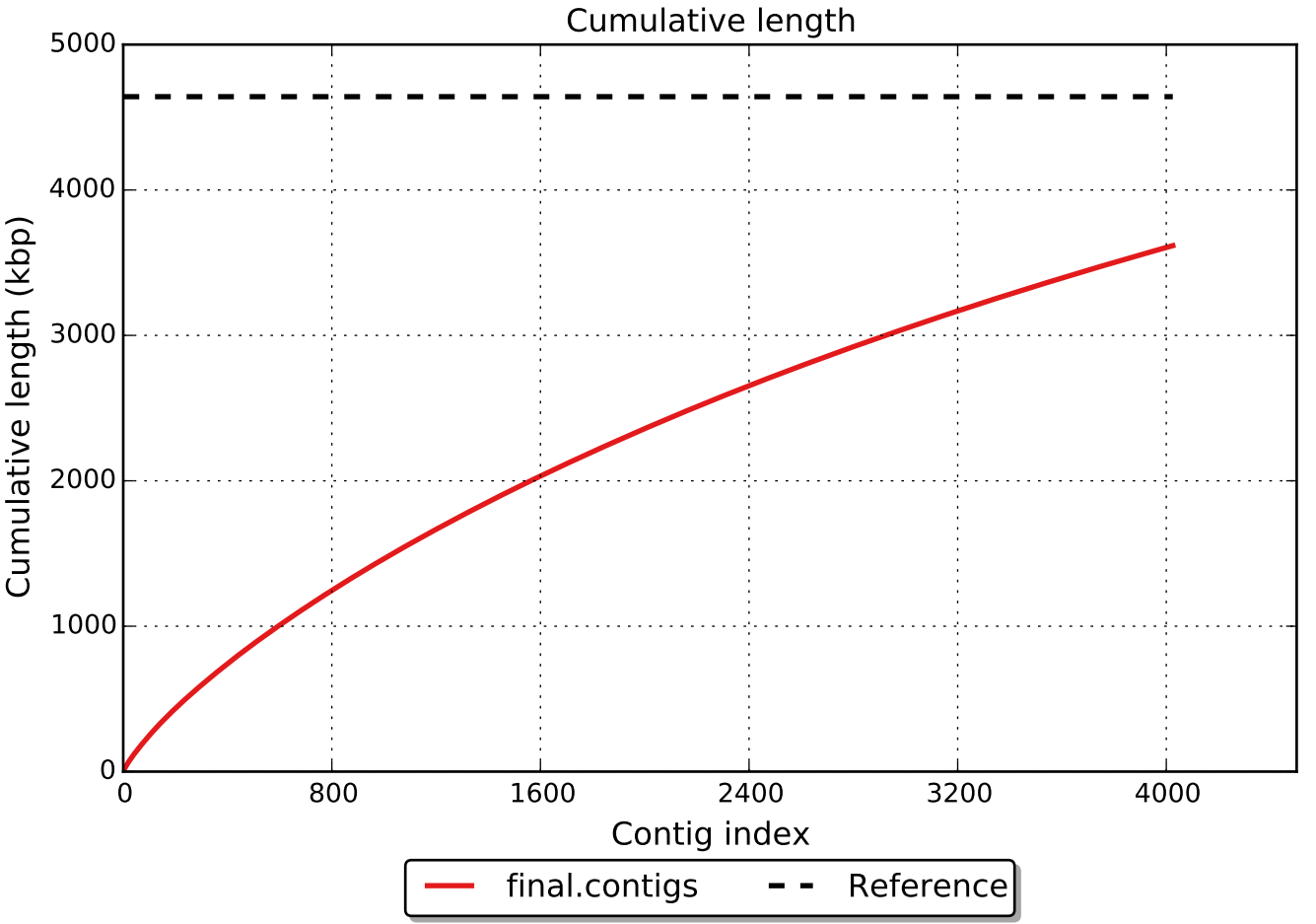
Unaligned report

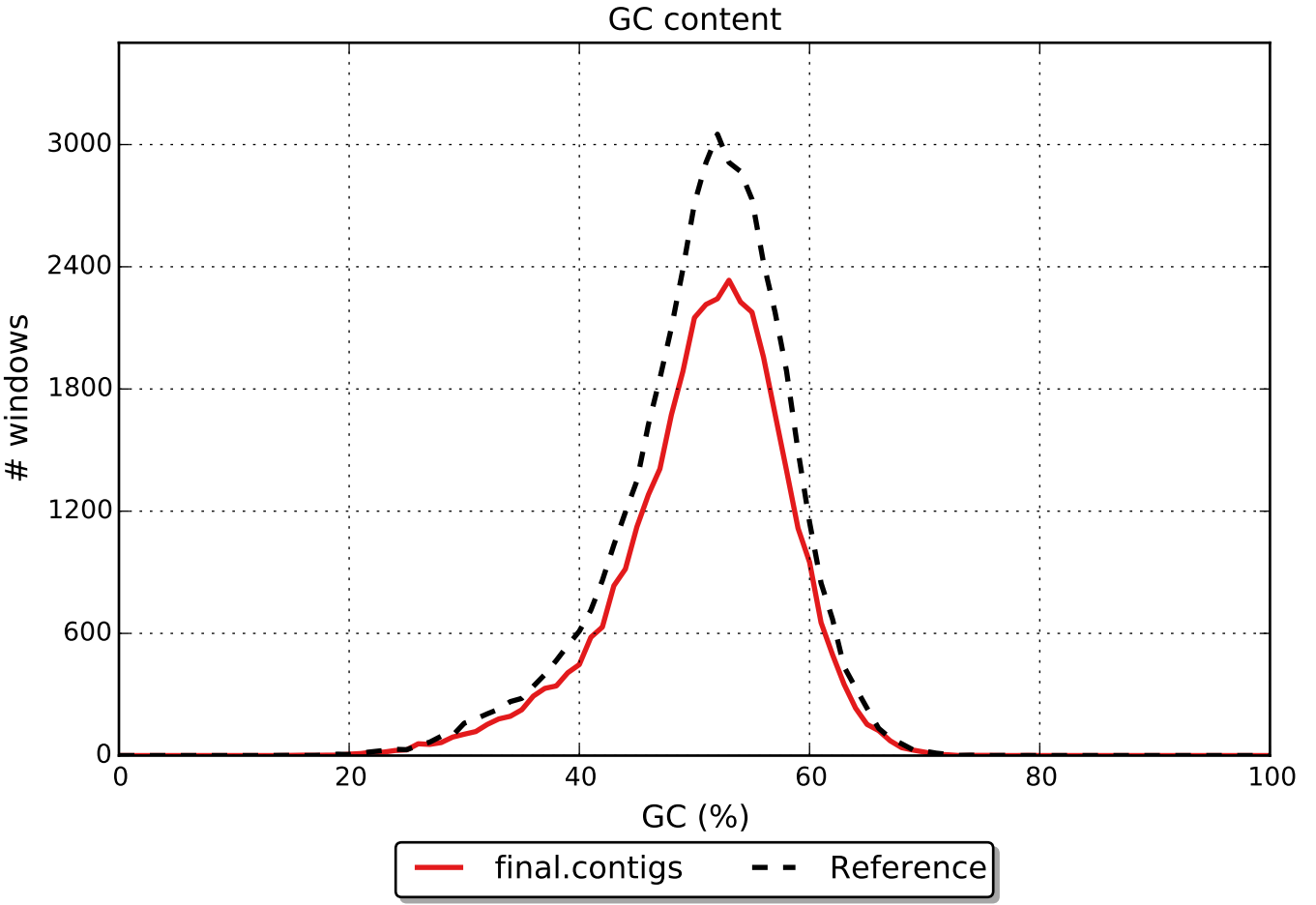
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	750
# N's	0

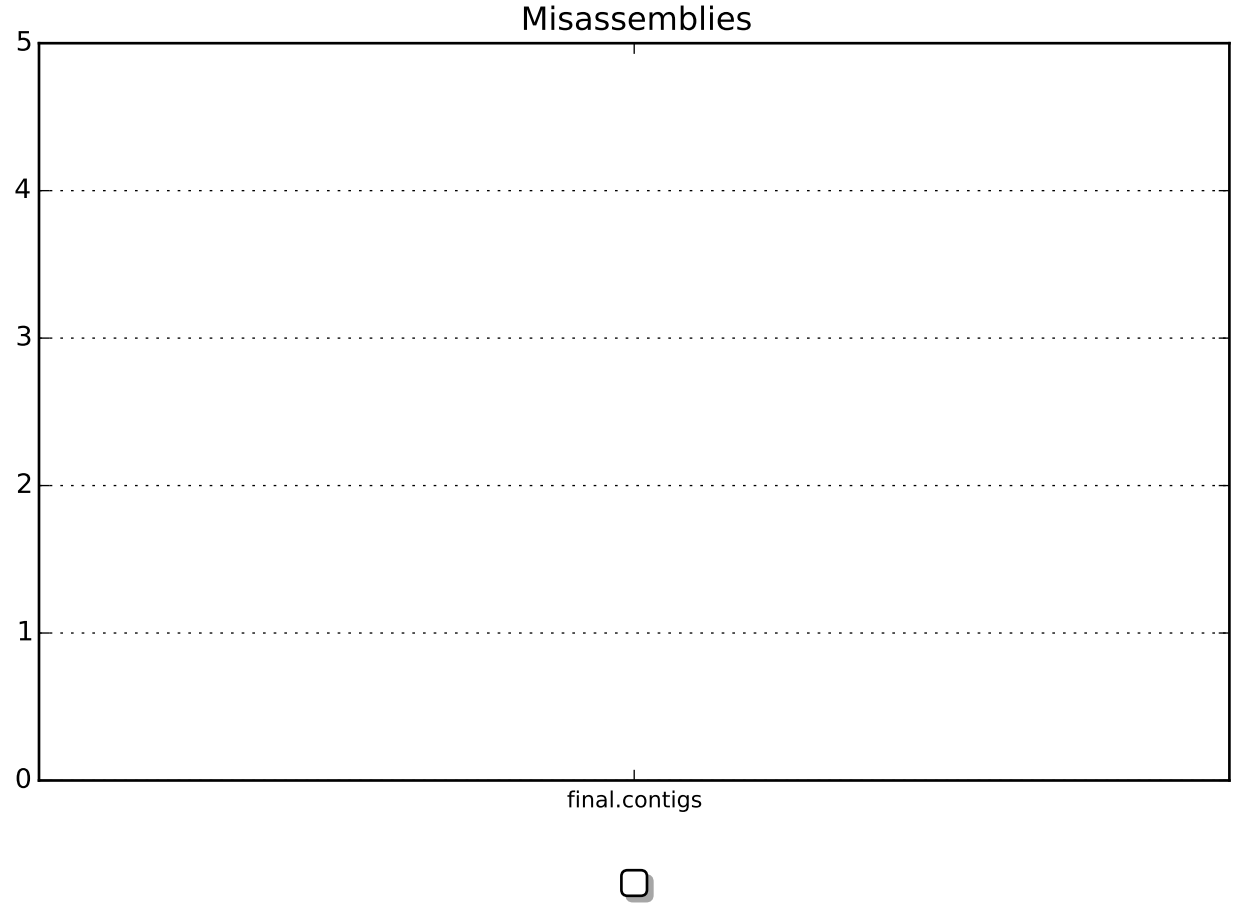
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

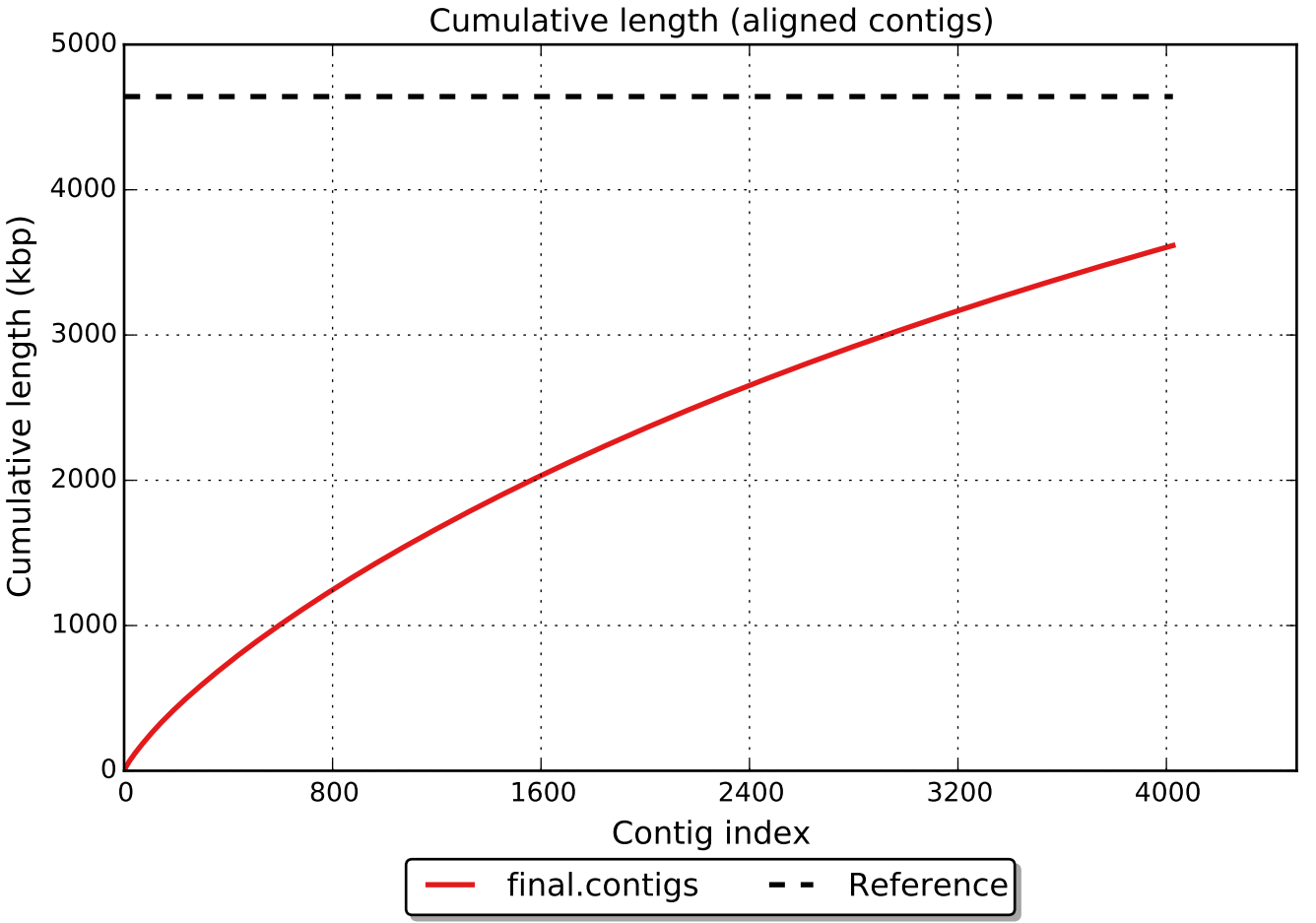

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

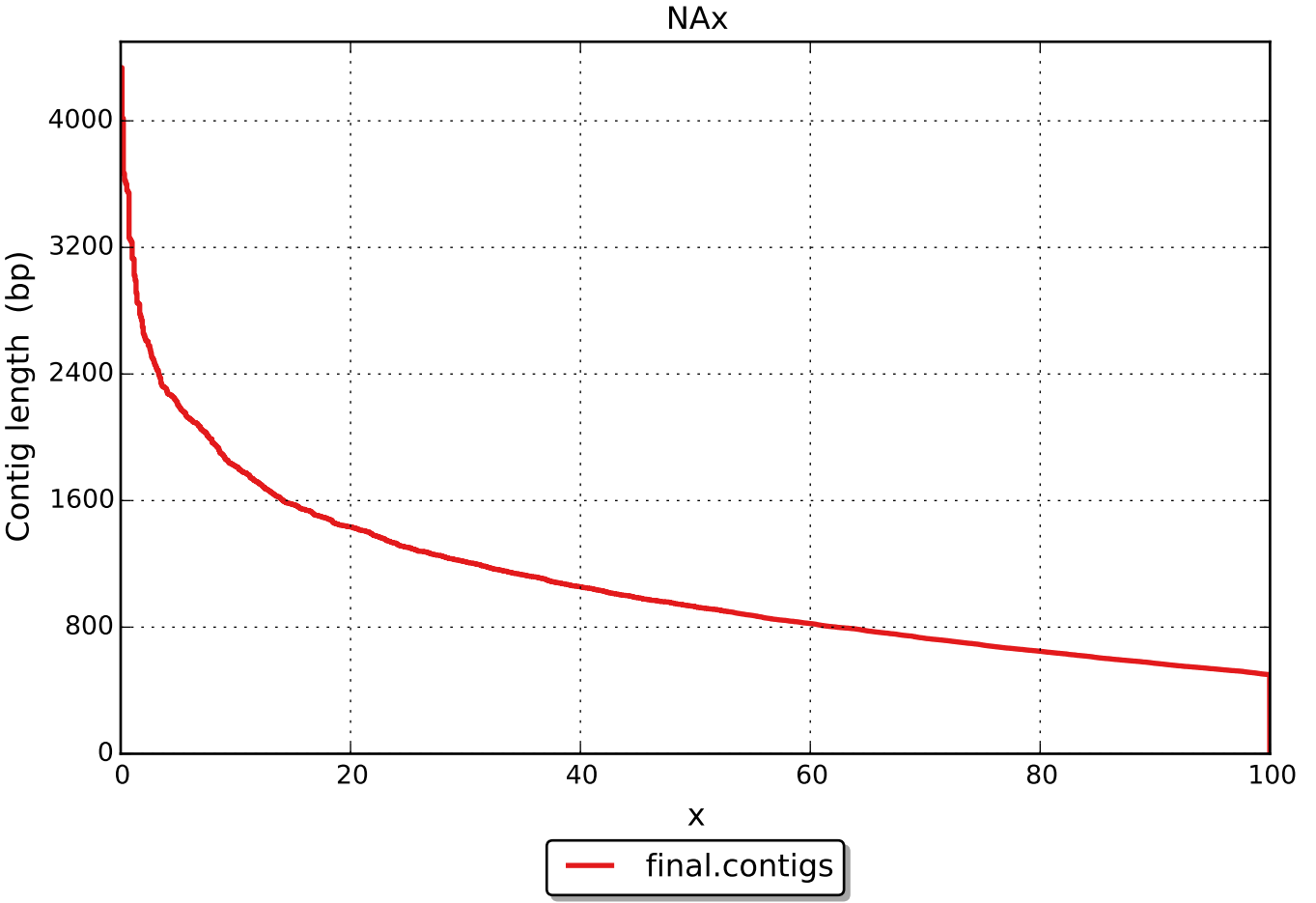

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

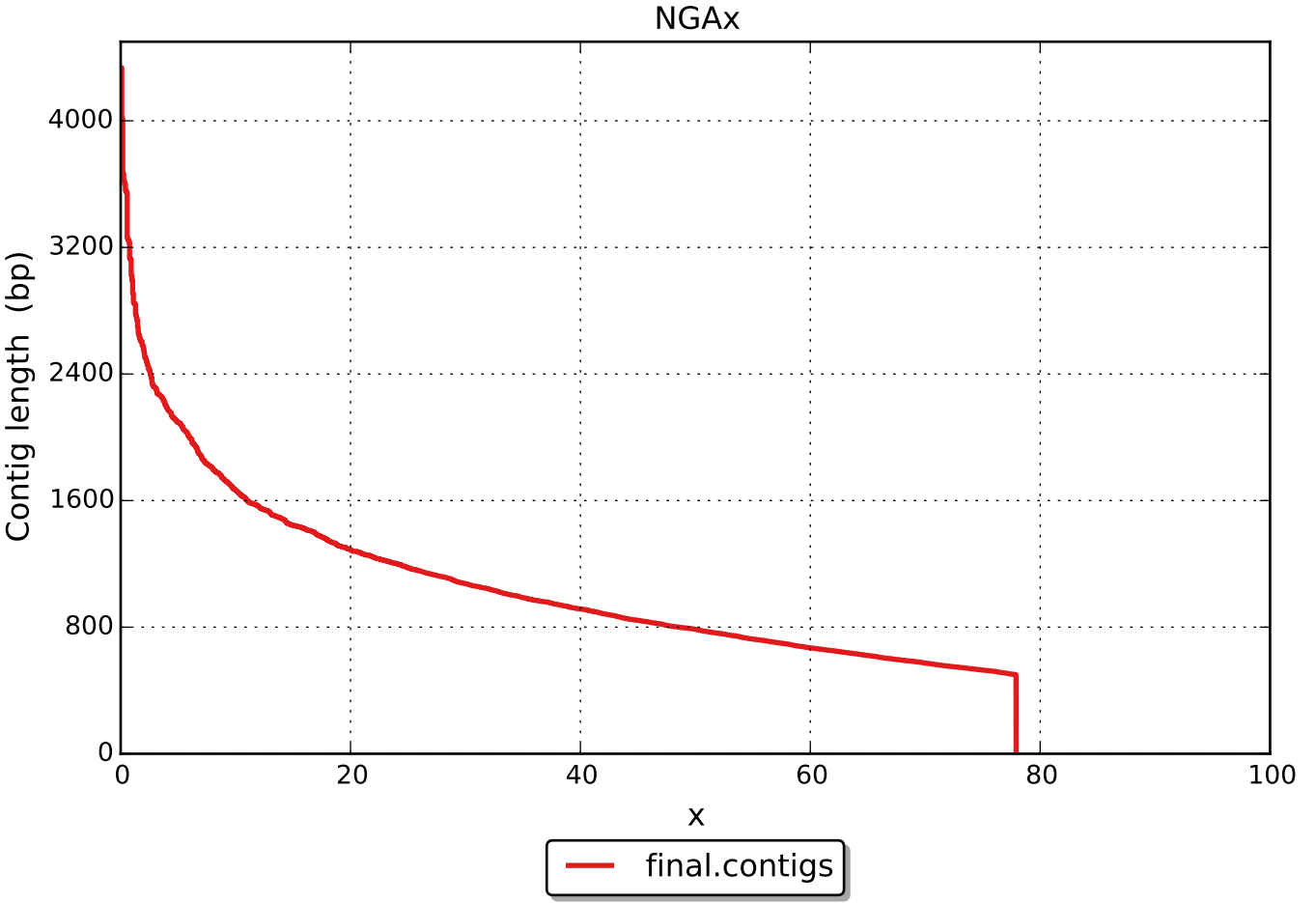

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs