Report

	final.contigs
# contigs (>= 1000 bp)	151
# contigs (>= 5000 bp)	118
# contigs (>= 10000 bp)	100
# contigs (>= 25000 bp)	68
# contigs (>= 50000 bp)	30
Total length (>= 1000 bp)	4552910
Total length (>= 5000 bp)	4478121
Total length (>= 10000 bp)	4348753
Total length (>= 25000 bp)	3834342
Total length (>= 50000 bp)	2542059
# contigs	167
Largest contig	177939
Total length	4563894
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	55538
NG50	55538
N75	30485
NG75	30196
L50	26
LG50	26
L75	54
LG75	55
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.221
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	67.86
# indels per 100 kbp	9.50
Largest alignment	177939
NA50	55538
NGA50	55538
NA75	30485
NGA75	30196
LA50	26
LGA50	26
LA75	54
LGA75	55

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

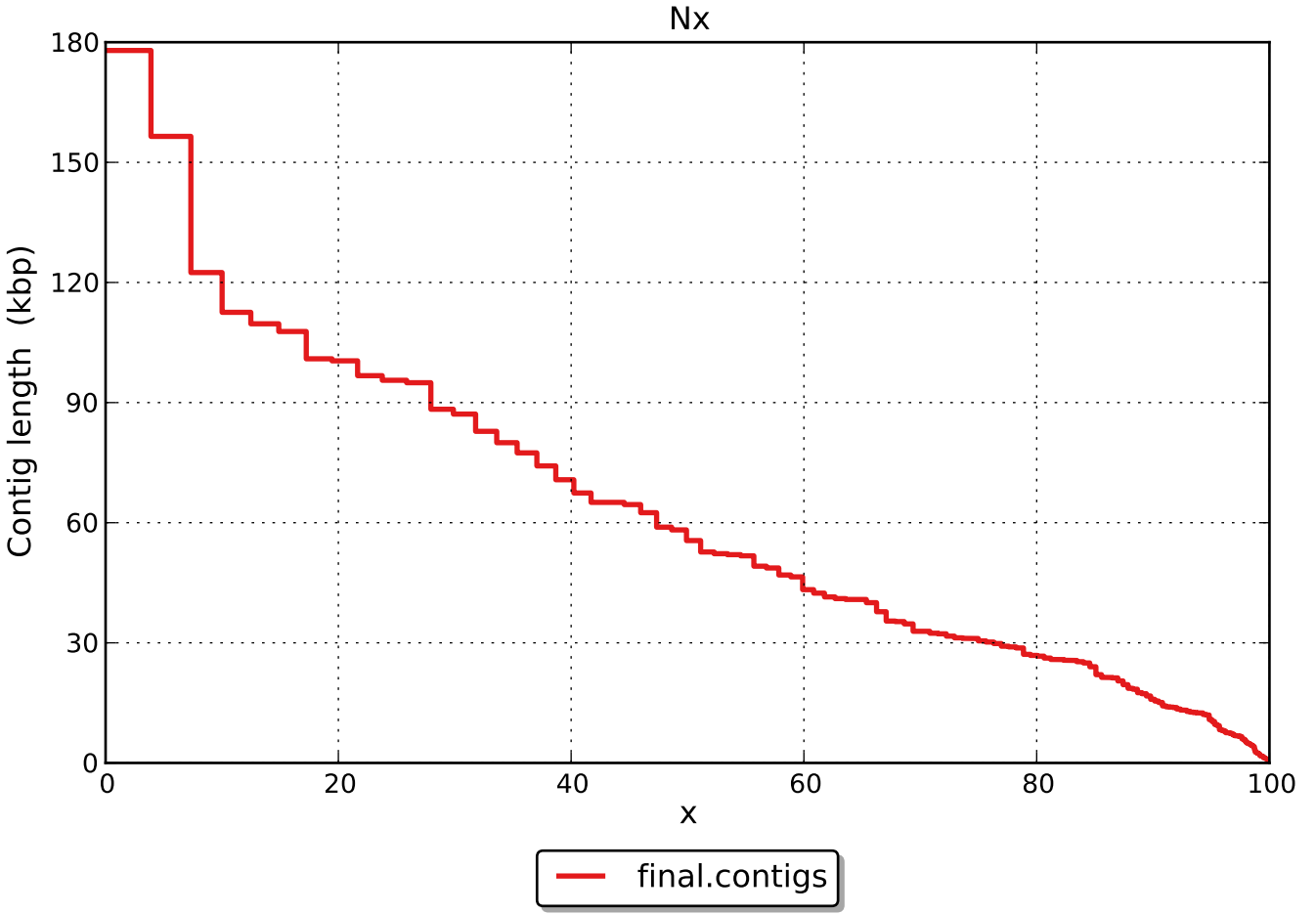
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# mismatches	3094
# indels	433
# short indels	432
# long indels	1
Indels length	727

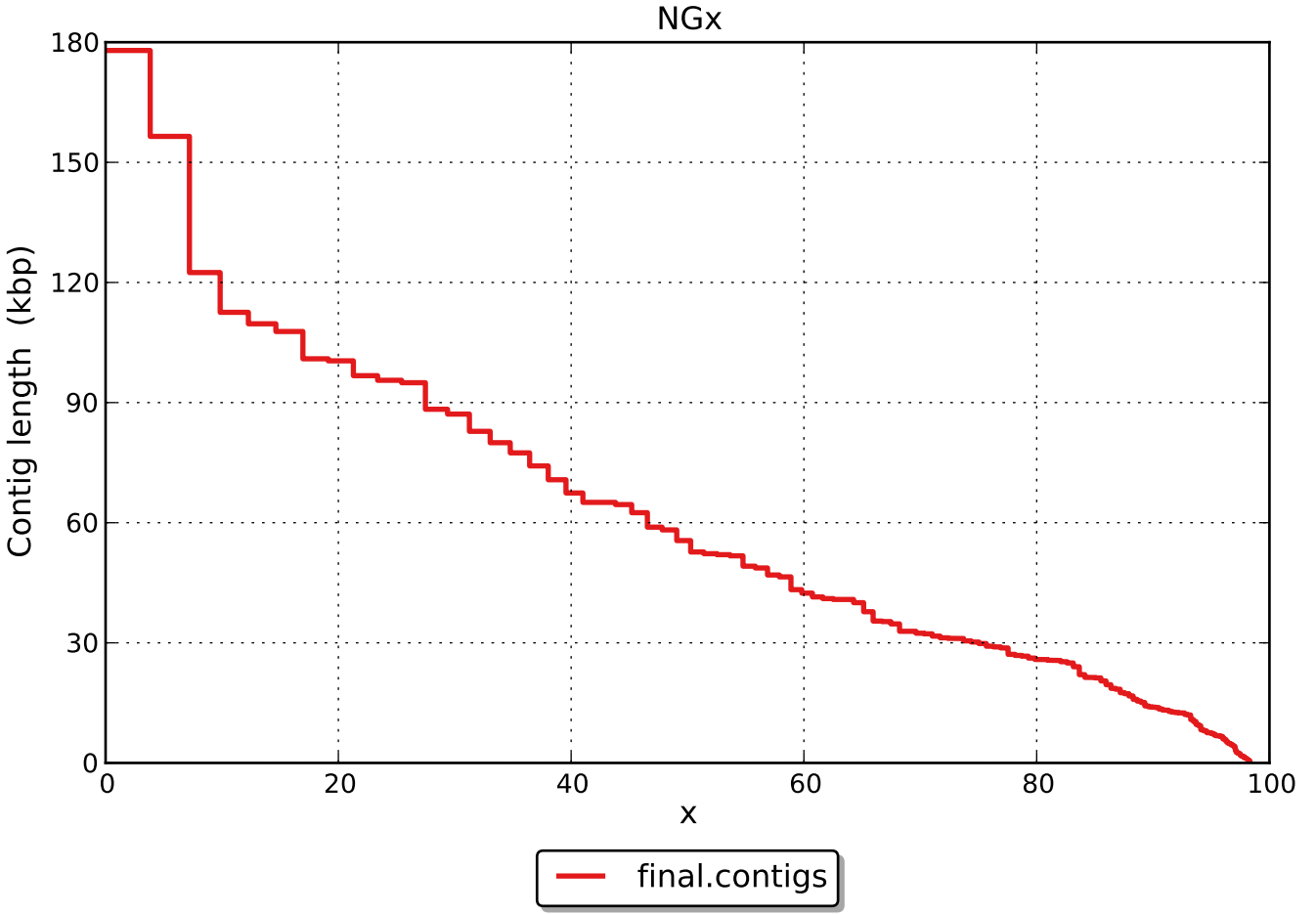
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

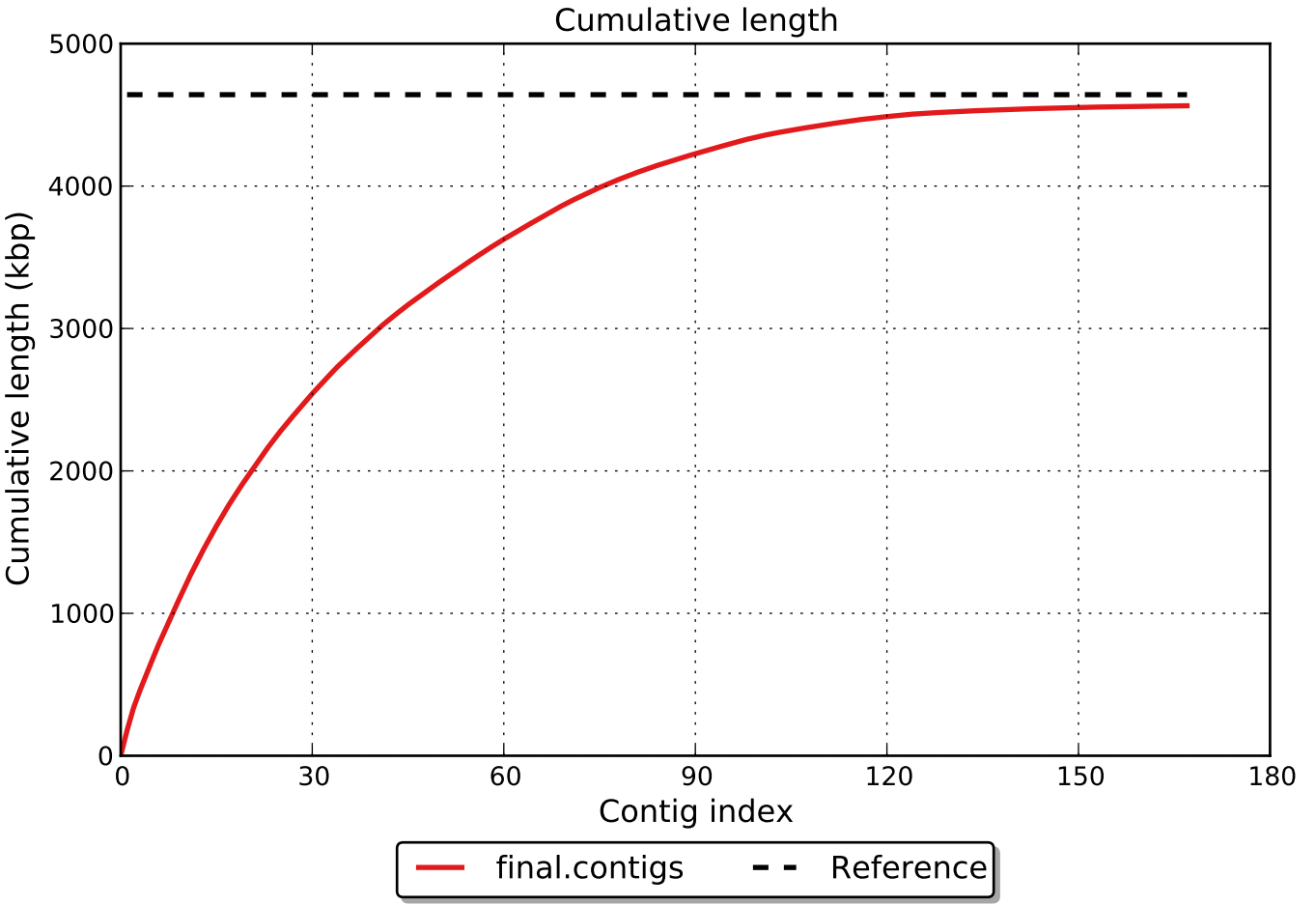
Unaligned report

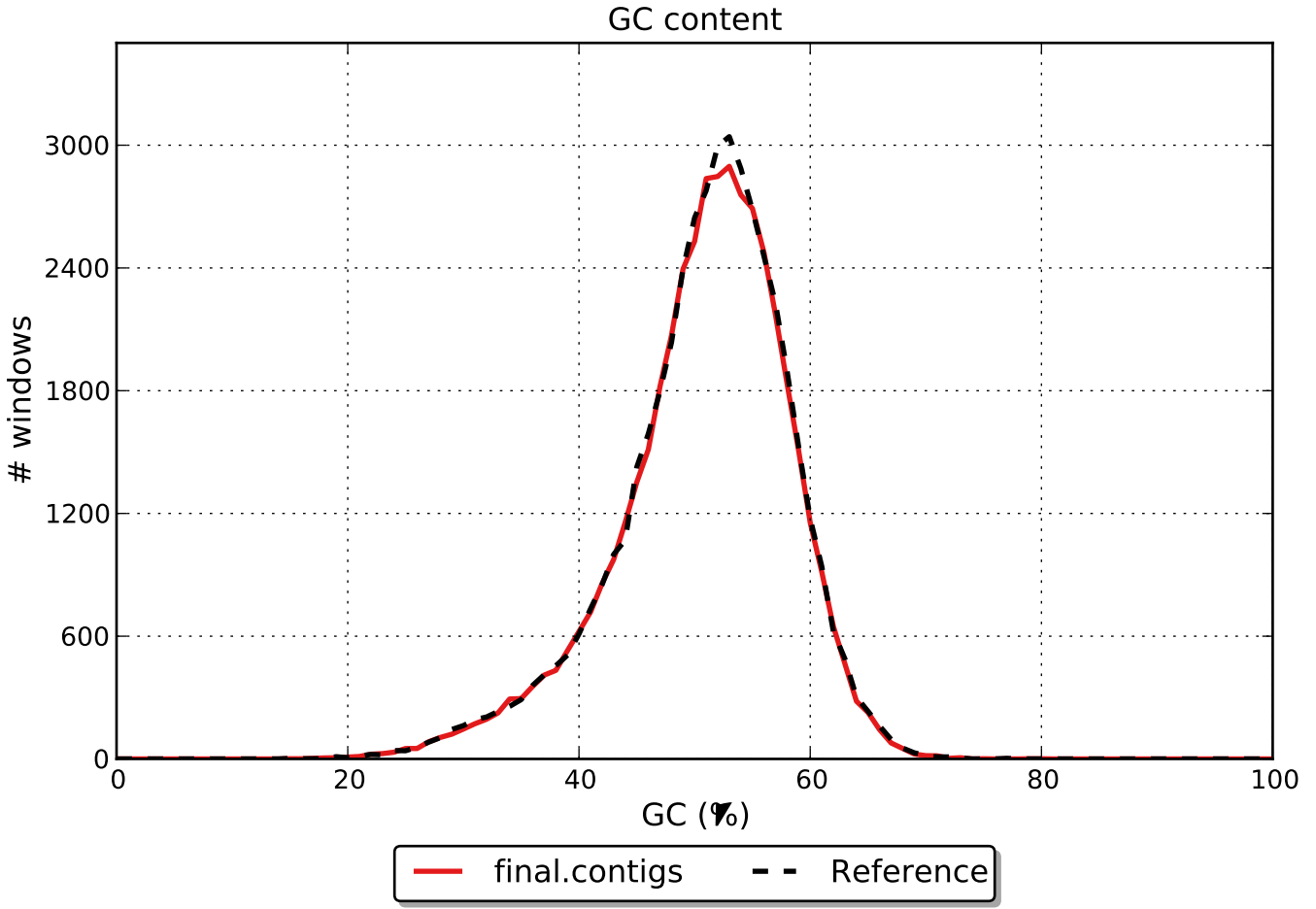
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

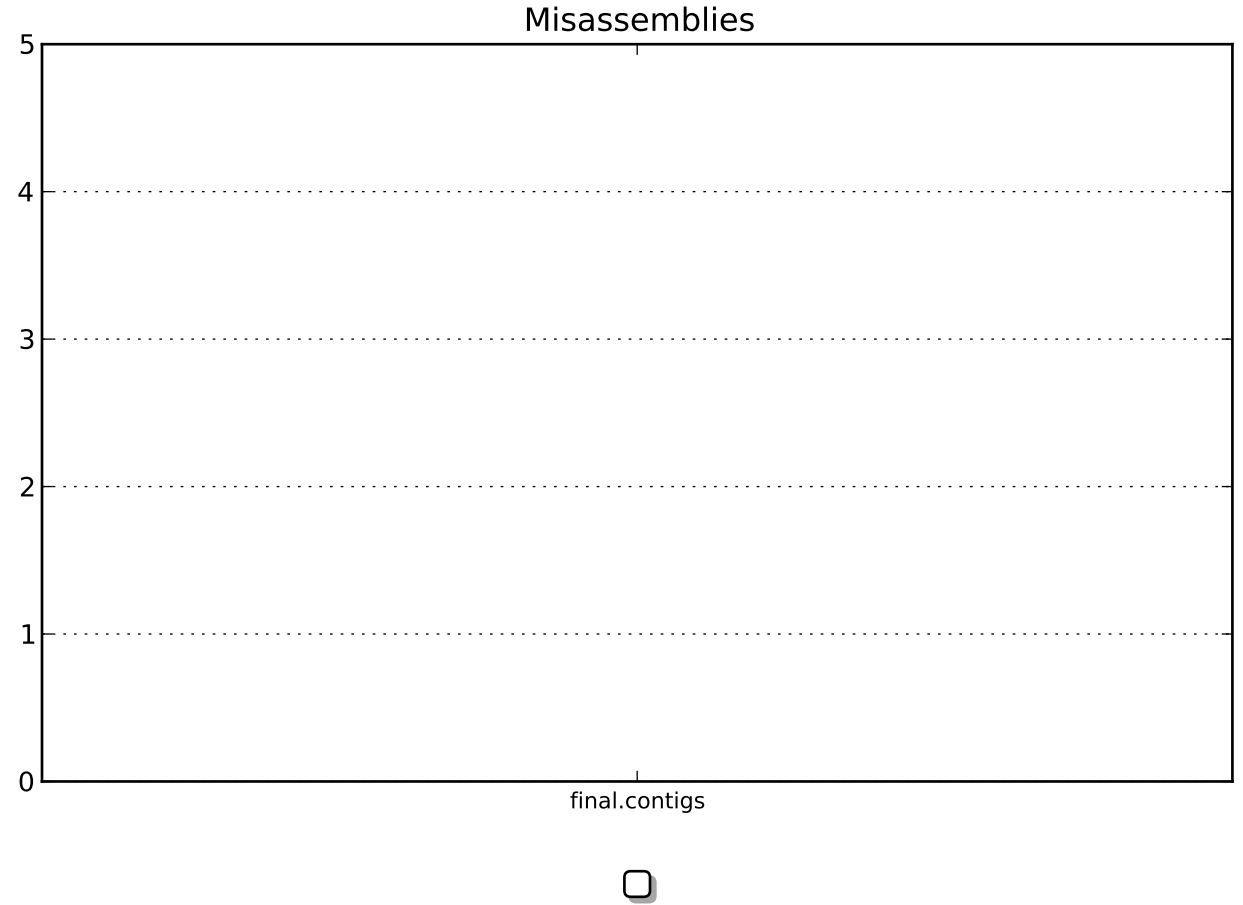
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

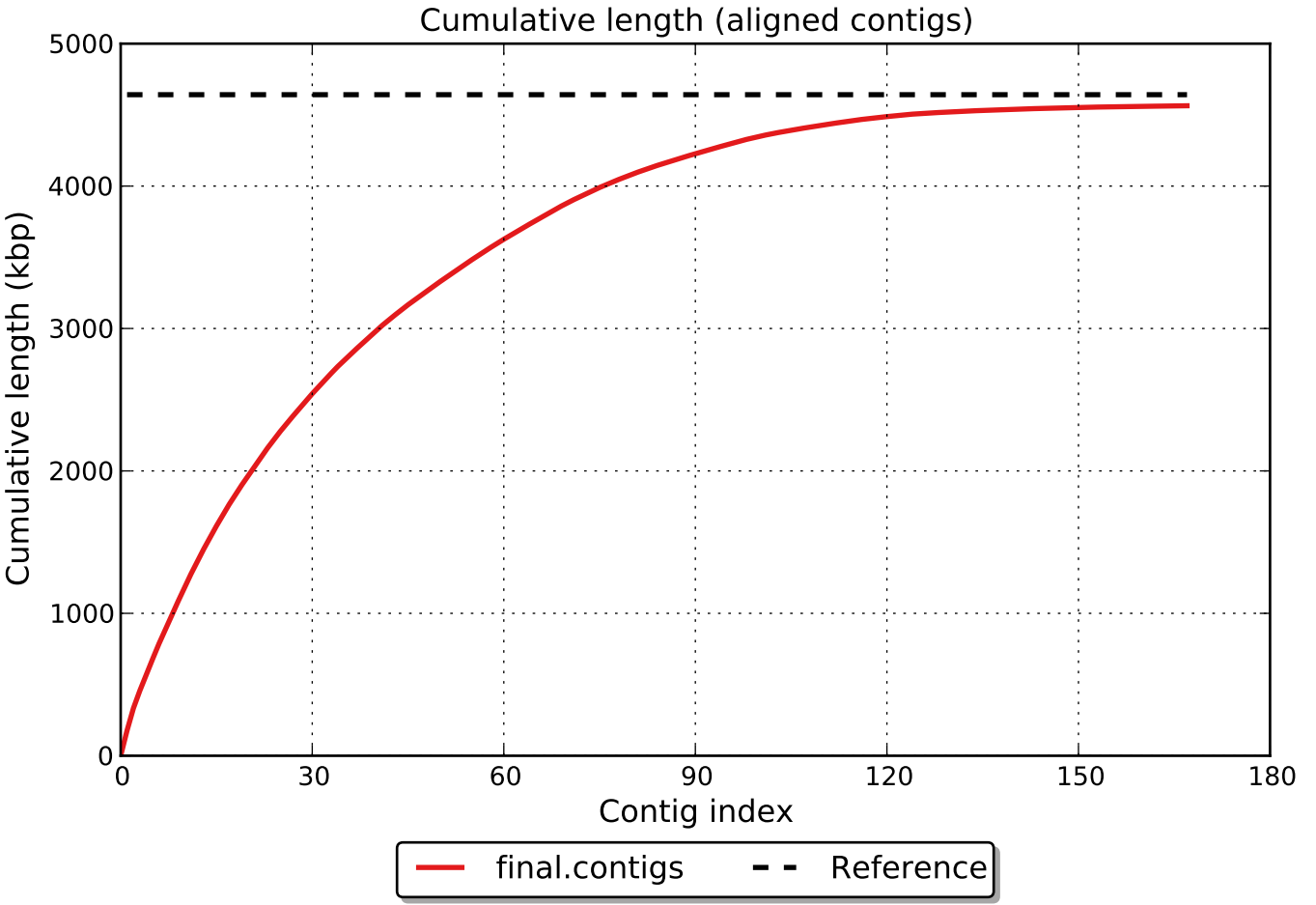

Nx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

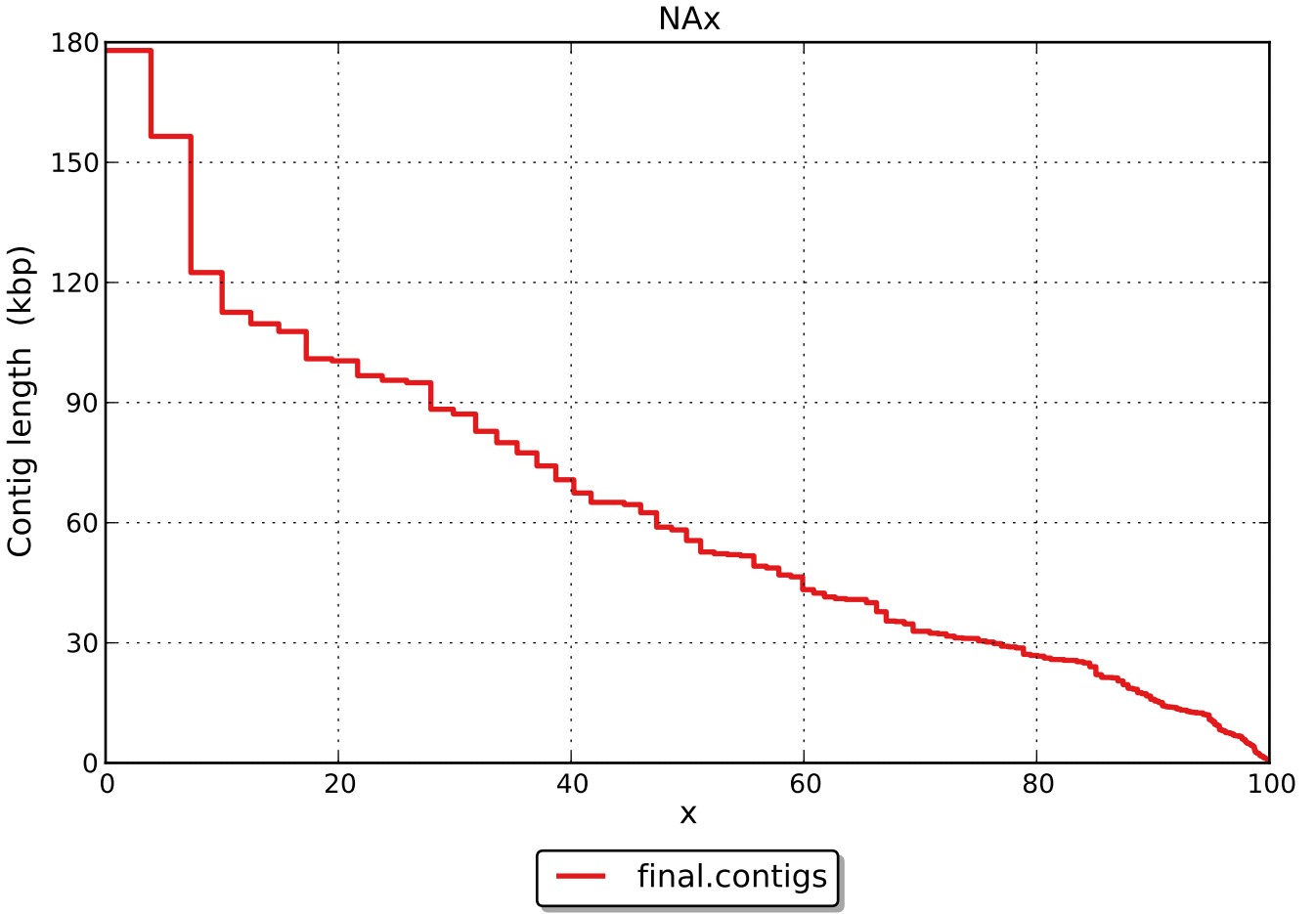

NGx
Contig length (kbp)
180
150
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs

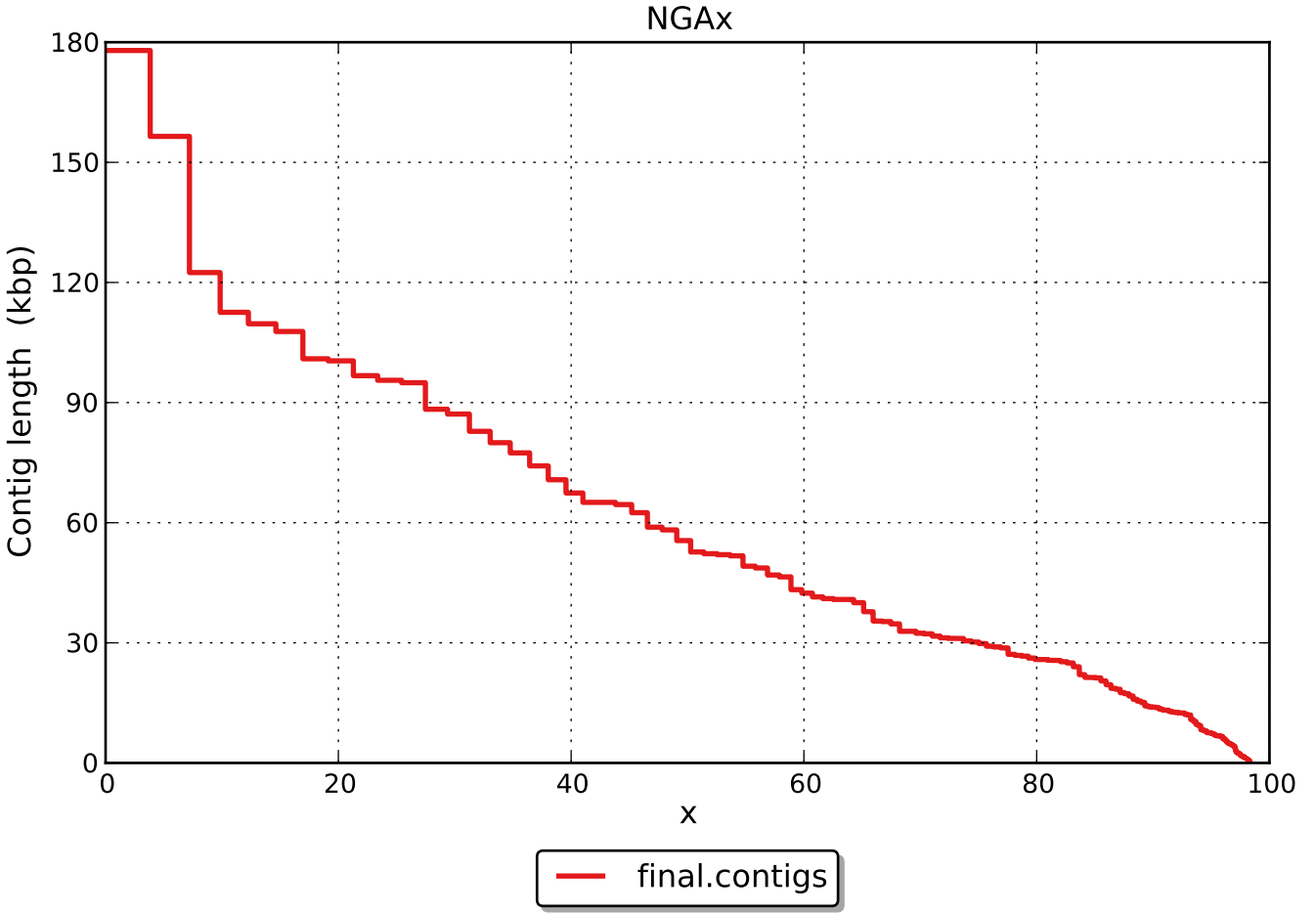

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
30
60
90
120
150
180
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
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
30
60
90
120
150
180
Contig index
final.contigs
Reference


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


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