Report

	final.contigs
# contigs (>= 1000 bp)	351
# contigs (>= 5000 bp)	237
# contigs (>= 10000 bp)	154
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	6
Total length (>= 1000 bp)	4558643
Total length (>= 5000 bp)	4232041
Total length (>= 10000 bp)	3637276
Total length (>= 25000 bp)	1963920
Total length (>= 50000 bp)	379345
# contigs	380
Largest contig	94038
Total length	4581351
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	22582
NG50	21954
N75	12278
NG75	11457
L50	67
LG50	68
L75	136
LG75	140
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.147
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.40
# indels per 100 kbp	0.00
Largest alignment	94038
NA50	22582
NGA50	21954
NA75	12278
NGA75	11457
LA50	67
LGA50	68
LA75	136
LGA75	140

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

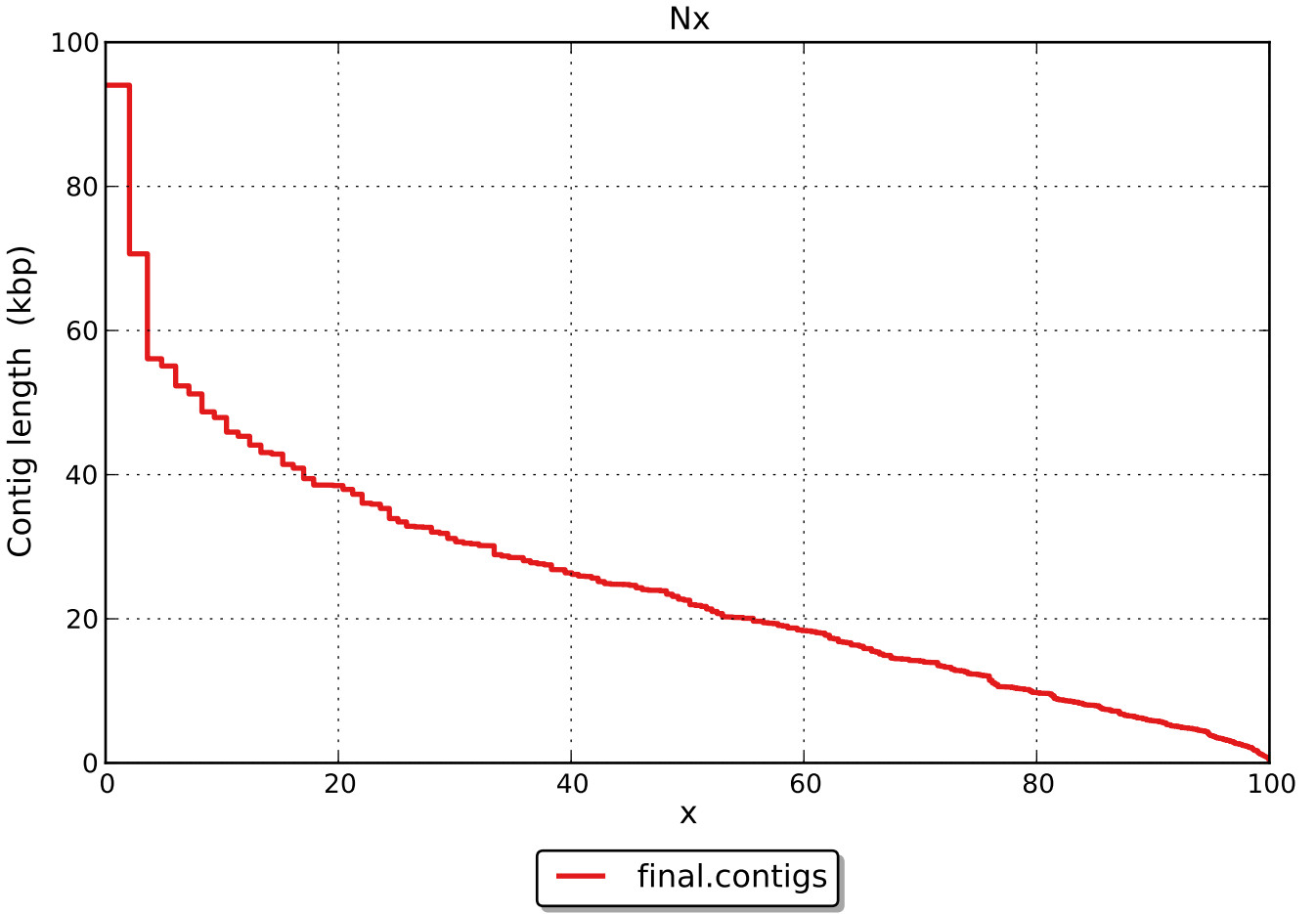
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	15109
# local misassemblies	0
# mismatches	18
# indels	0
# short indels	0
# long indels	0
Indels length	0

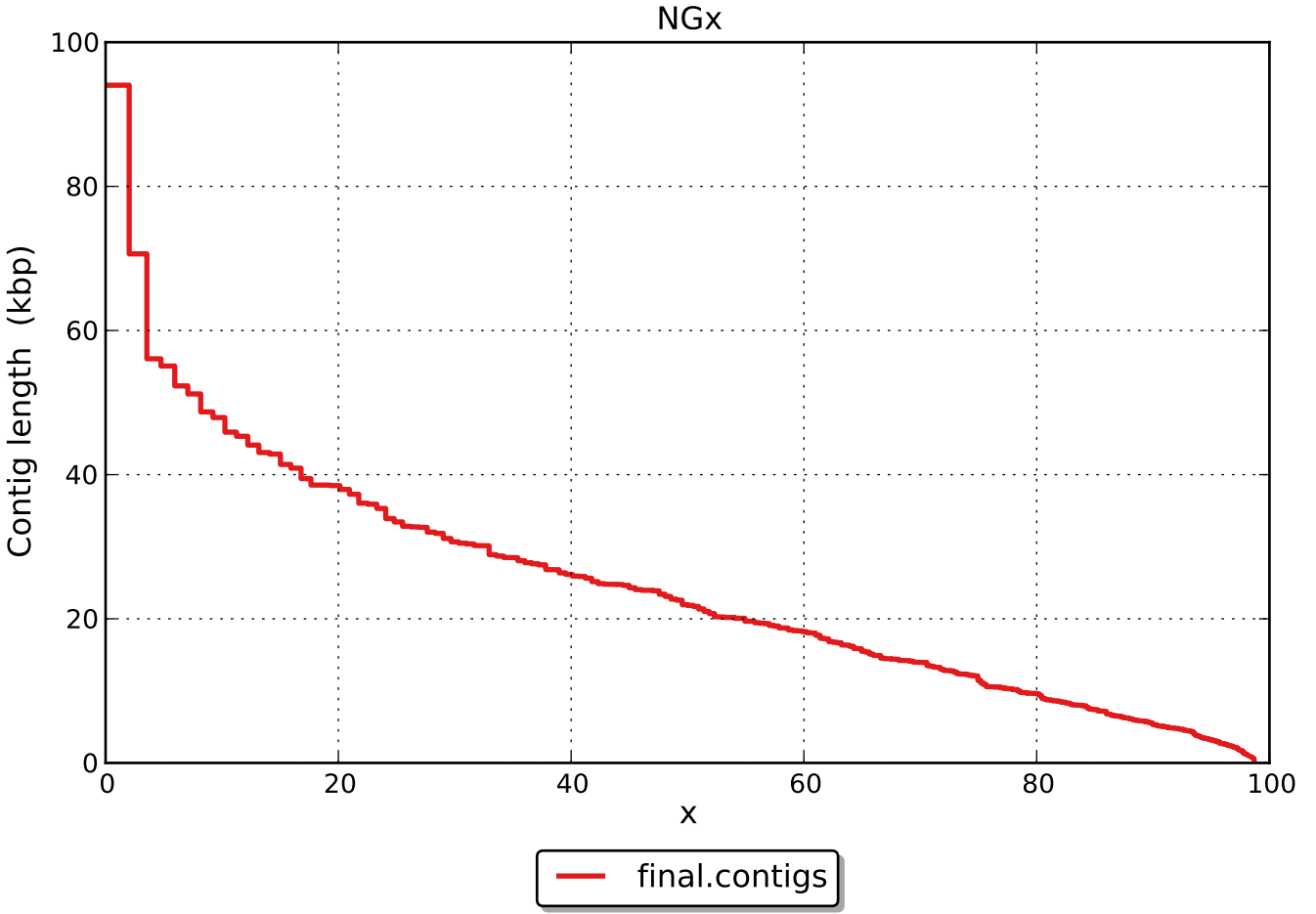
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

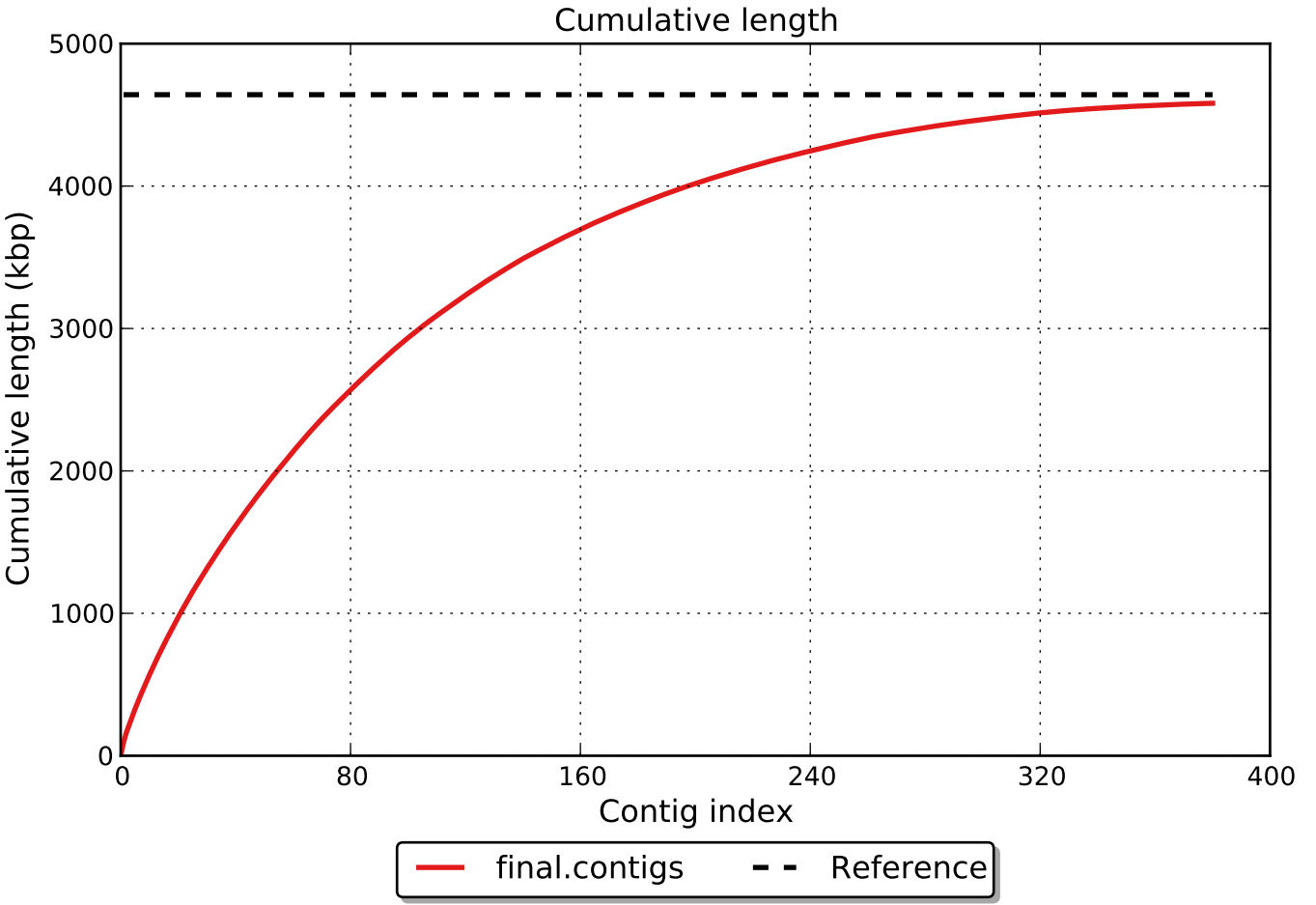
Unaligned report

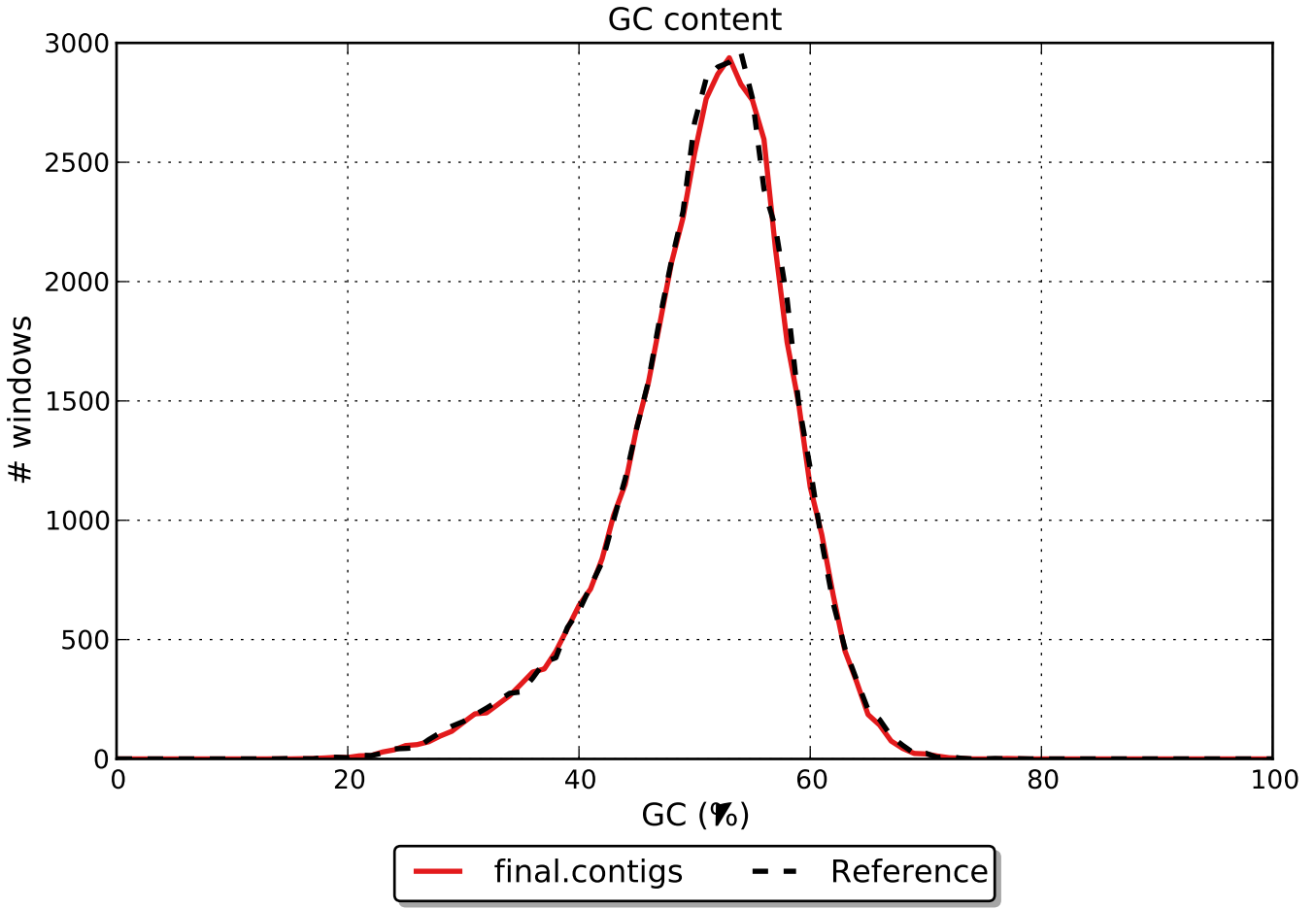
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

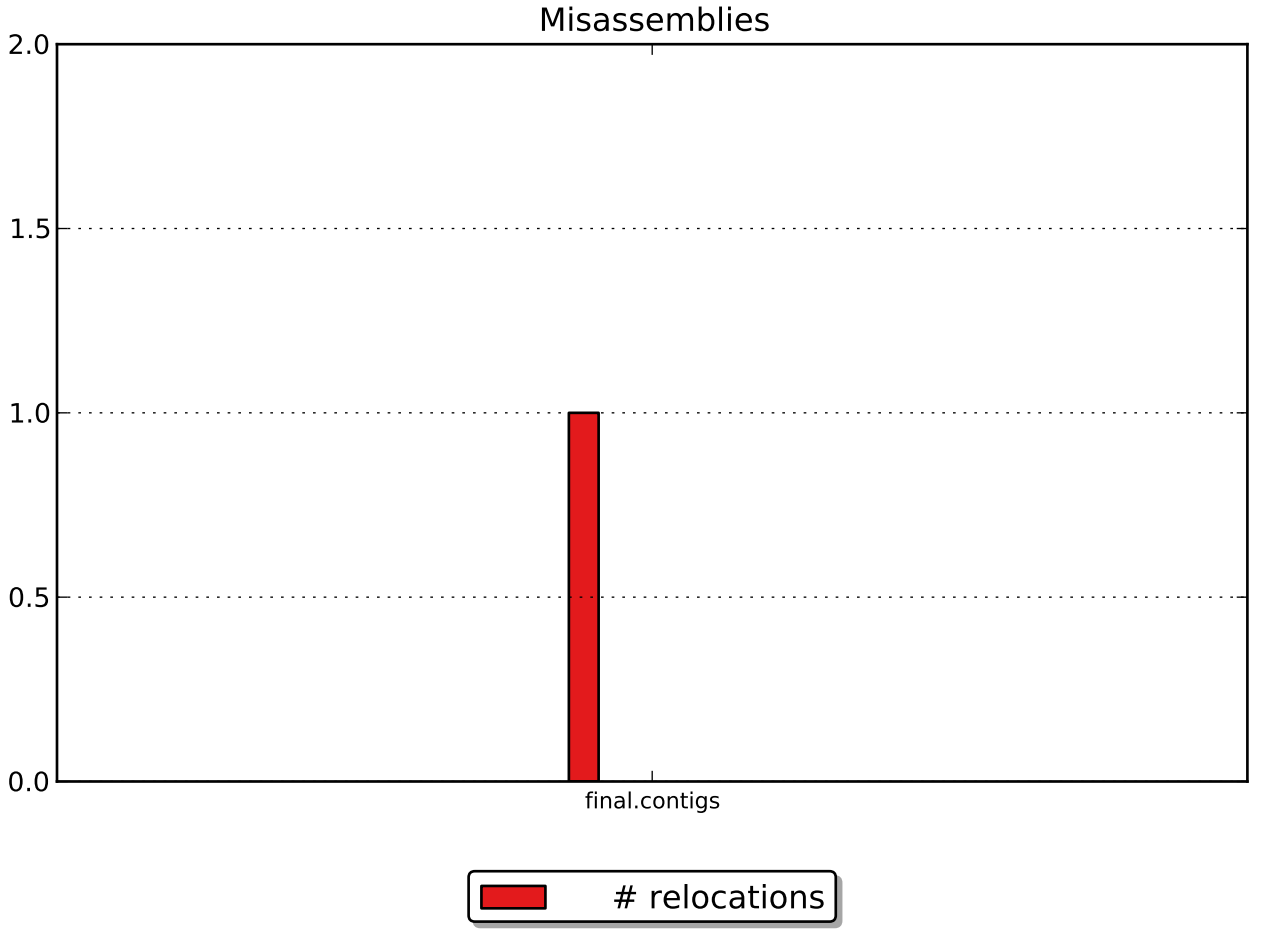
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

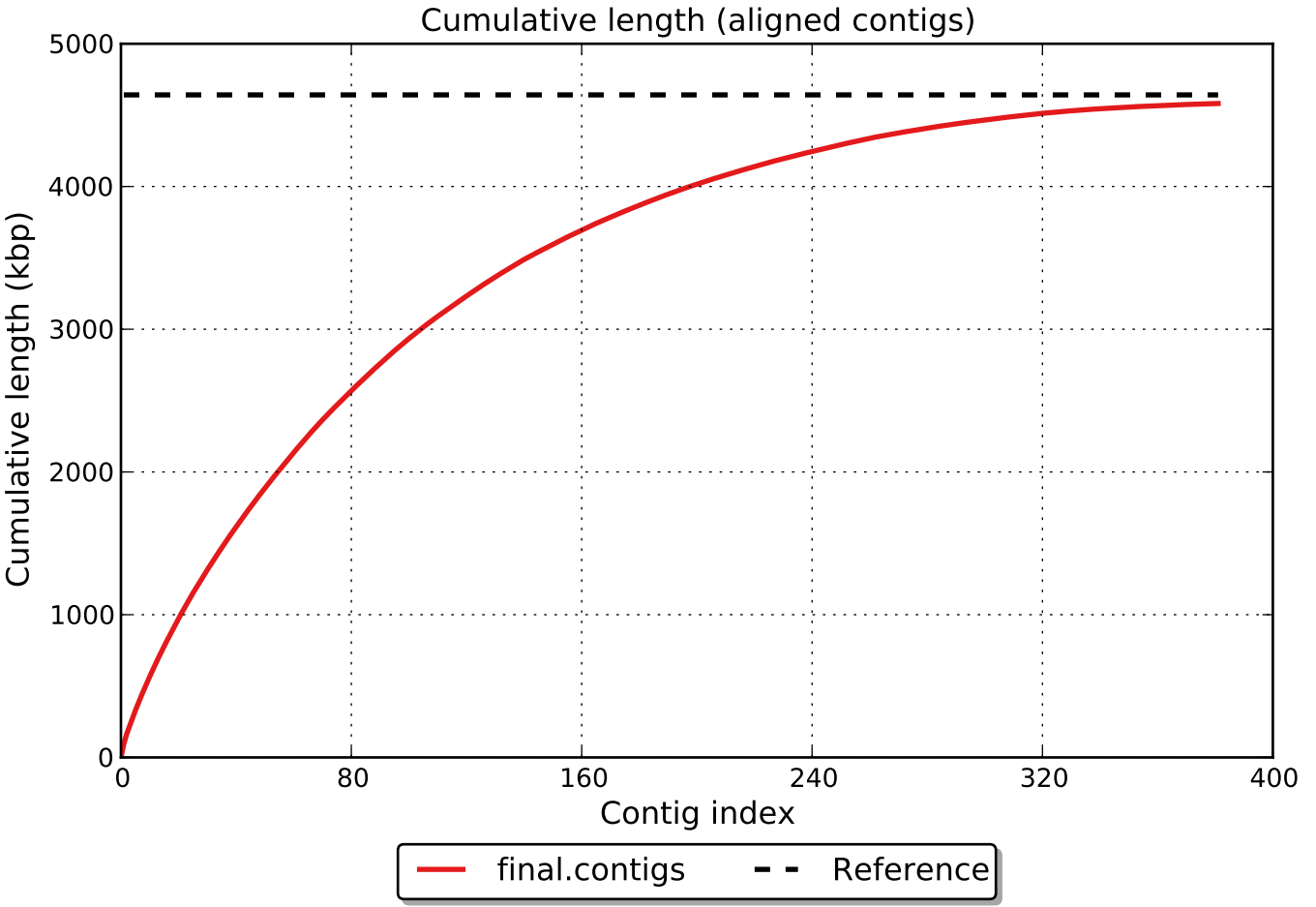

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

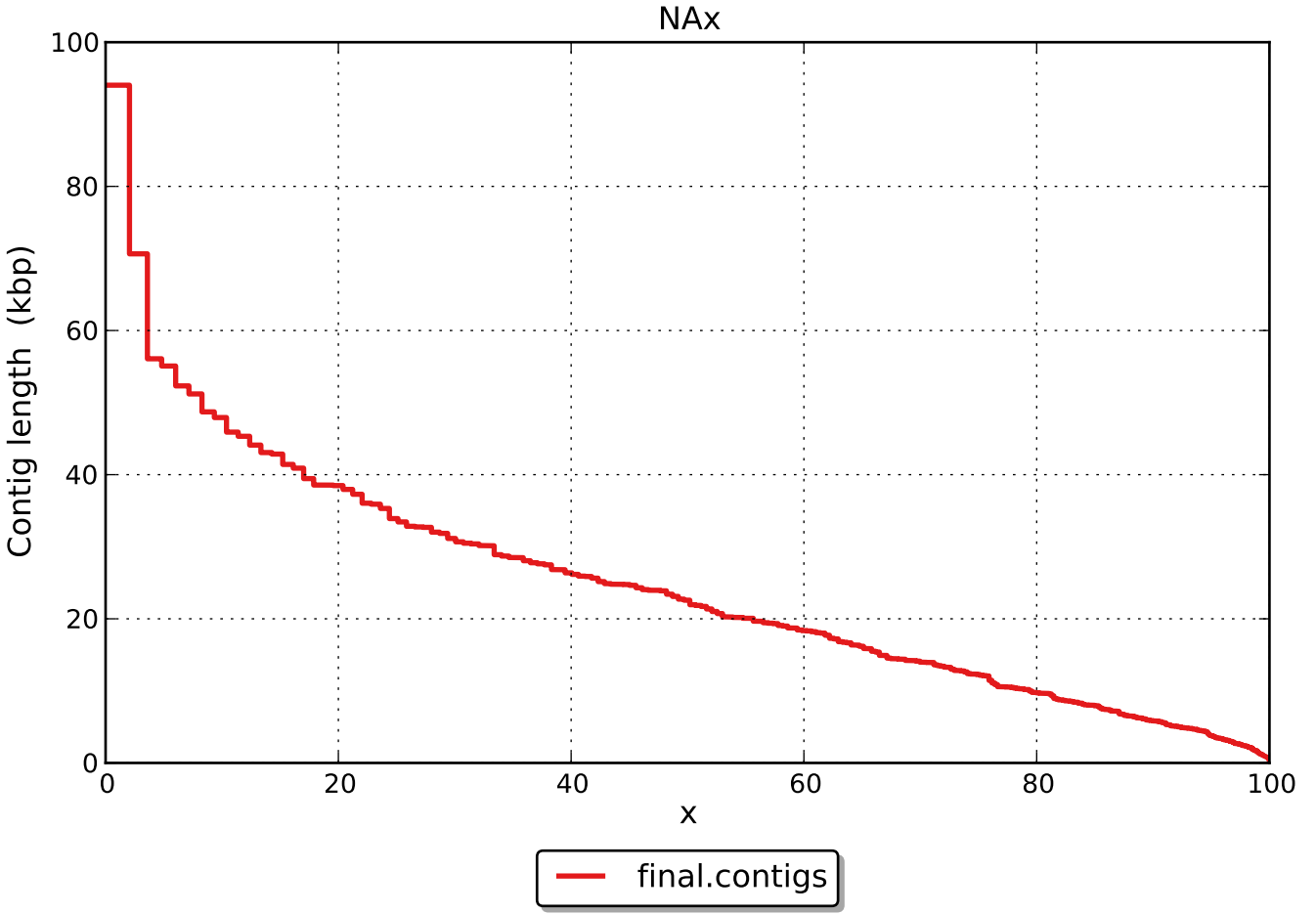

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

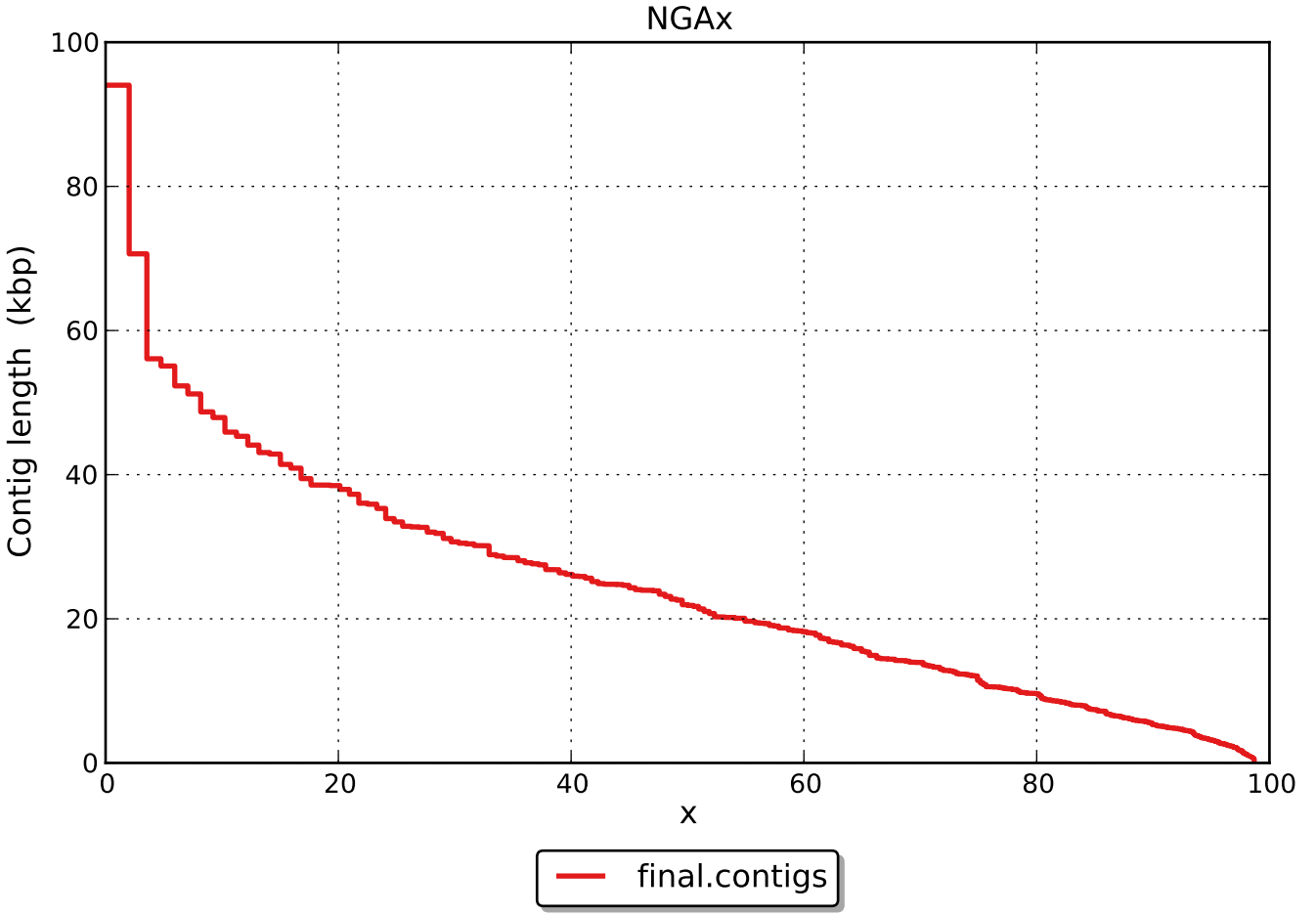

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


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