Report

	final.contigs
# contigs (>= 0 bp)	794
# contigs (>= 1000 bp)	400
Total length (>= 0 bp)	1214059
Total length (>= 1000 bp)	947137
# contigs	794
Largest contig	9129
Total length	1214059
Reference length	641799
GC (%)	26.26
Reference GC (%)	26.30
N50	2143
NG50	3540
N75	1089
NG75	2776
L50	172
LG50	69
L75	366
LG75	121
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	9065
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.209
Duplication ratio	2.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	823.97
# indels per 100 kbp	0.33
Largest alignment	9129
NA50	708
NGA50	2106
NGA75	1092
LA50	344
LGA50	93
LGA75	199

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

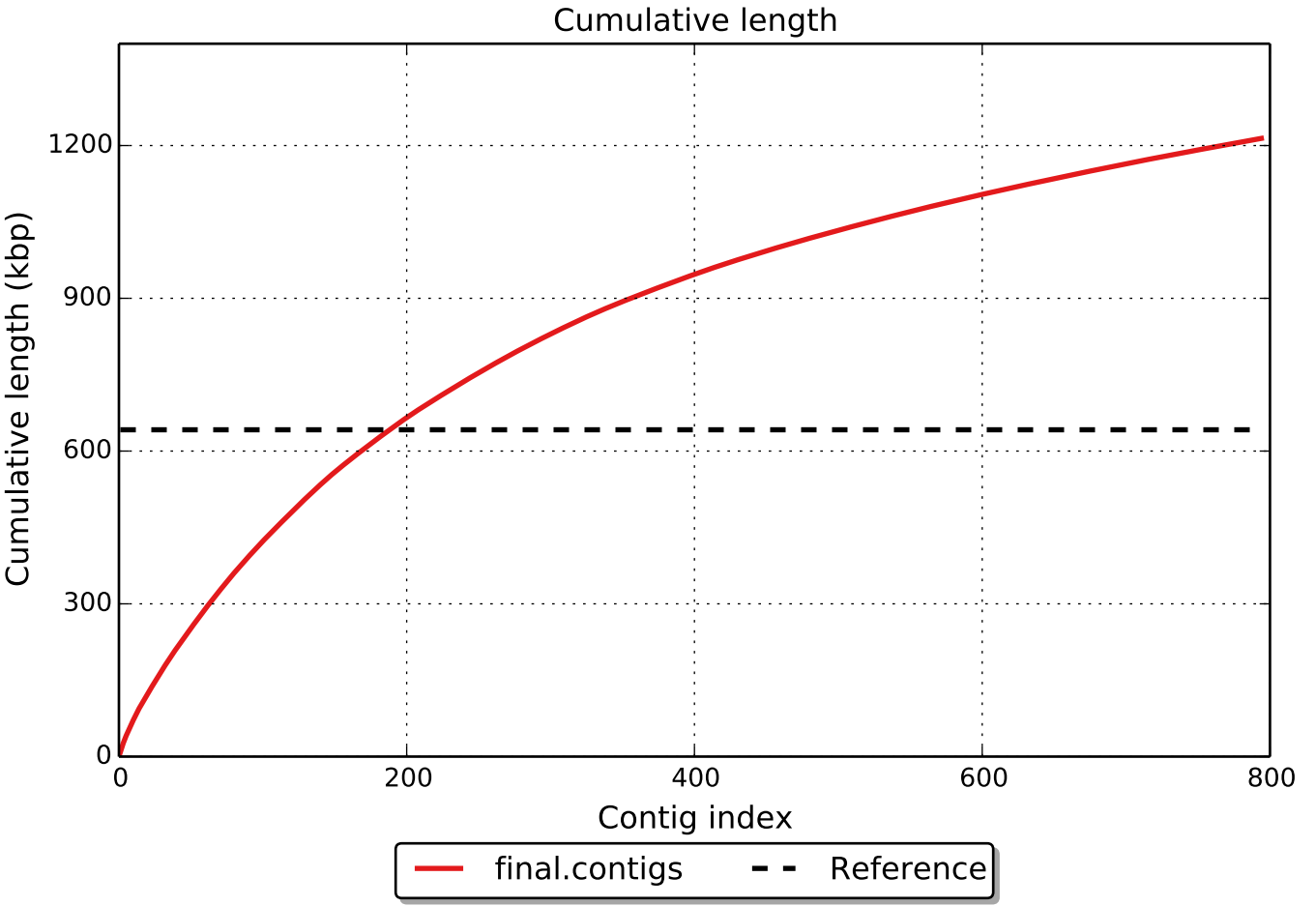
	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	9065
# local misassemblies	0
# mismatches	4982
# indels	2
# short indels	2
# long indels	0
Indels length	2

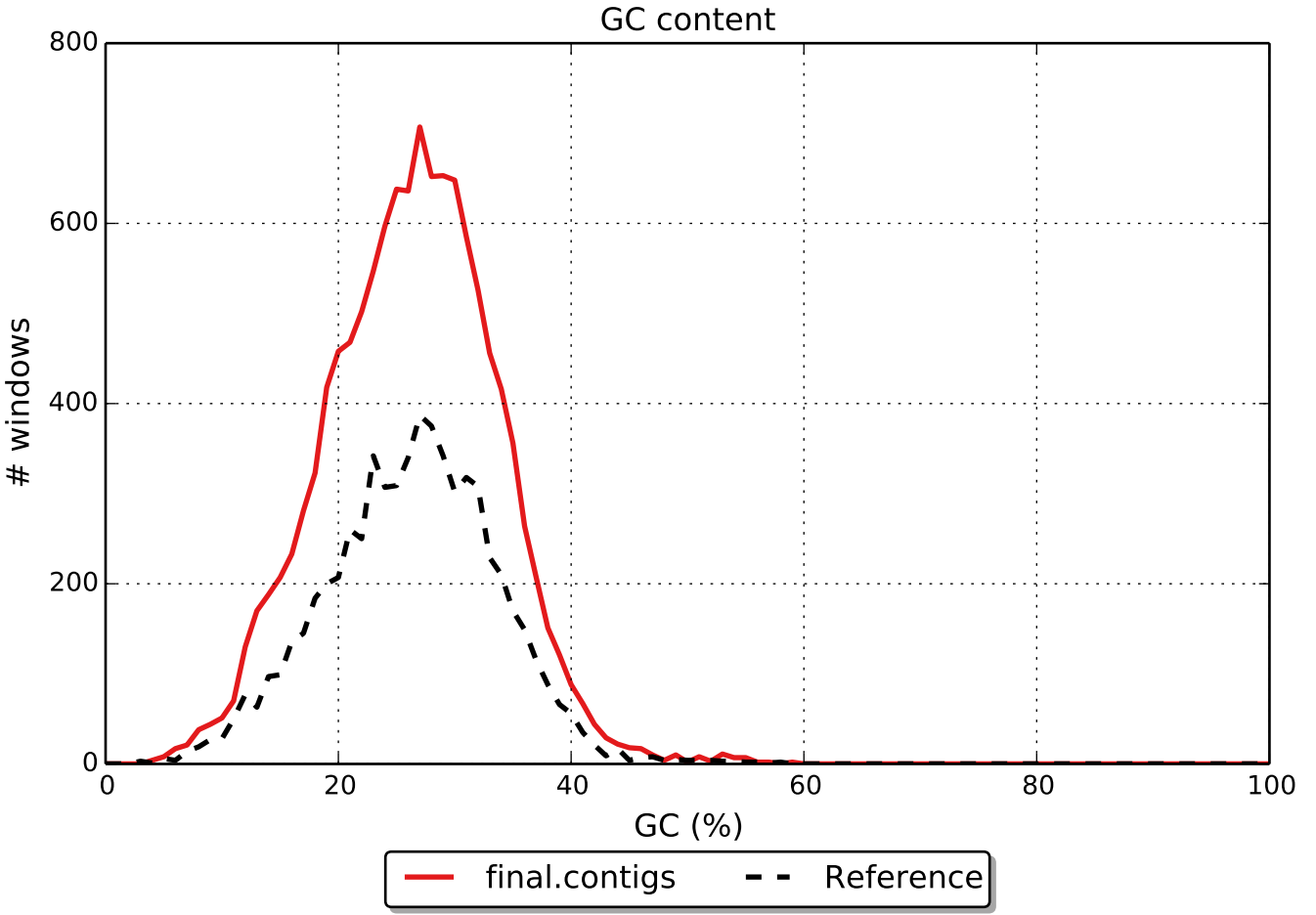
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

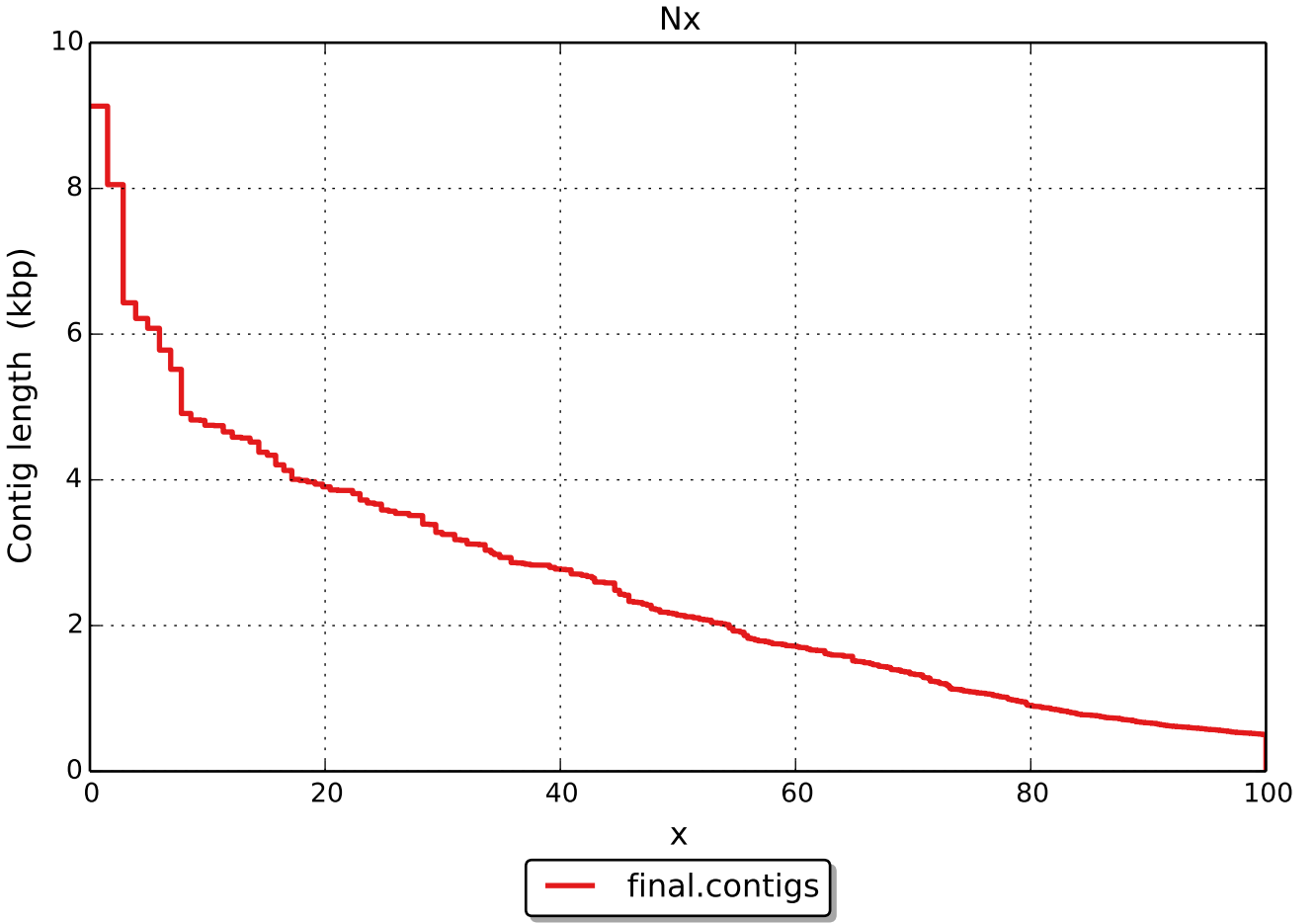
Unaligned report

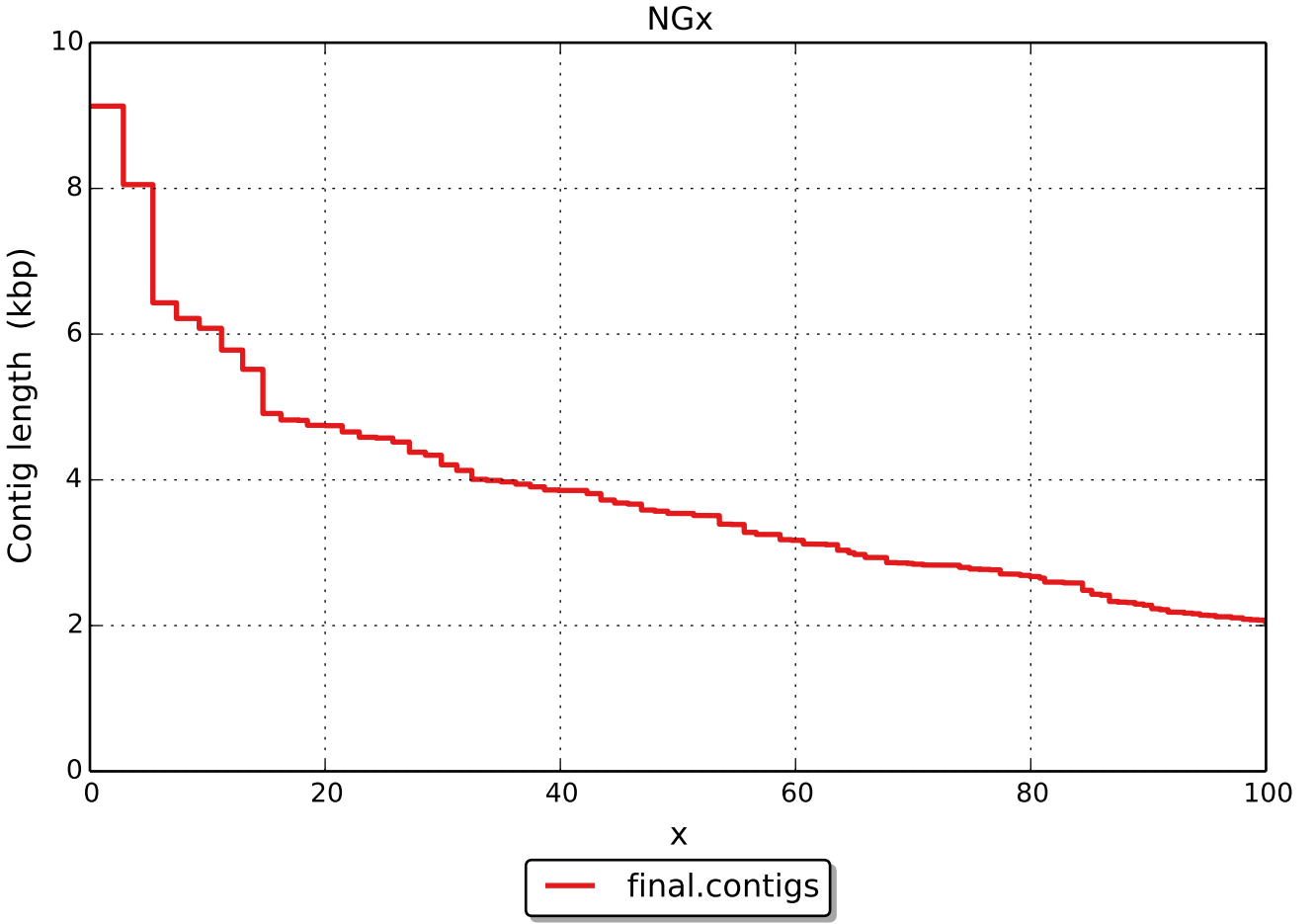
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

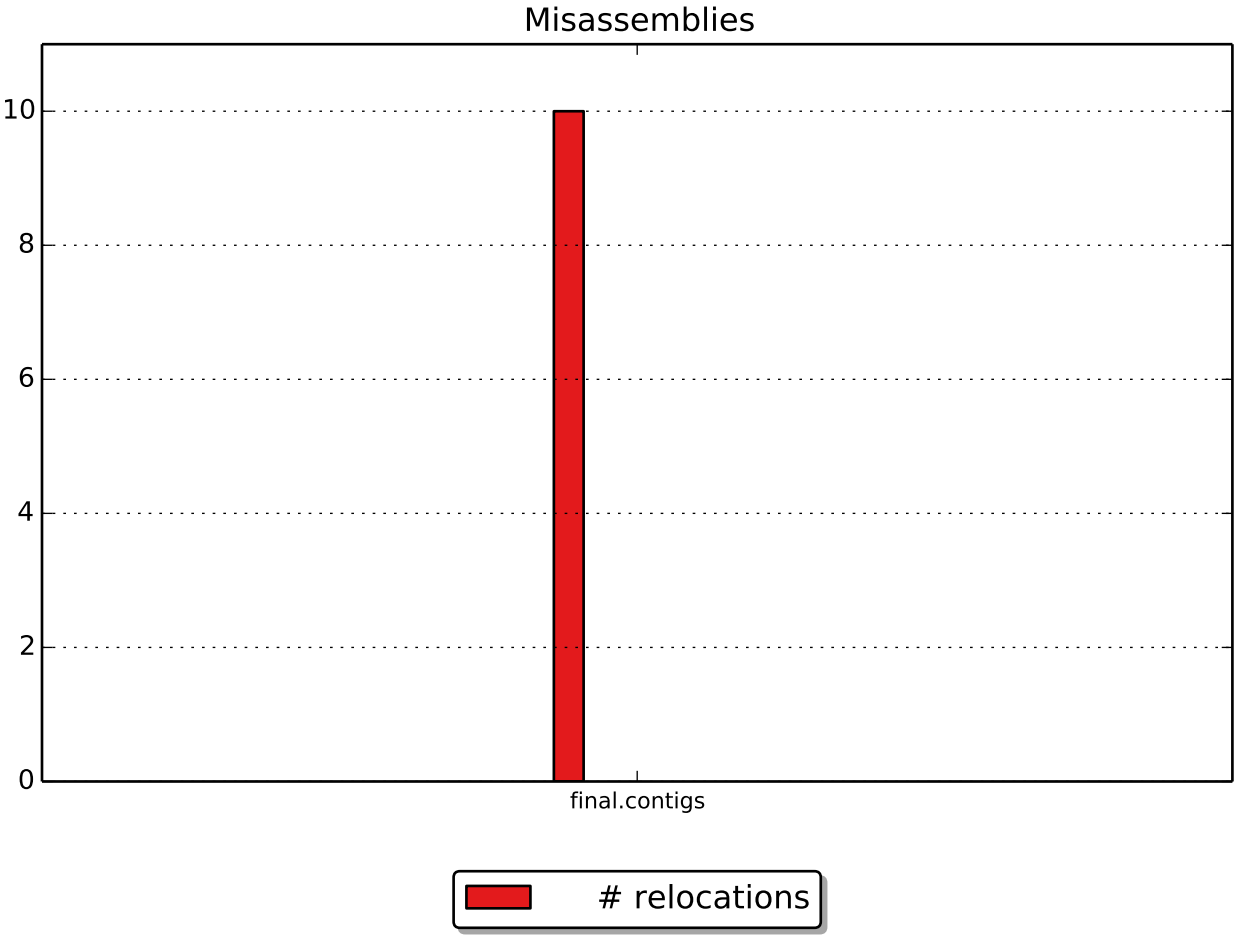
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

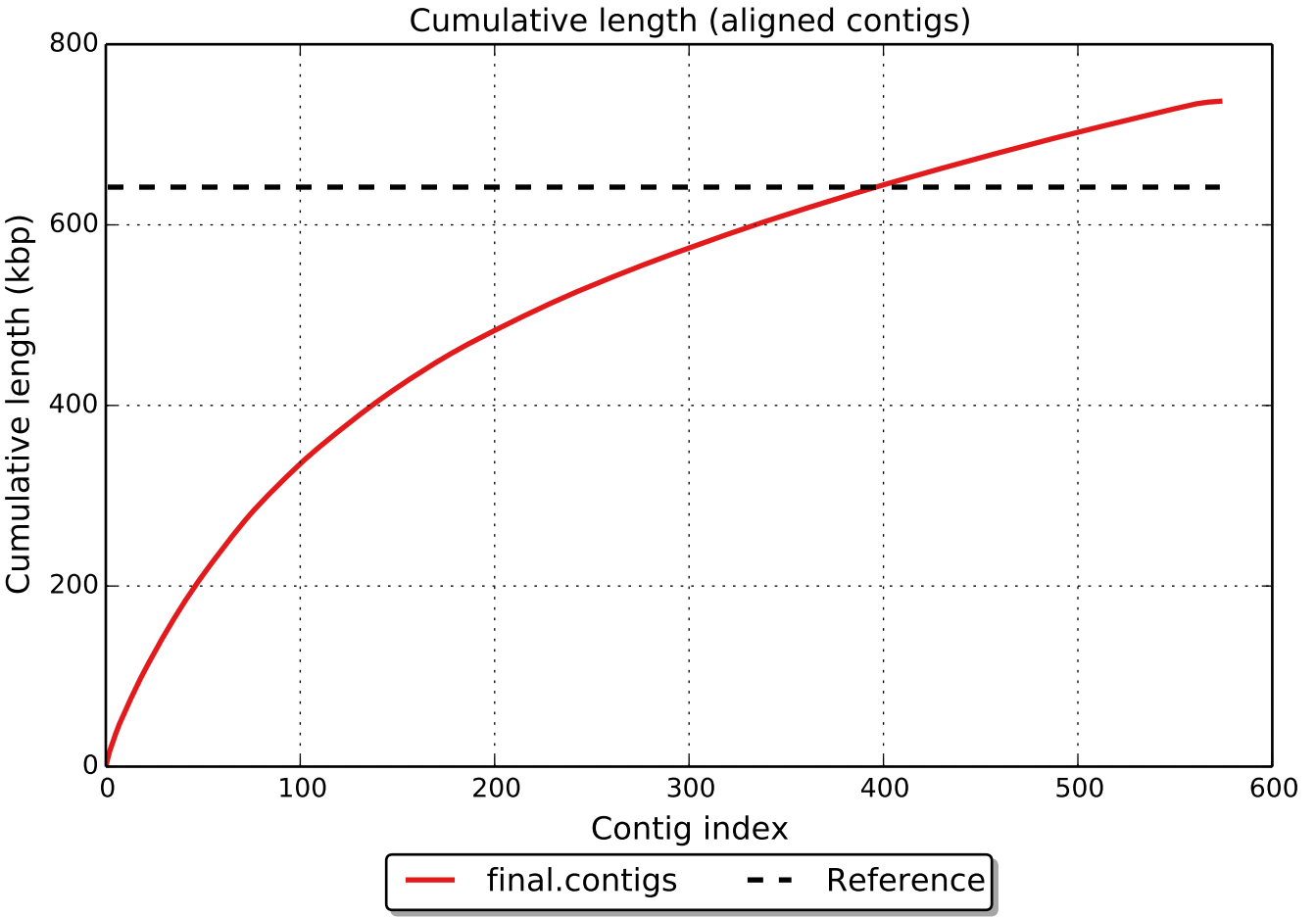

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
Contig index
final.contigs
Reference

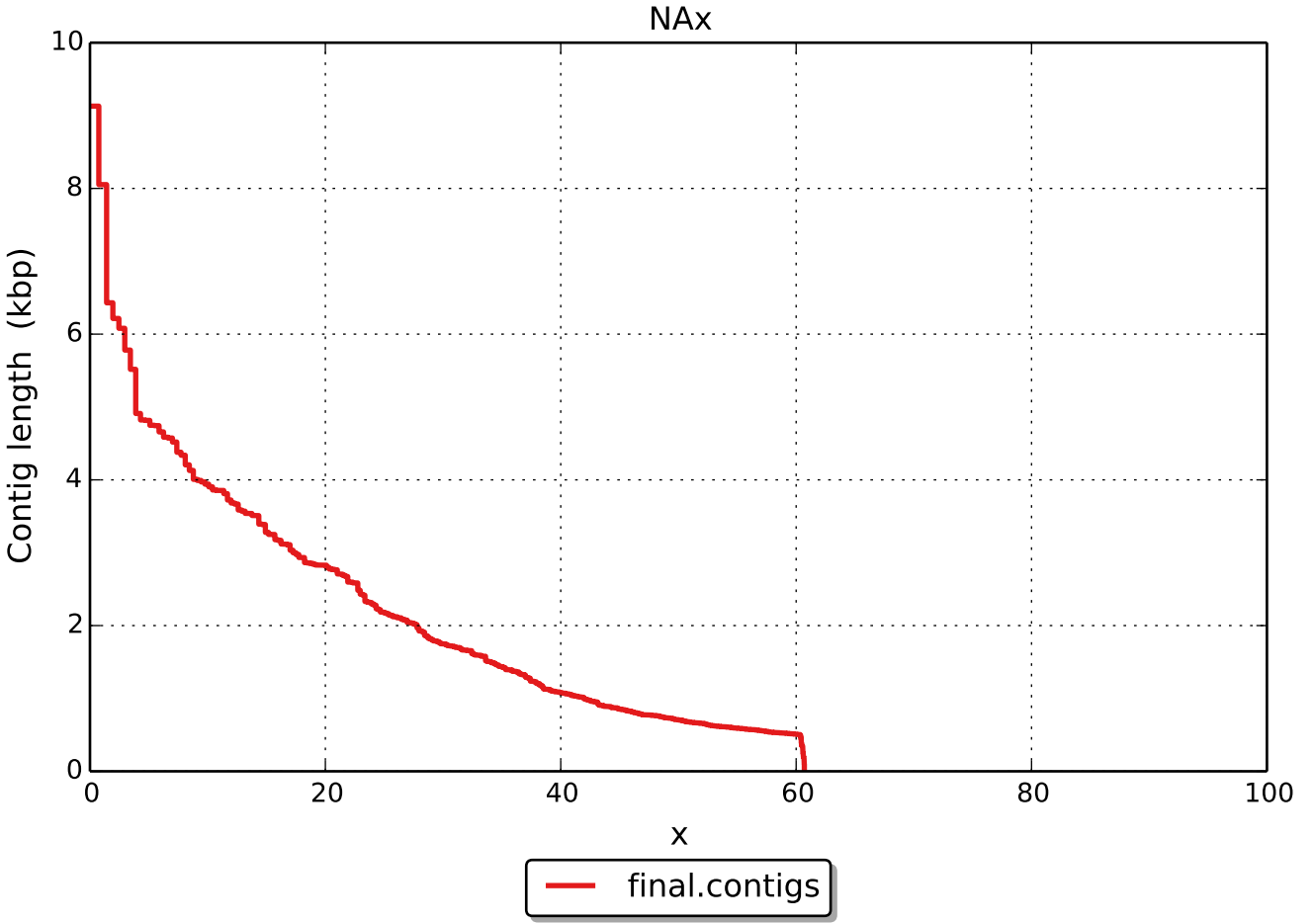

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

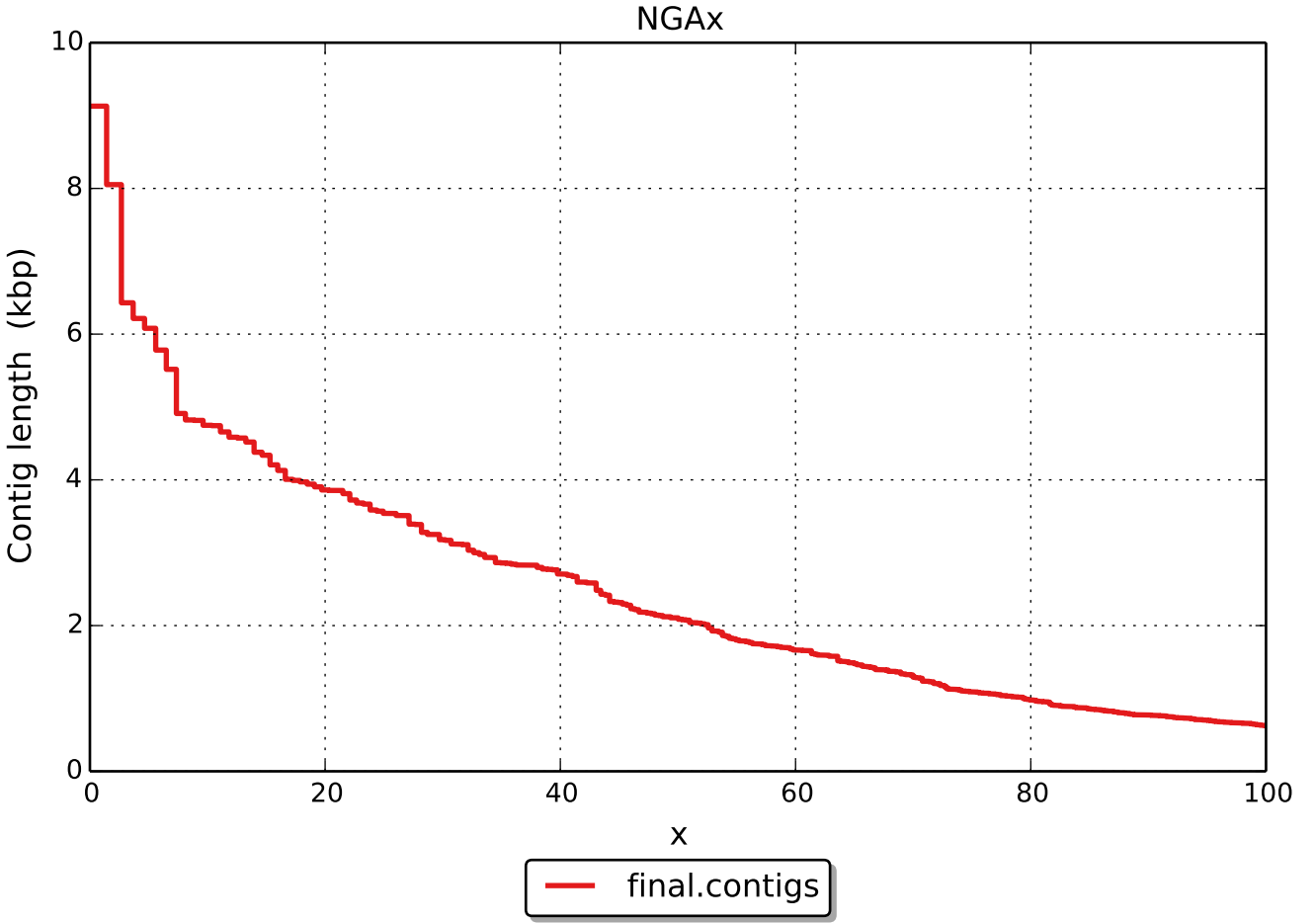

Nx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
10
8
6
4
2
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
800
600
400
200
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
10
8
6
4
2
0
0
20
40
60
80
100
x
final.contigs