Report

	final.contigs
# contigs (>= 0 bp)	749
# contigs (>= 1000 bp)	253
Total length (>= 0 bp)	790680
Total length (>= 1000 bp)	446581
# contigs	749
Largest contig	5595
Total length	790680
Reference length	615980
GC (%)	25.38
Reference GC (%)	25.35
N50	1155
NG50	1449
N75	732
NG75	971
L50	206
LG50	137
L75	425
LG75	269
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	8535
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.789
Duplication ratio	1.383
# N's per 100 kbp	0.00
# mismatches per 100 kbp	923.96
# indels per 100 kbp	0.35
Largest alignment	5595
NA50	1150
NGA50	1449
NA75	730
NGA75	969
LA50	206
LGA50	137
LA75	426
LGA75	270

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

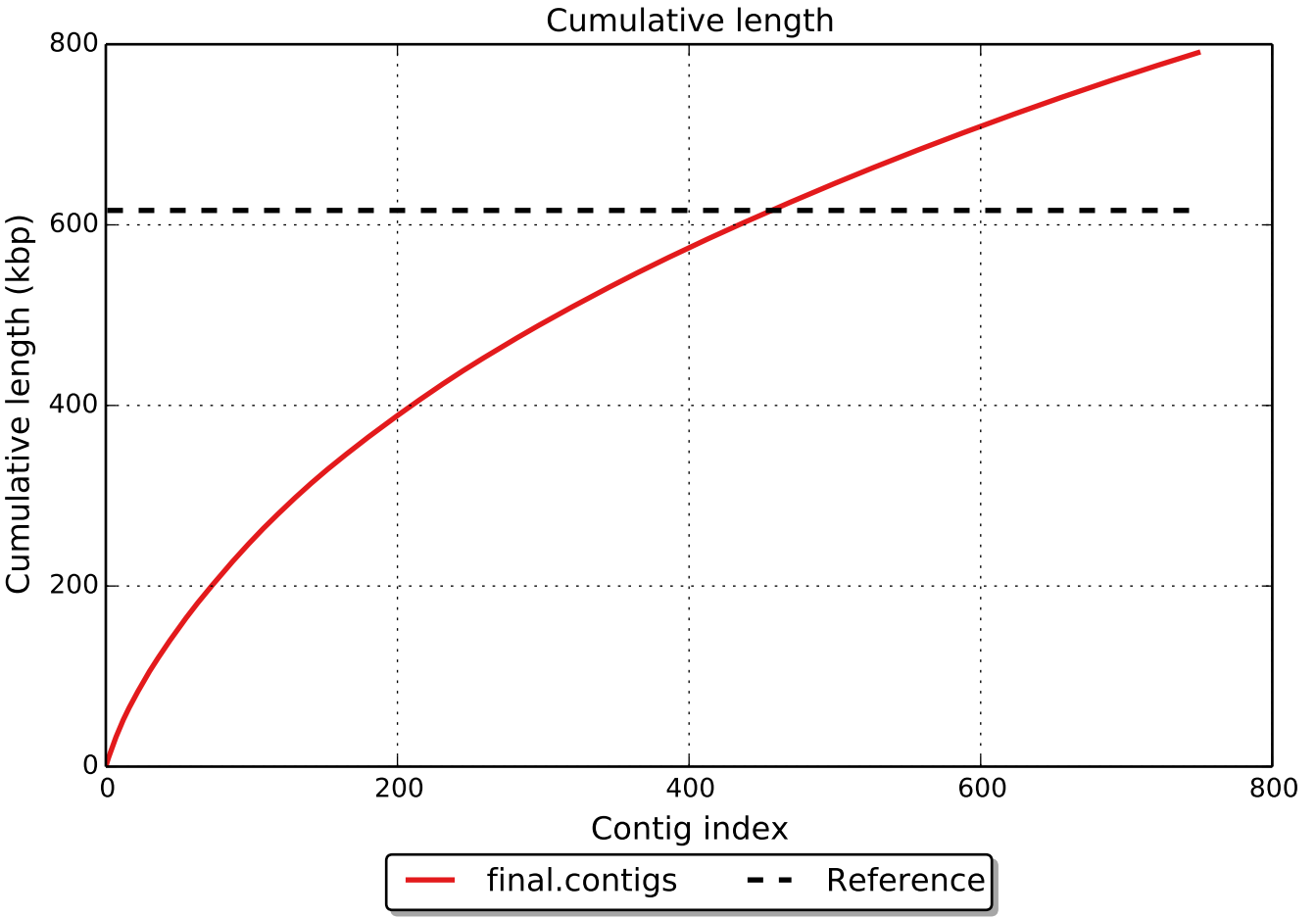
	final.contigs
# misassemblies	9
# relocations	9
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	9
Misassembled contigs length	8535
# local misassemblies	0
# mismatches	5281
# indels	2
# short indels	2
# long indels	0
Indels length	2

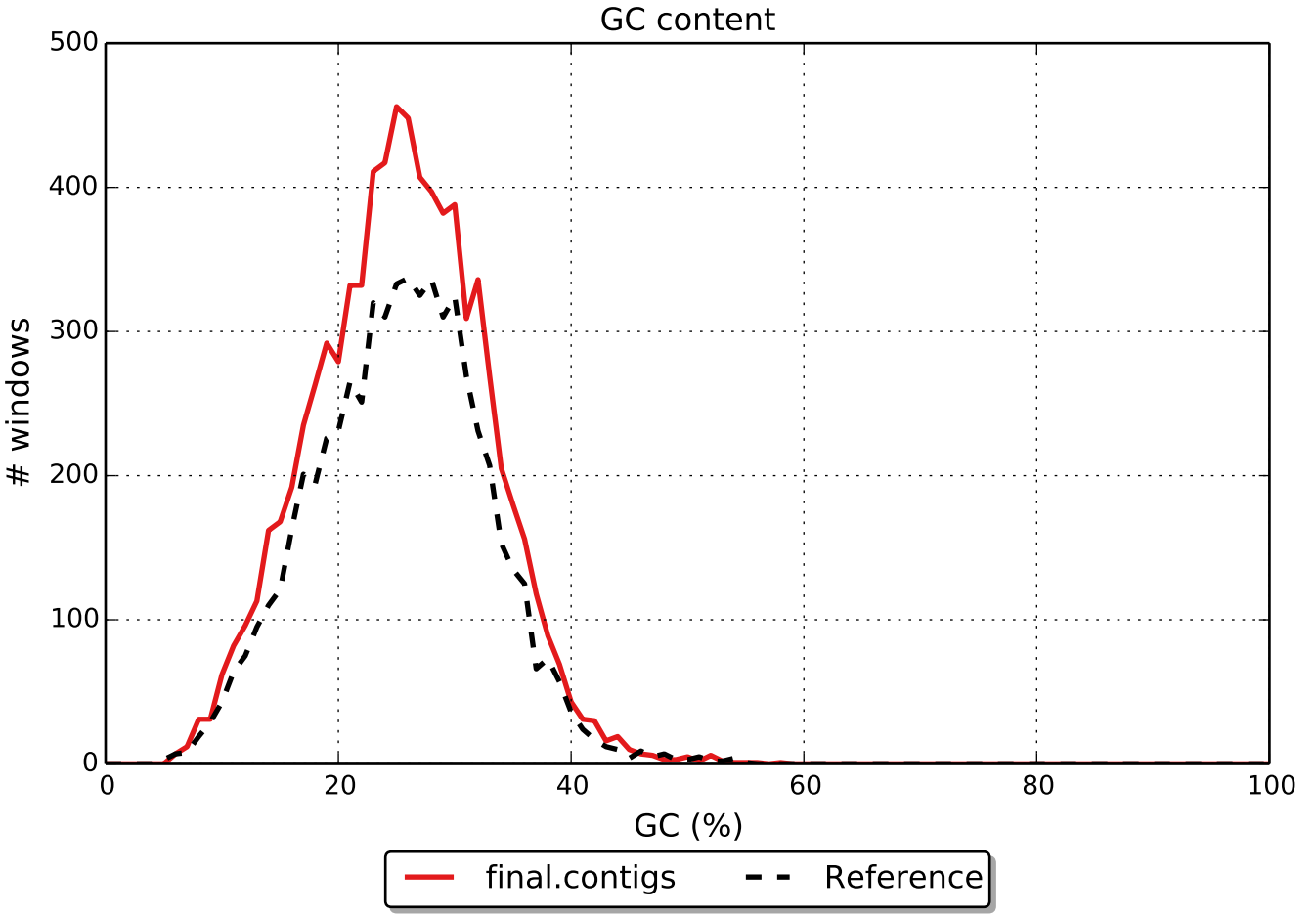
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

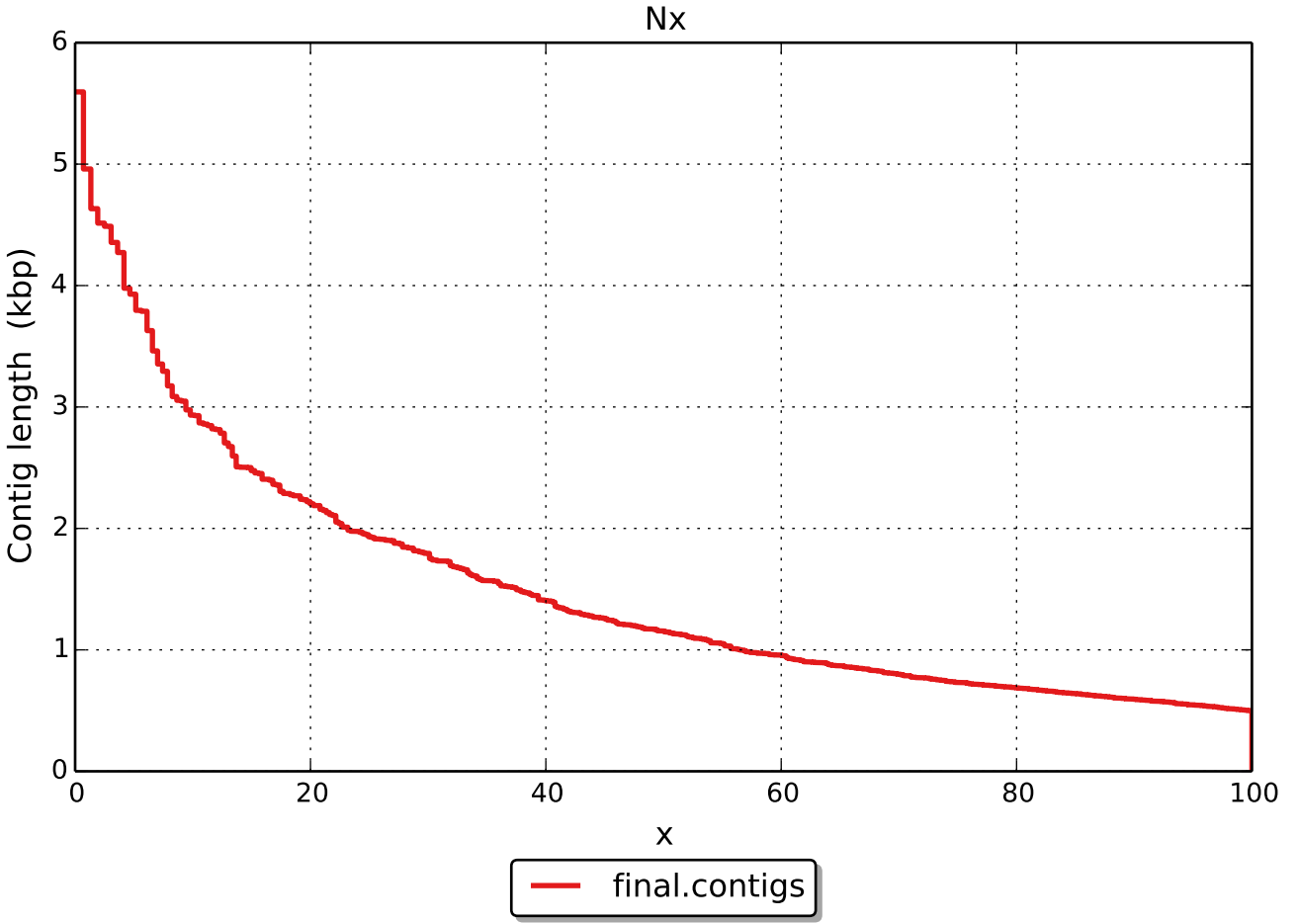
Unaligned report

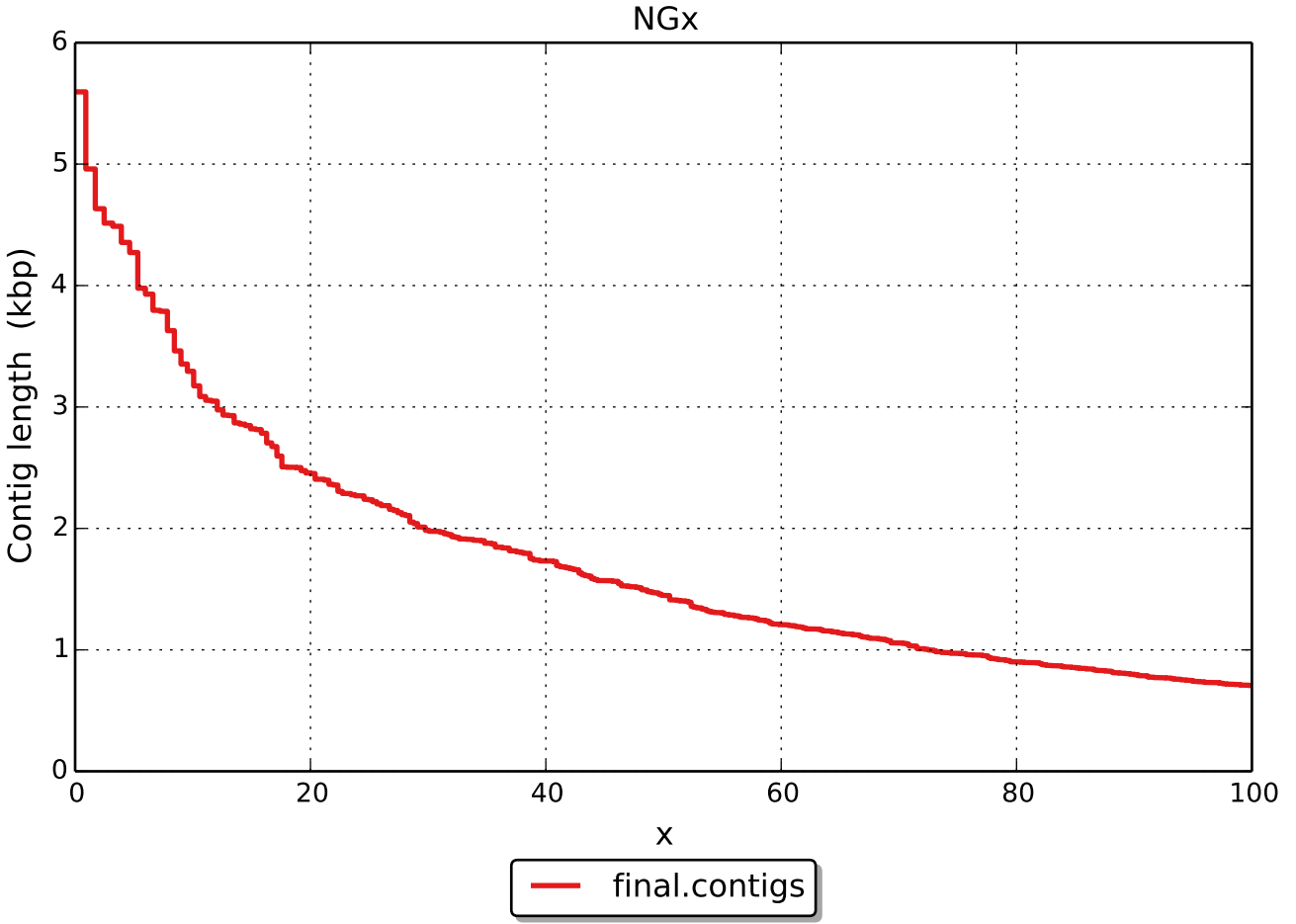
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

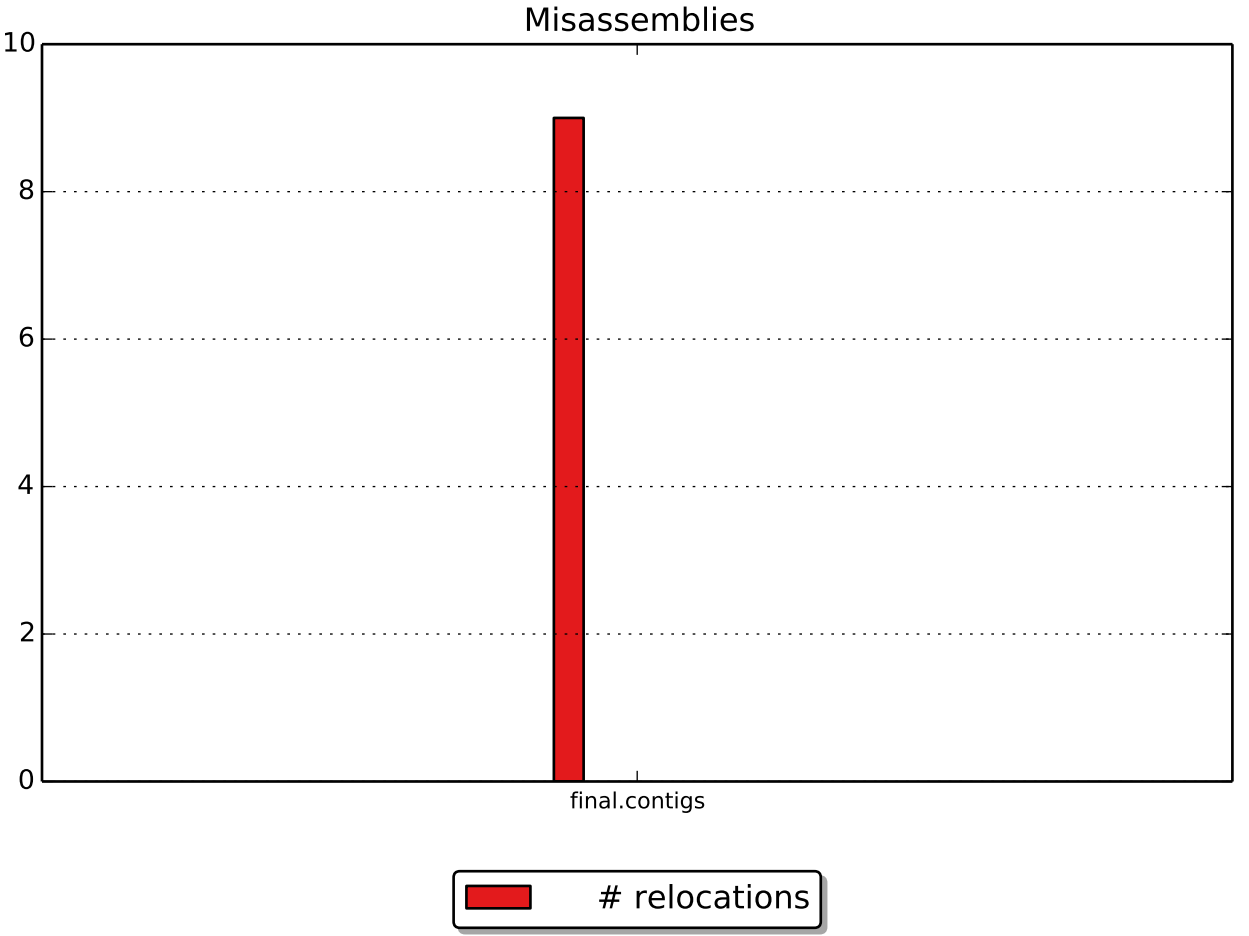
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

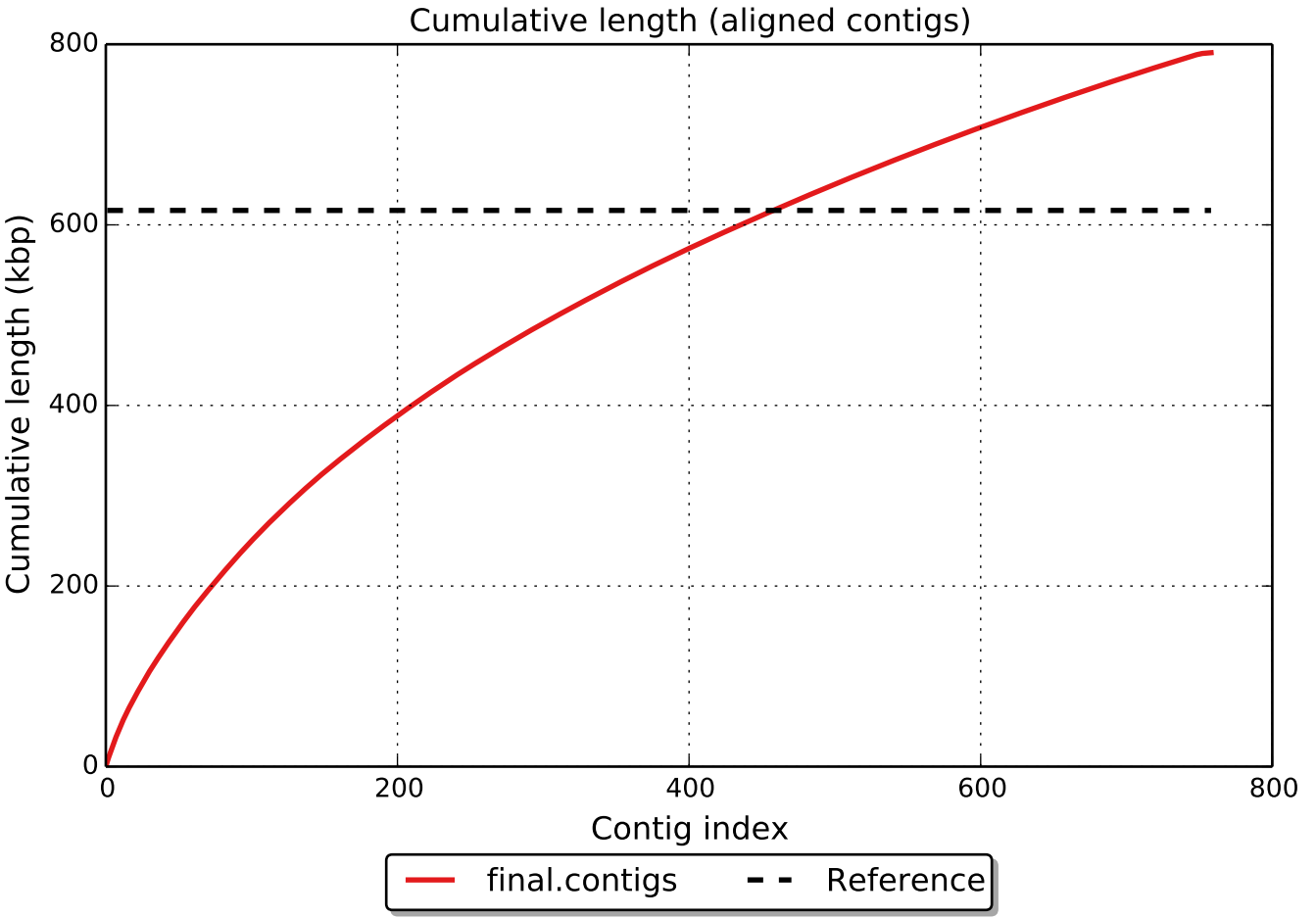

Cumulative length
Cumulative length (kbp)
800
600
400
200
0
0
200
400
600
800
Contig index
final.contigs
Reference

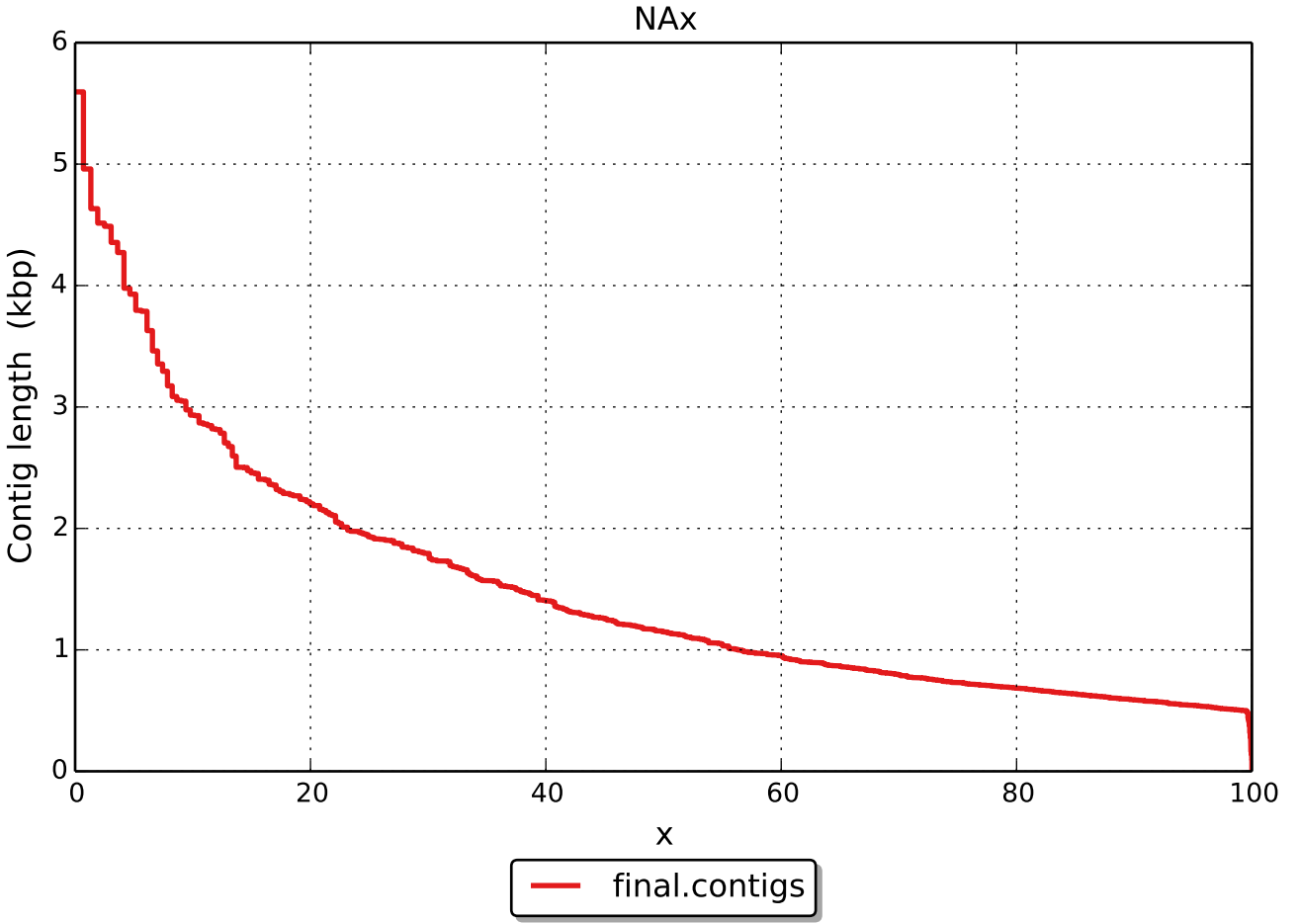

GC content
windows
GC (%)
0
100
200
300
400
500
0
20
40
60
80
100
final.contigs
Reference

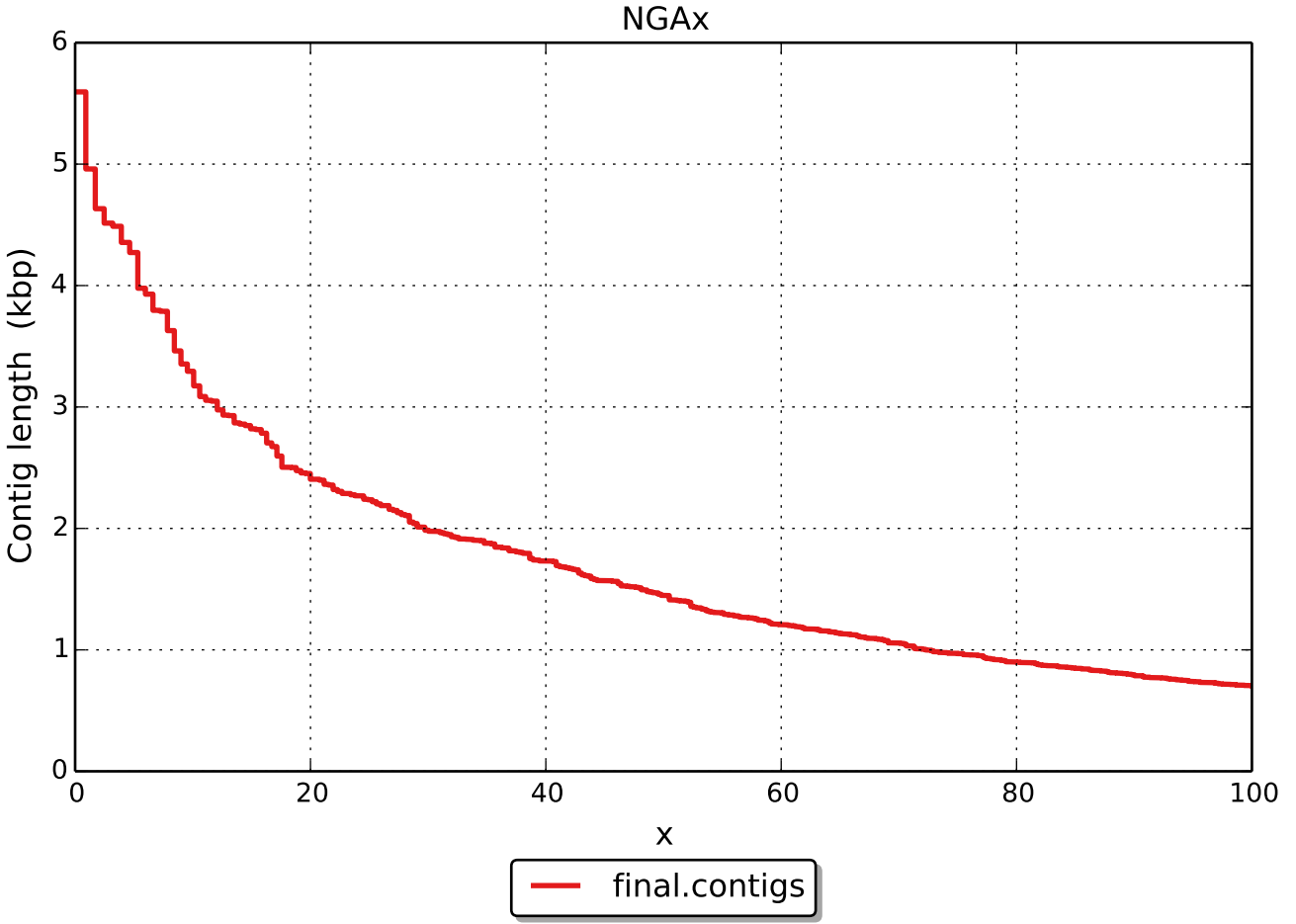

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
1
2
3
4
5
6
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
200
400
600
800
Contig index
final.contigs
Reference


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


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