Report

	final.contigs
# contigs (>= 0 bp)	975
# contigs (>= 1000 bp)	485
Total length (>= 0 bp)	1337010
Total length (>= 1000 bp)	1057848
# contigs	767
Largest contig	9818
Total length	1260254
Reference length	1283598
GC (%)	26.31
Reference GC (%)	26.29
N50	2043
NG50	2012
N75	1285
NG75	1254
L50	188
LG50	193
L75	386
LG75	400
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	8348
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.685
Duplication ratio	1.037
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.30
# indels per 100 kbp	0.08
Largest alignment	9818
NA50	2043
NGA50	2012
NA75	1285
NGA75	1254
LA50	188
LGA50	194
LA75	387
LGA75	401

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

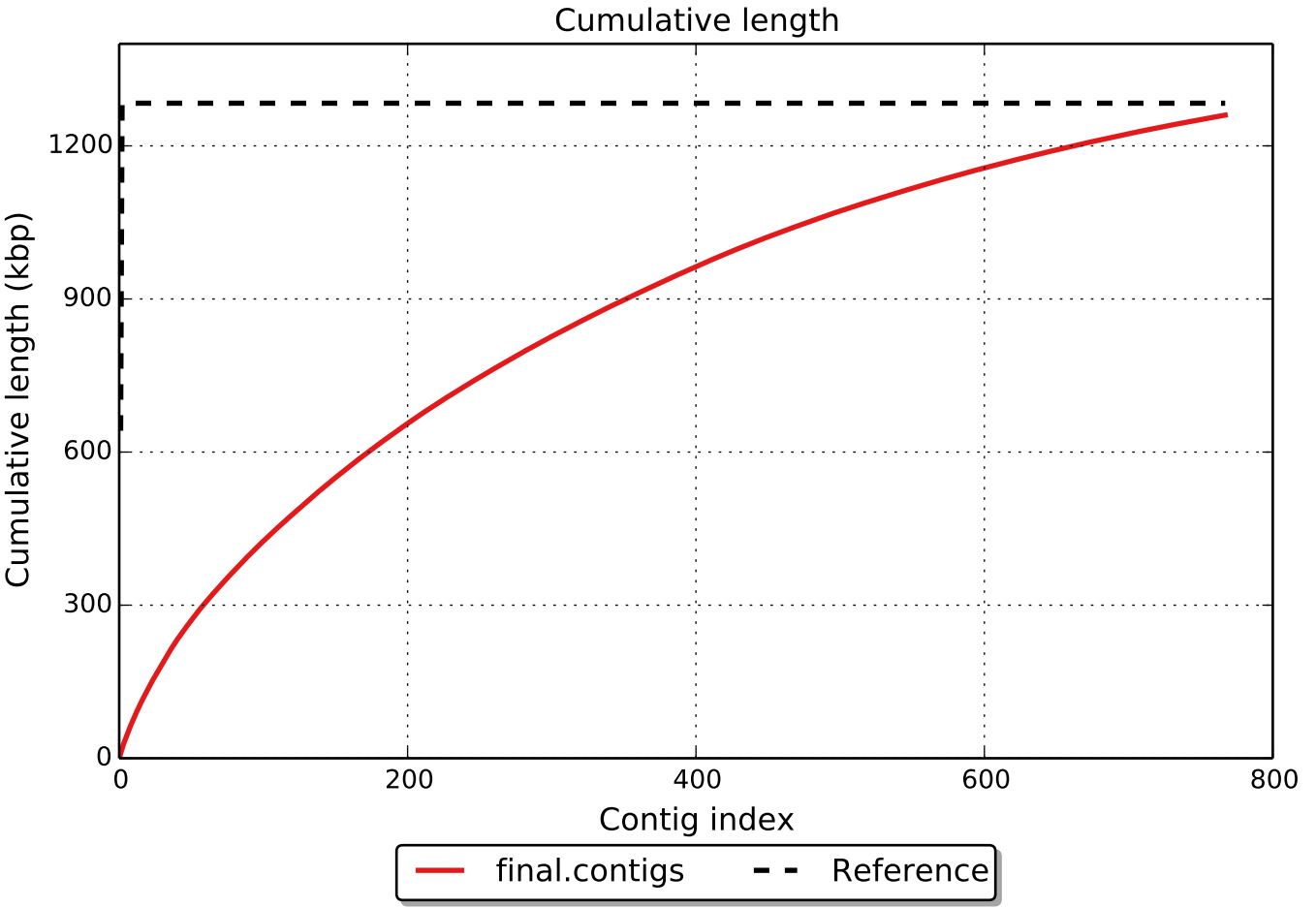
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	8348
# local misassemblies	0
# mismatches	186
# indels	1
# short indels	0
# long indels	1
Indels length	14

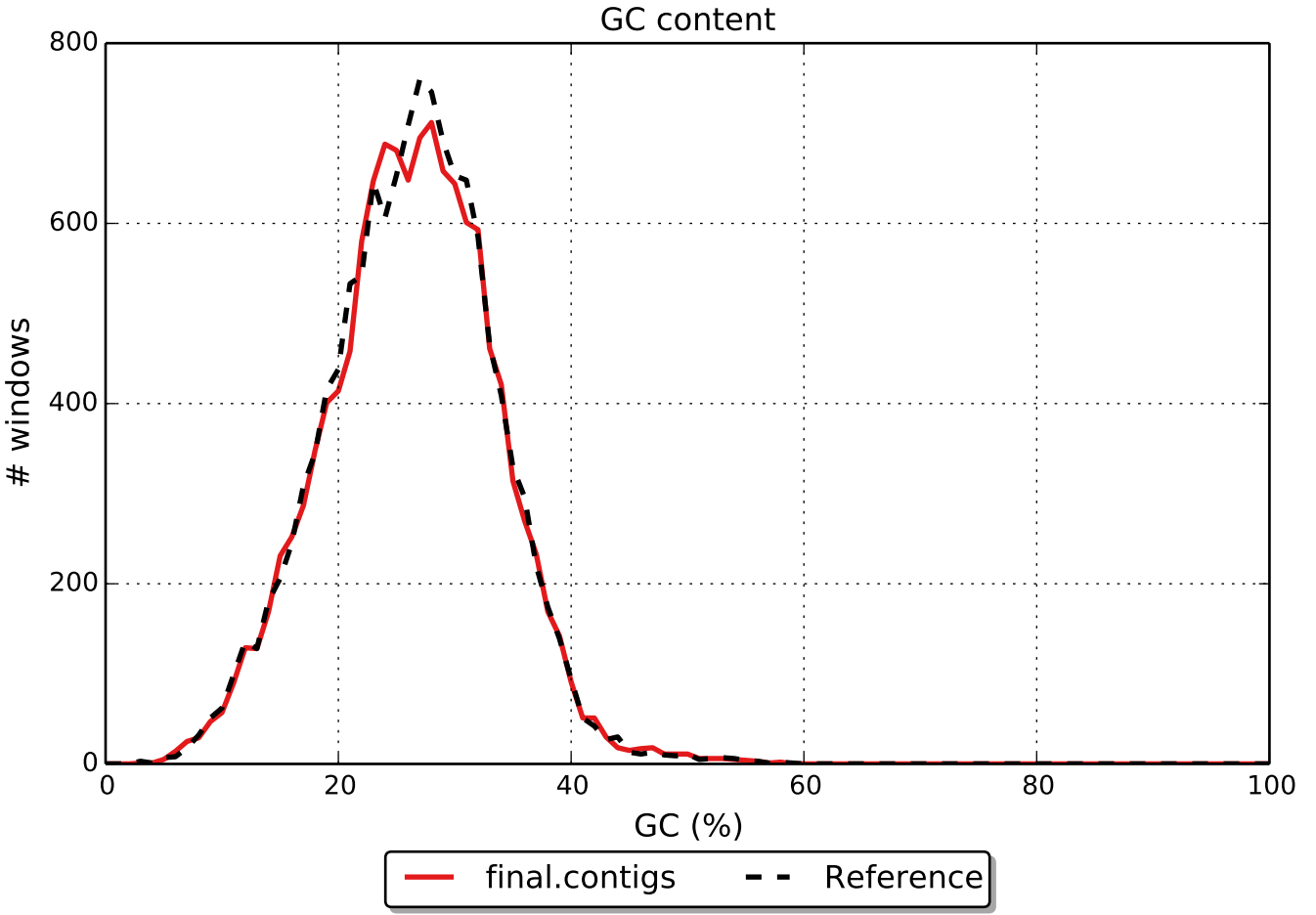
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

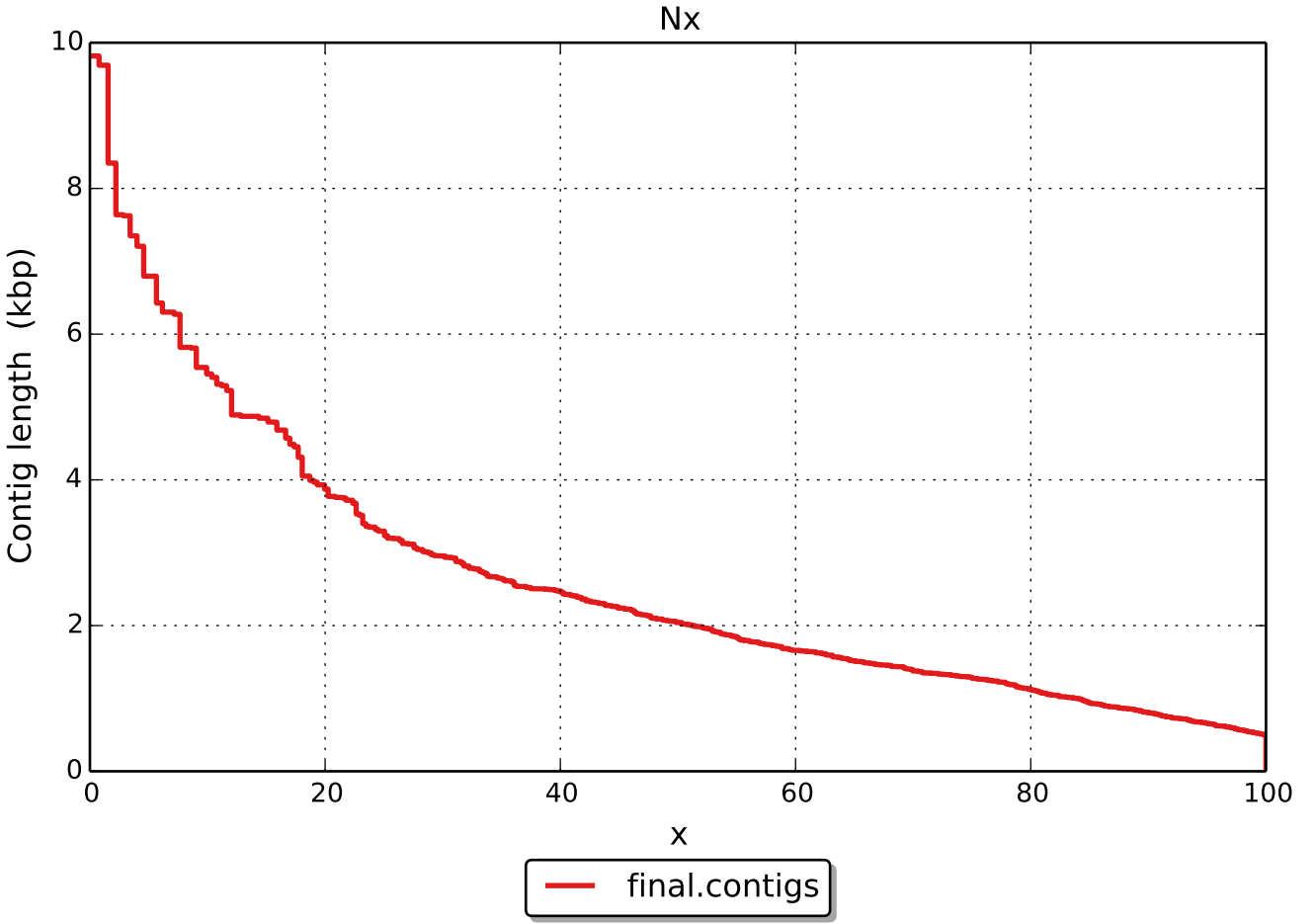
Unaligned report

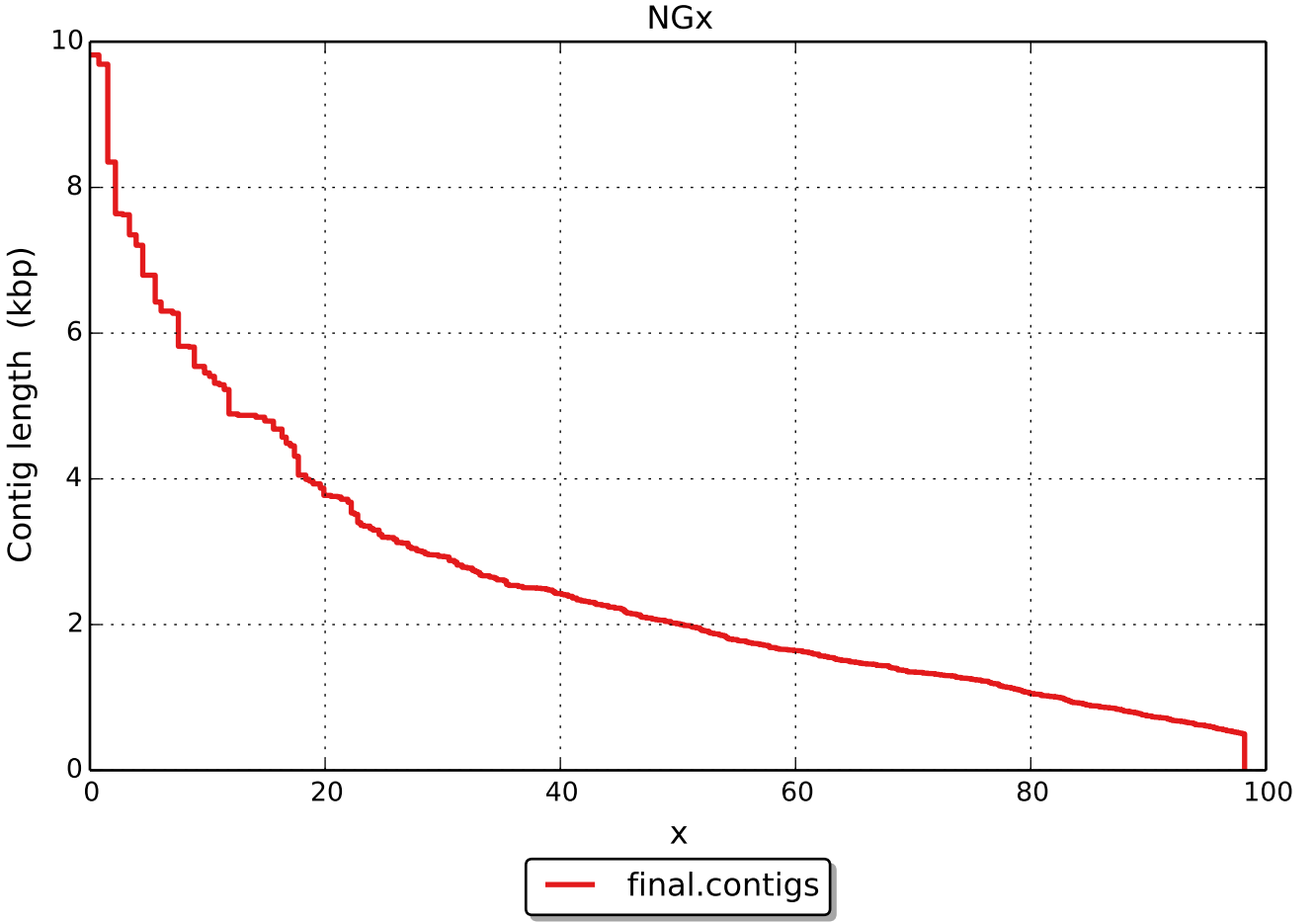
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

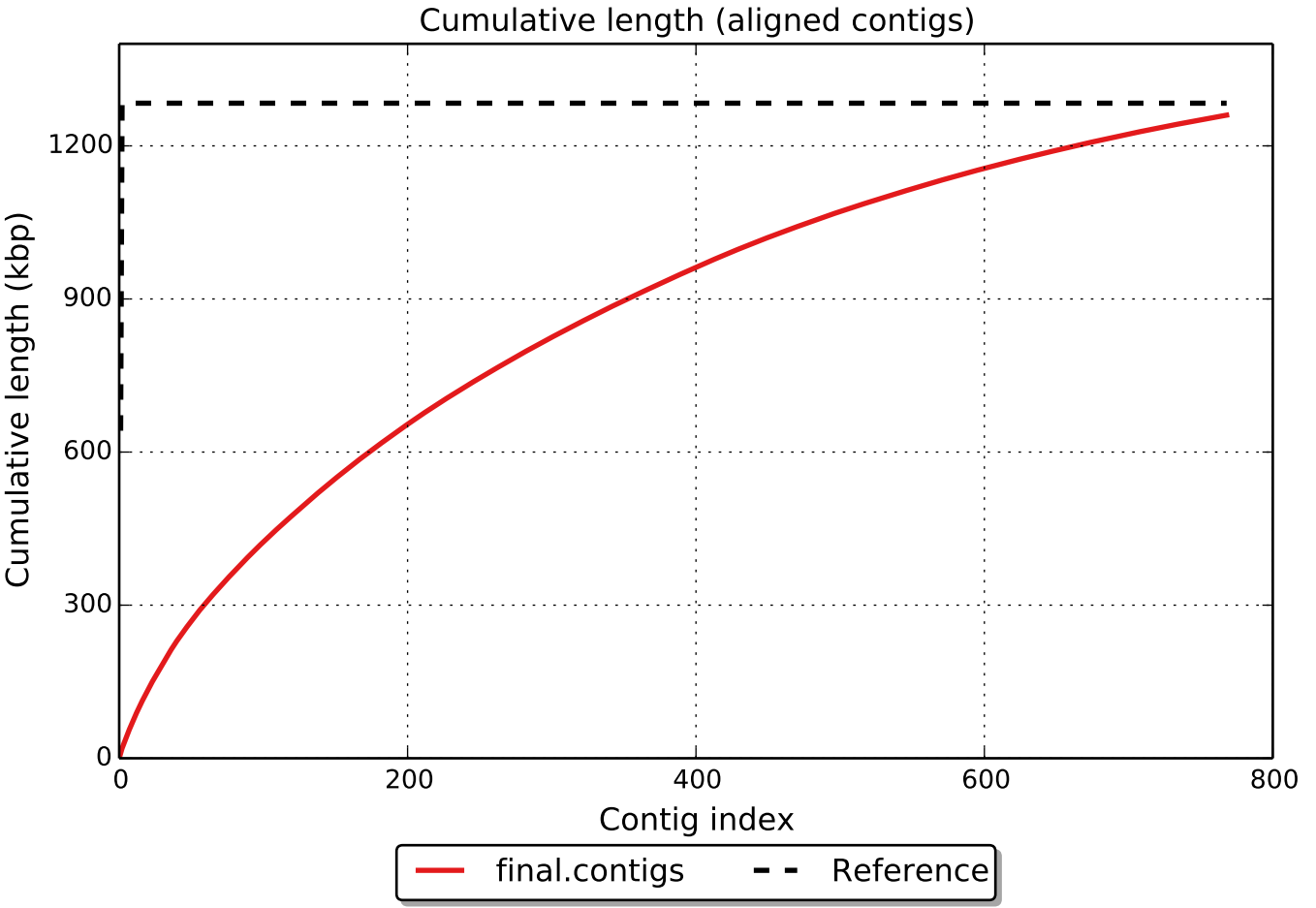

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
Contig index
final.contigs
Reference

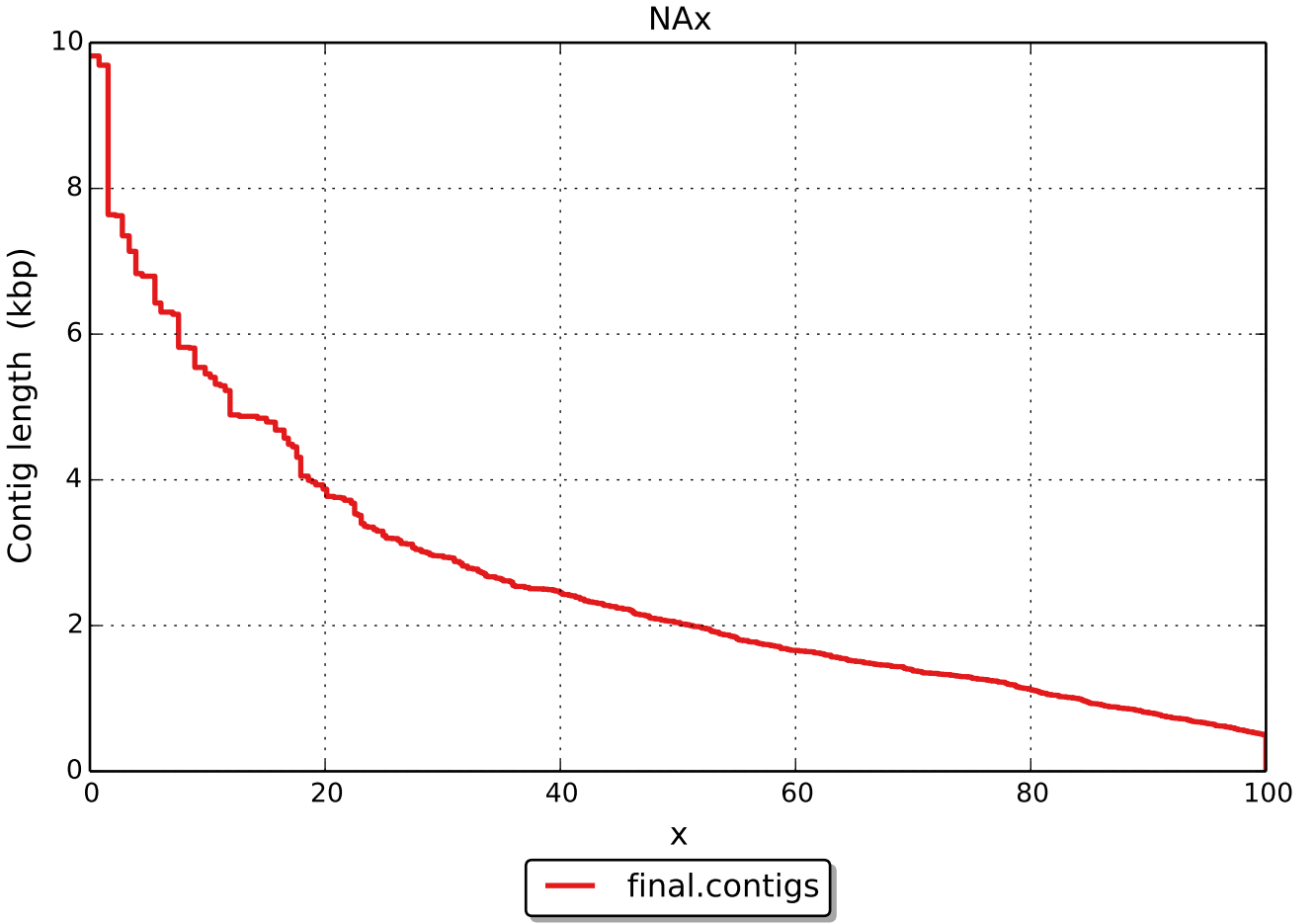

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

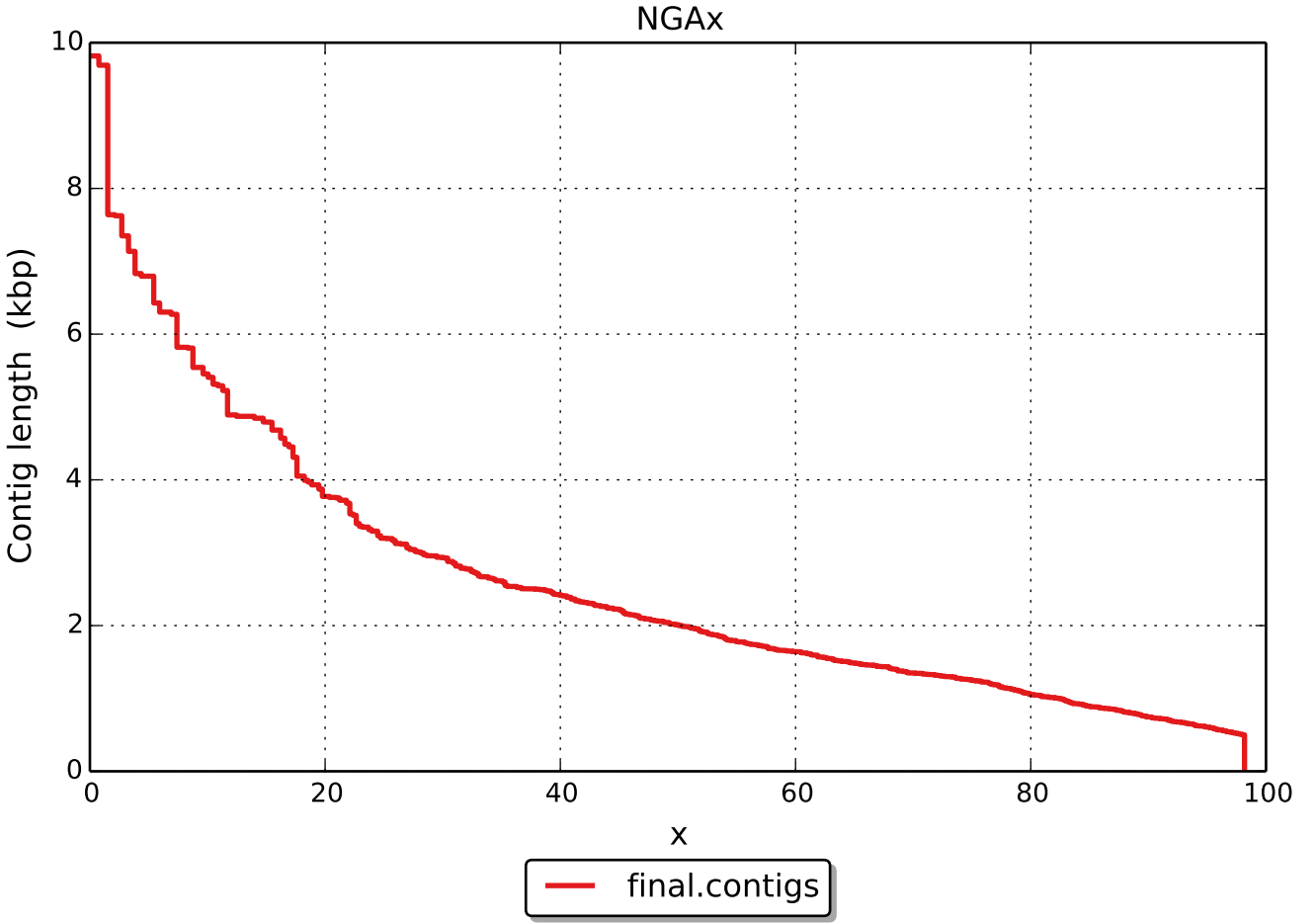

Nx
Contig length (kbp)
0
2
4
6
8
10
0
20
40
60
80
100
x
final.contigs


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

Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
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