Report

	final.contigs
# contigs (>= 0 bp)	1053
# contigs (>= 1000 bp)	482
Total length (>= 0 bp)	1276156
Total length (>= 1000 bp)	930688
# contigs	844
Largest contig	8031
Total length	1200225
Reference length	1231960
GC (%)	25.34
Reference GC (%)	25.34
N50	1711
NG50	1666
N75	1058
NG75	1011
L50	230
LG50	240
L75	453
LG75	476
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.268
Duplication ratio	1.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	73.45
# indels per 100 kbp	0.00
Largest alignment	8031
NA50	1711
NGA50	1666
NA75	1058
NGA75	1011
LA50	230
LGA50	240
LA75	453
LGA75	476

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

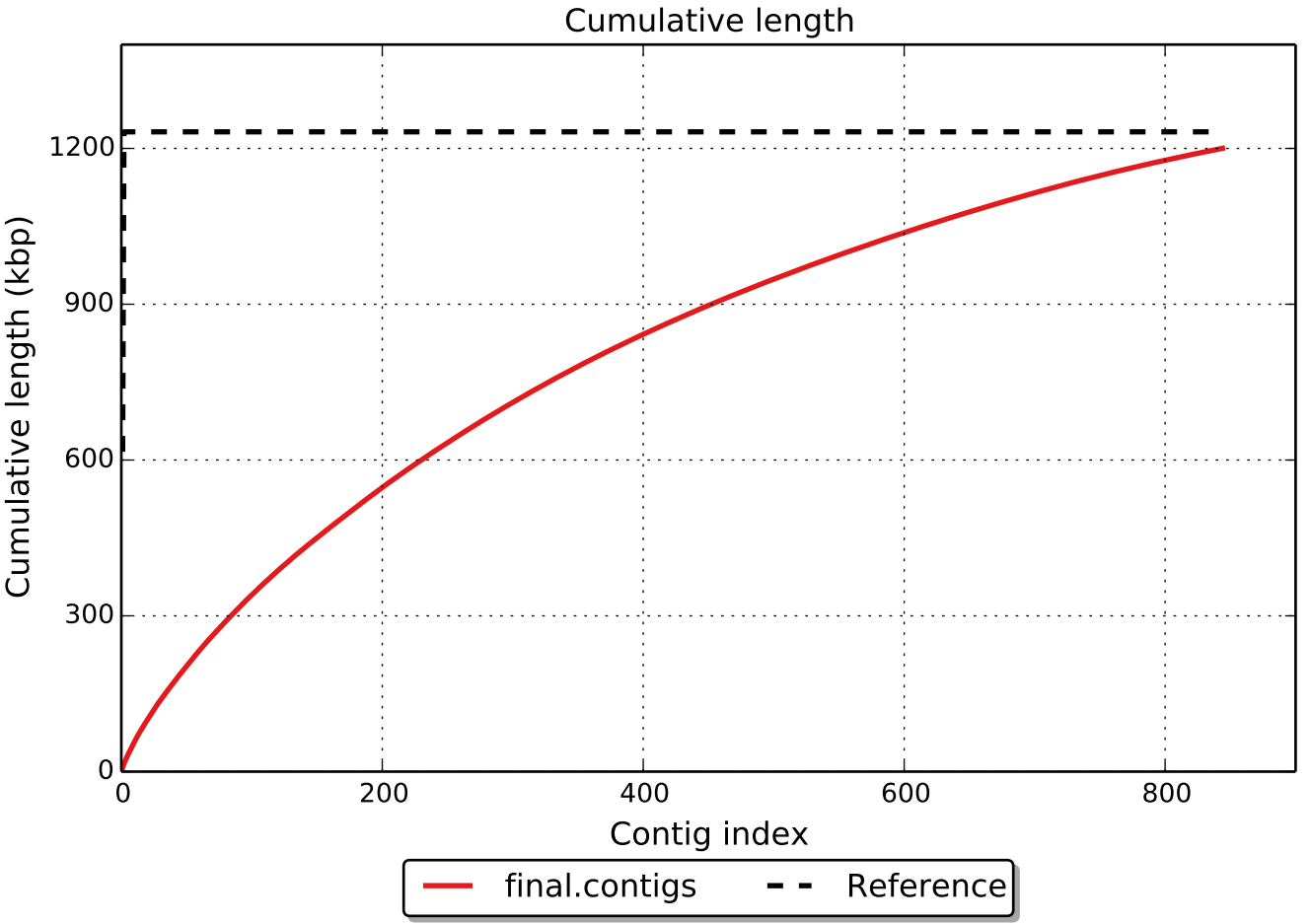
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	844
# indels	0
# short indels	0
# long indels	0
Indels length	0

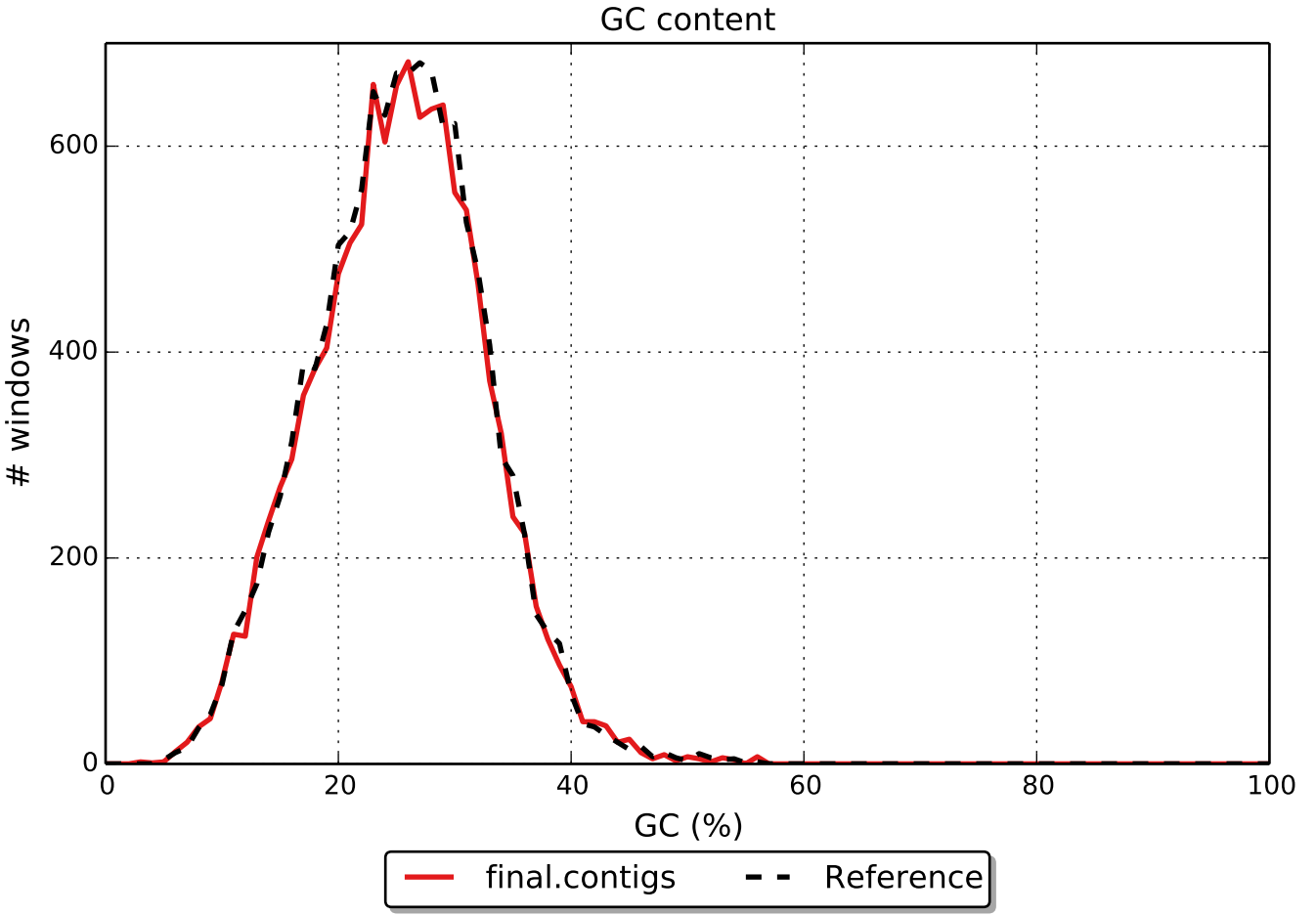
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

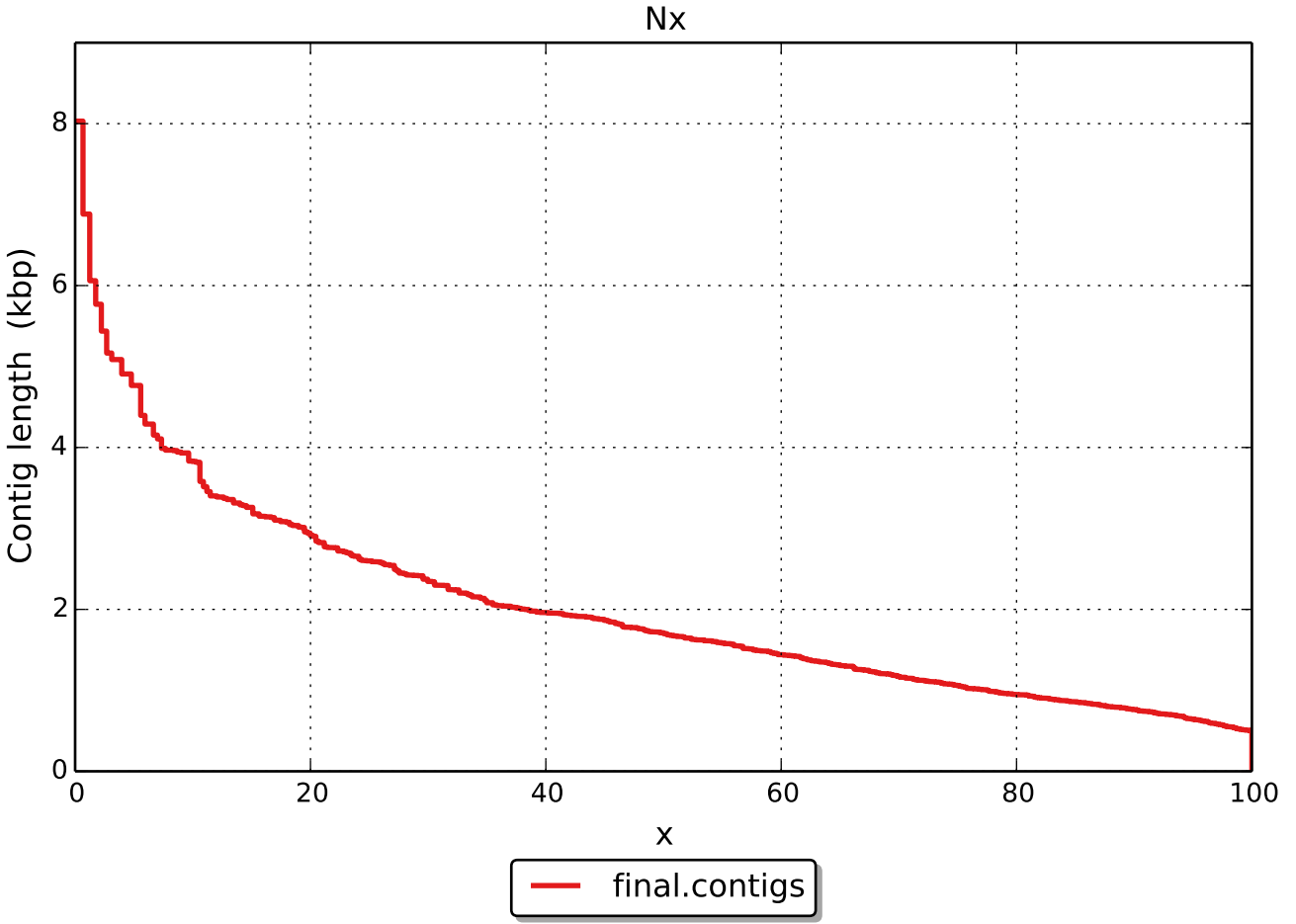
Unaligned report

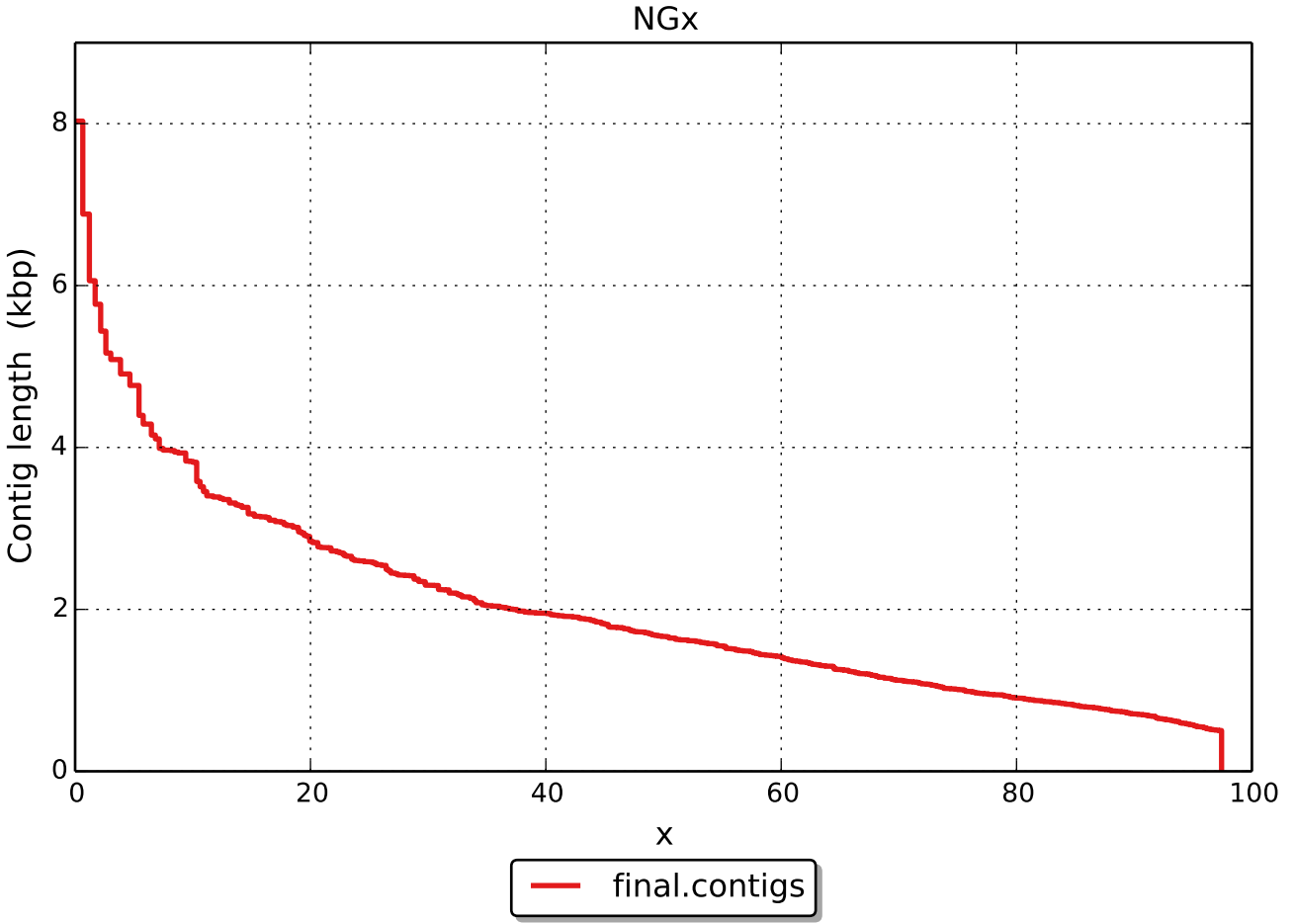
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

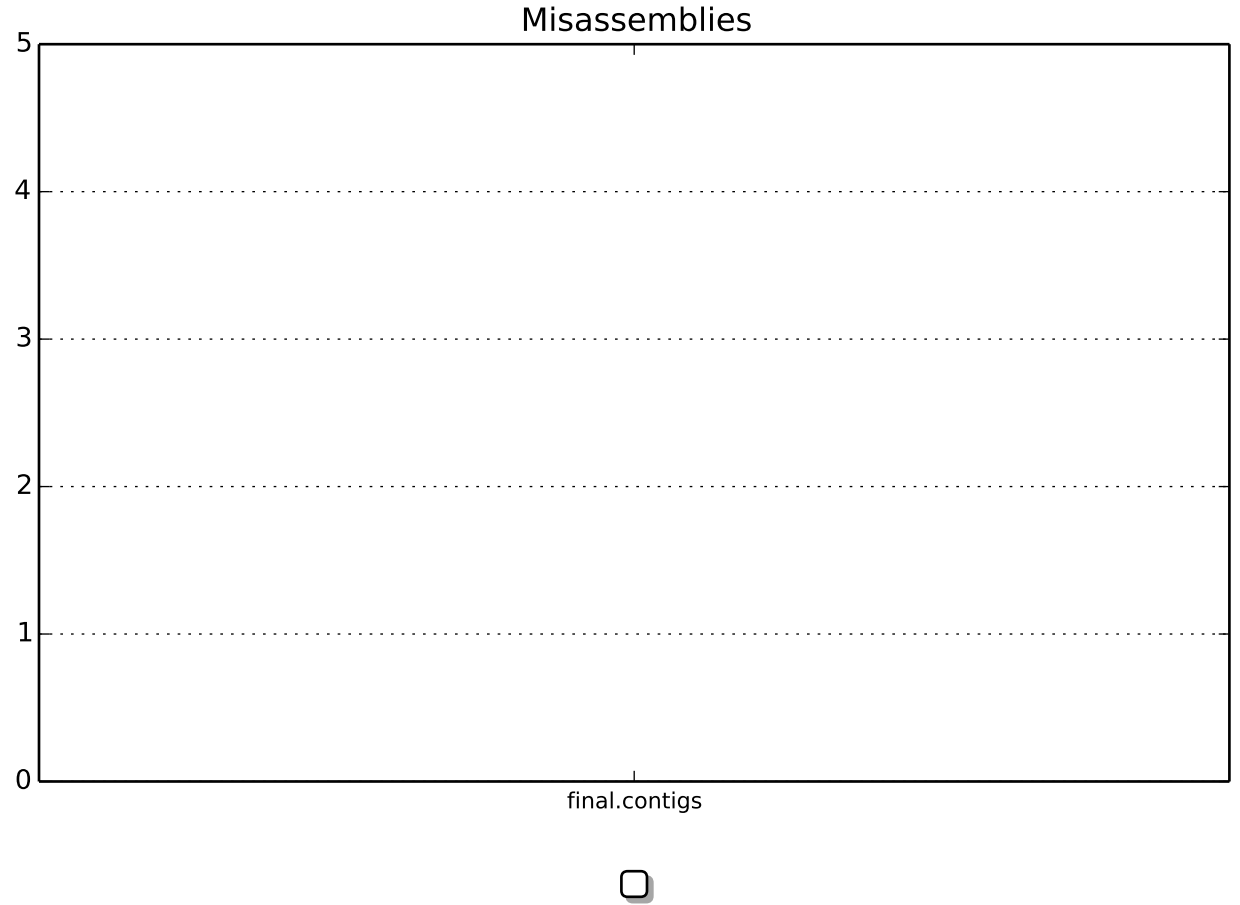
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

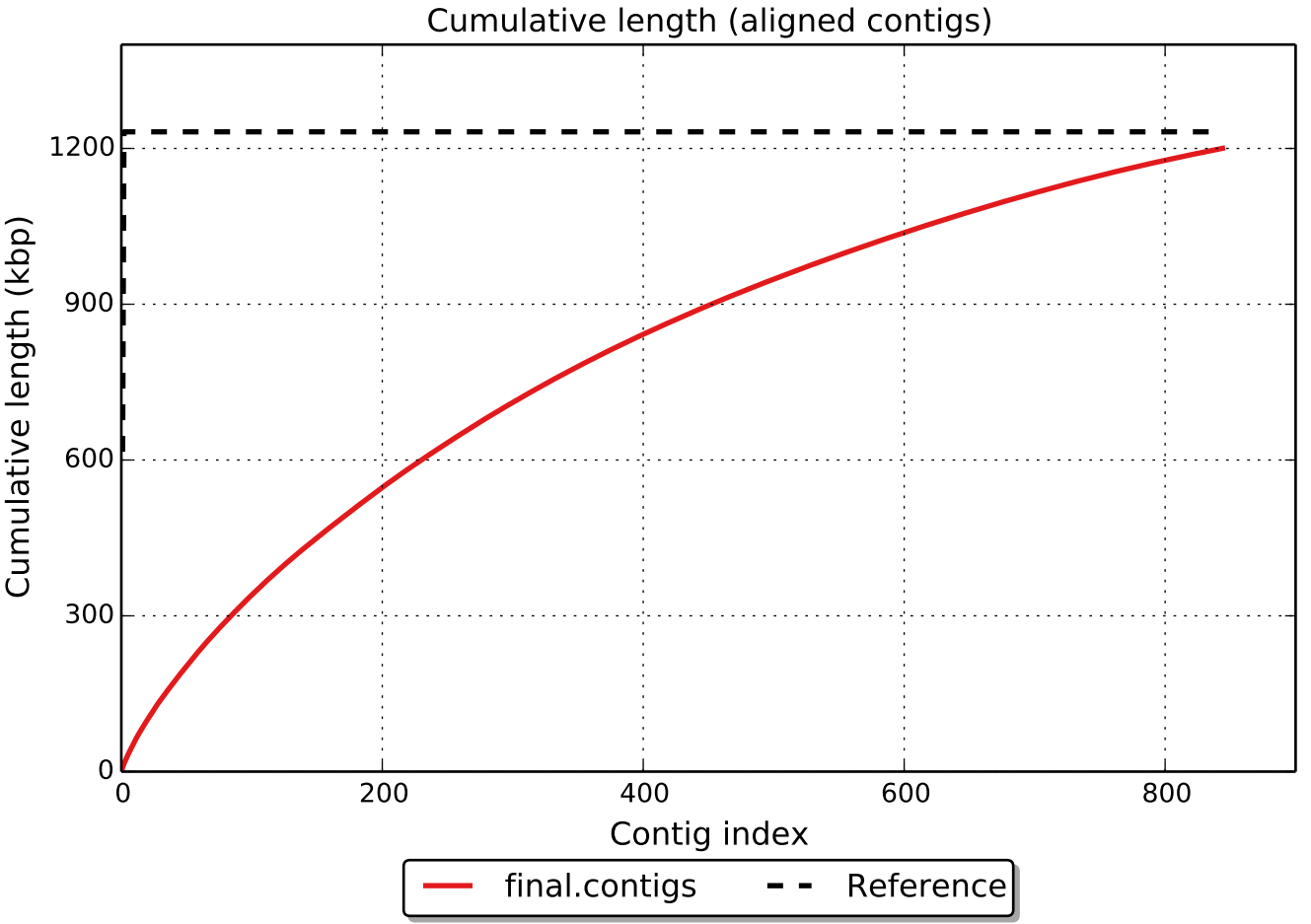

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
Contig index
final.contigs
Reference

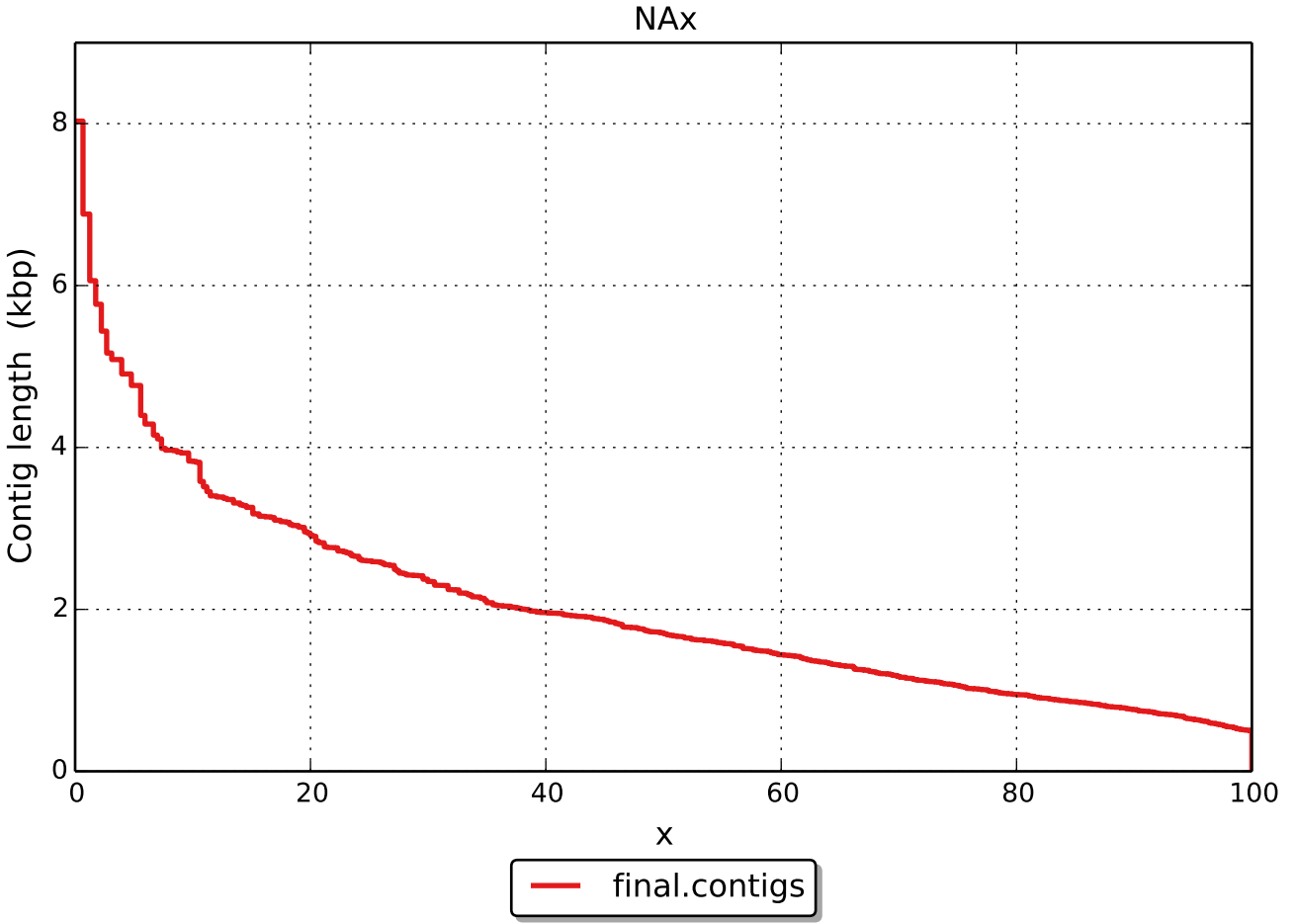

GC content
windows
GC (%)
0
200
400
600
0
20
40
60
80
100
final.contigs
Reference

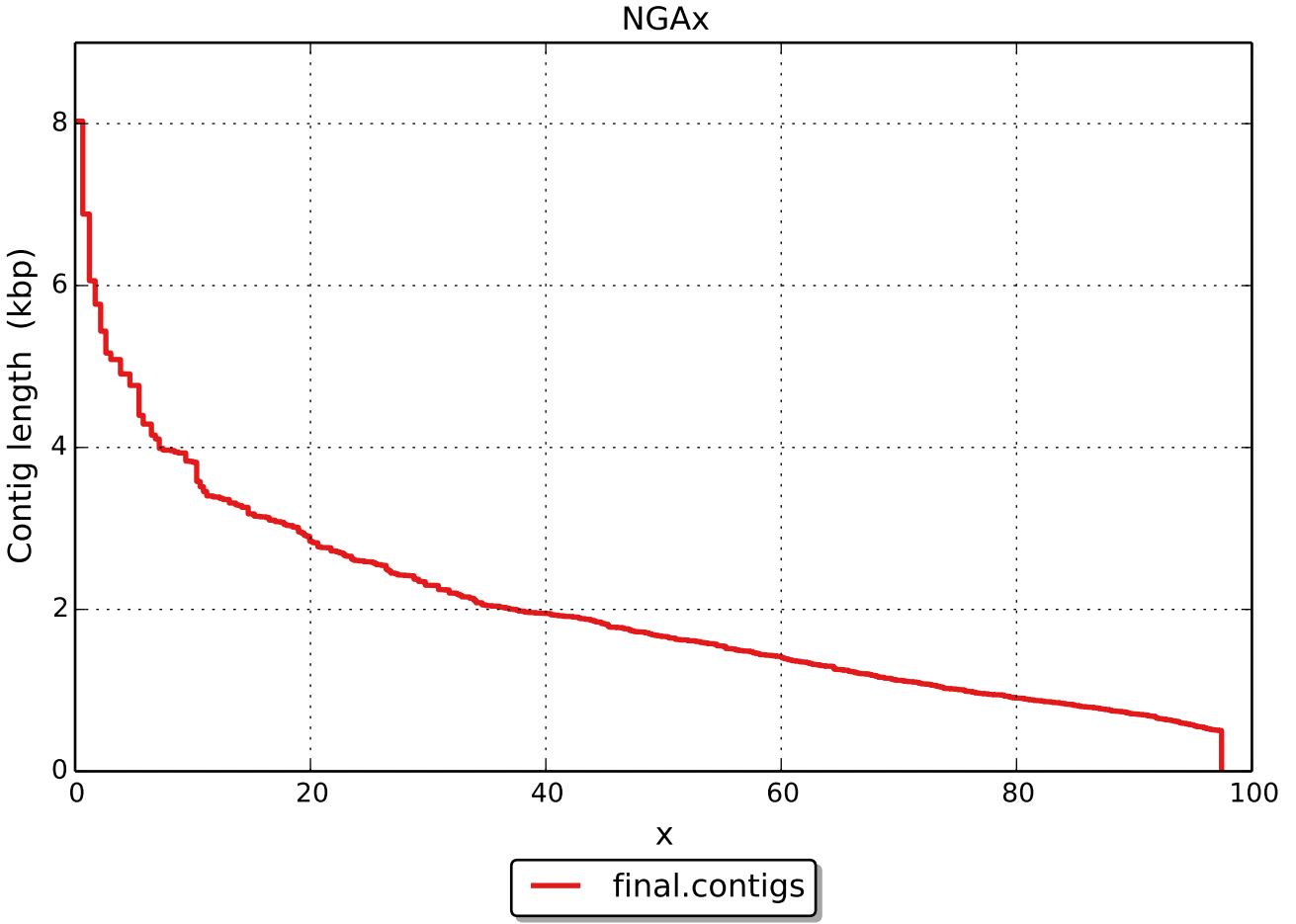

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


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


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


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