Report

	final.contigs
# contigs (>= 0 bp)	856
# contigs (>= 1000 bp)	484
Total length (>= 0 bp)	1210881
Total length (>= 1000 bp)	934344
# contigs	856
Largest contig	8031
Total length	1210881
Reference length	615980
GC (%)	25.34
Reference GC (%)	25.33
N50	1700
NG50	2587
N75	1045
NG75	1999
L50	233
LG50	88
L75	459
LG75	156
# misassemblies	28
# misassembled contigs	27
Misassembled contigs length	66201
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	916
Genome fraction (%)	96.530
Duplication ratio	2.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1656.05
# indels per 100 kbp	2.52
Largest alignment	8031
NA50	1664
NGA50	2425
NA75	1017
NGA75	1955
LA50	243
LGA50	92
LA75	474
LGA75	164

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

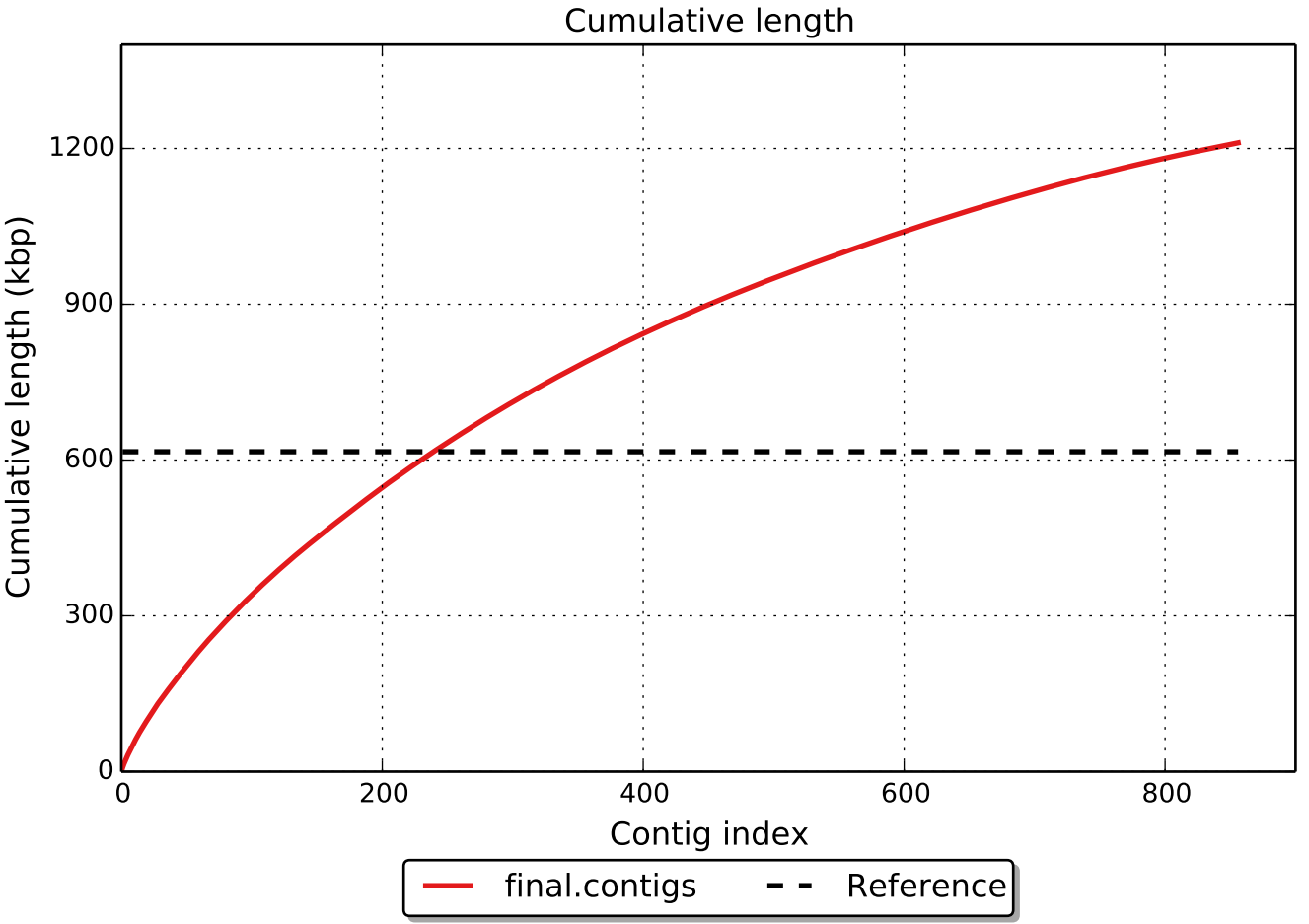
	final.contigs
# misassemblies	28
# relocations	28
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	27
Misassembled contigs length	66201
# local misassemblies	0
# mismatches	9847
# indels	15
# short indels	15
# long indels	0
Indels length	15

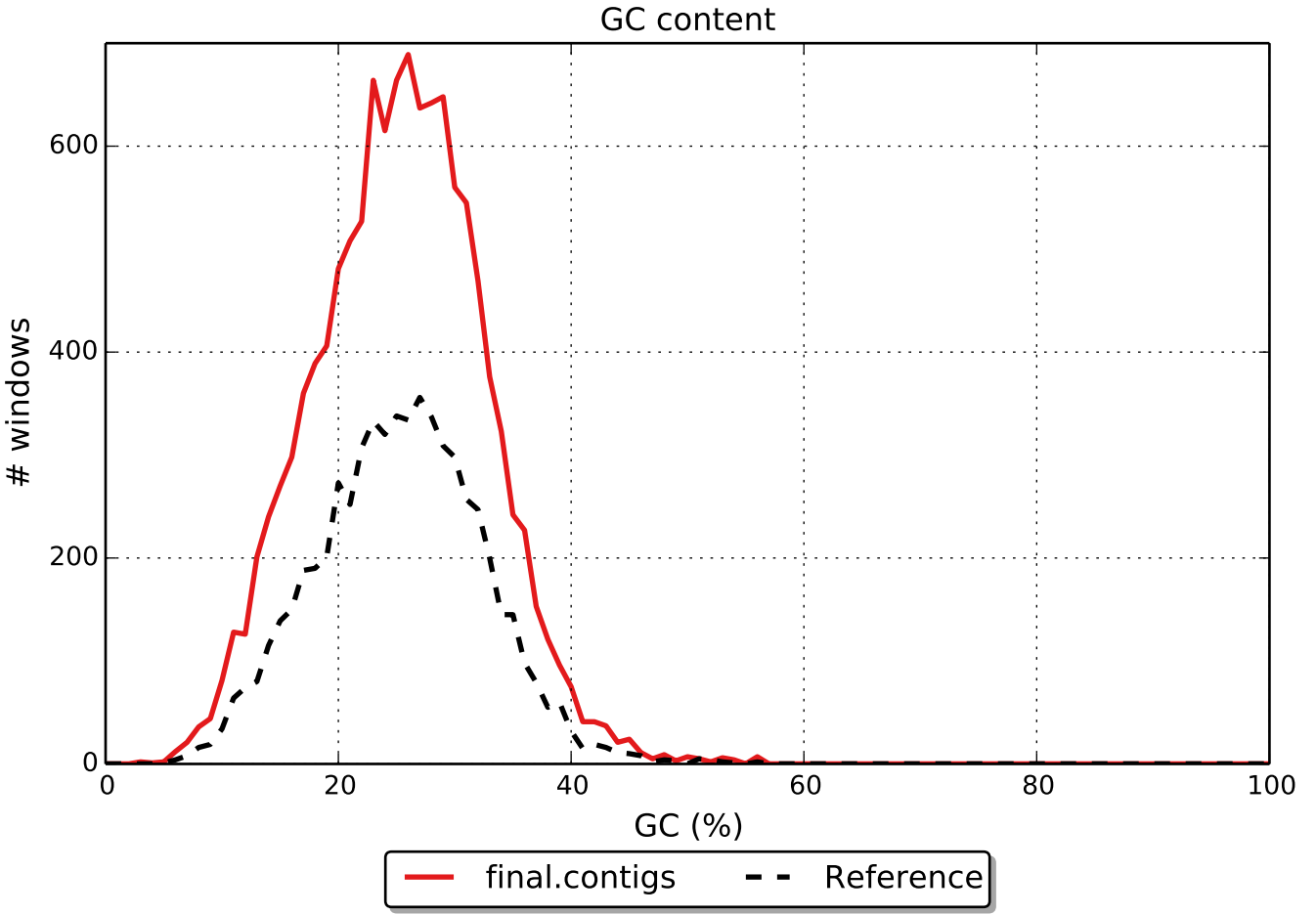
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

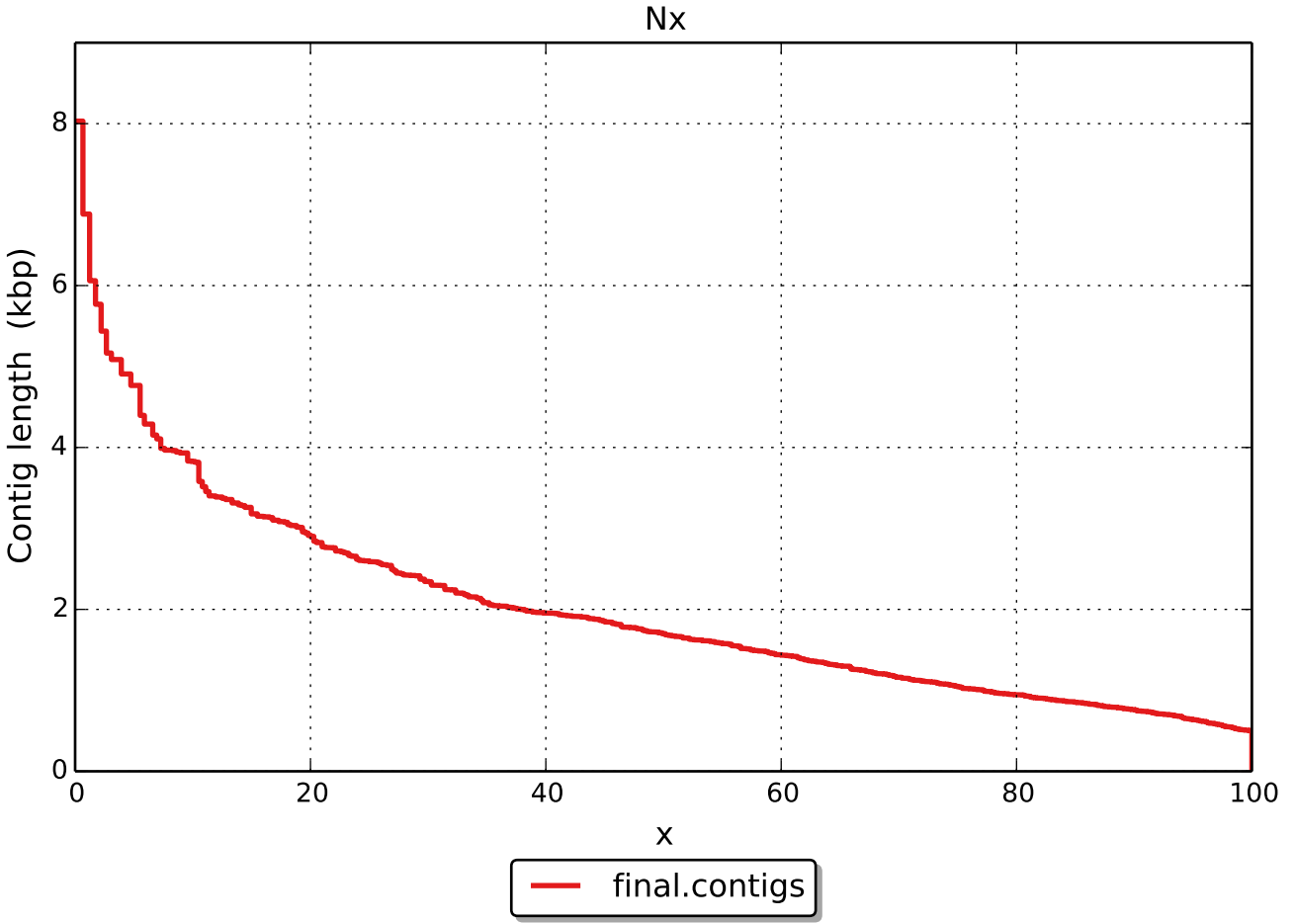
Unaligned report

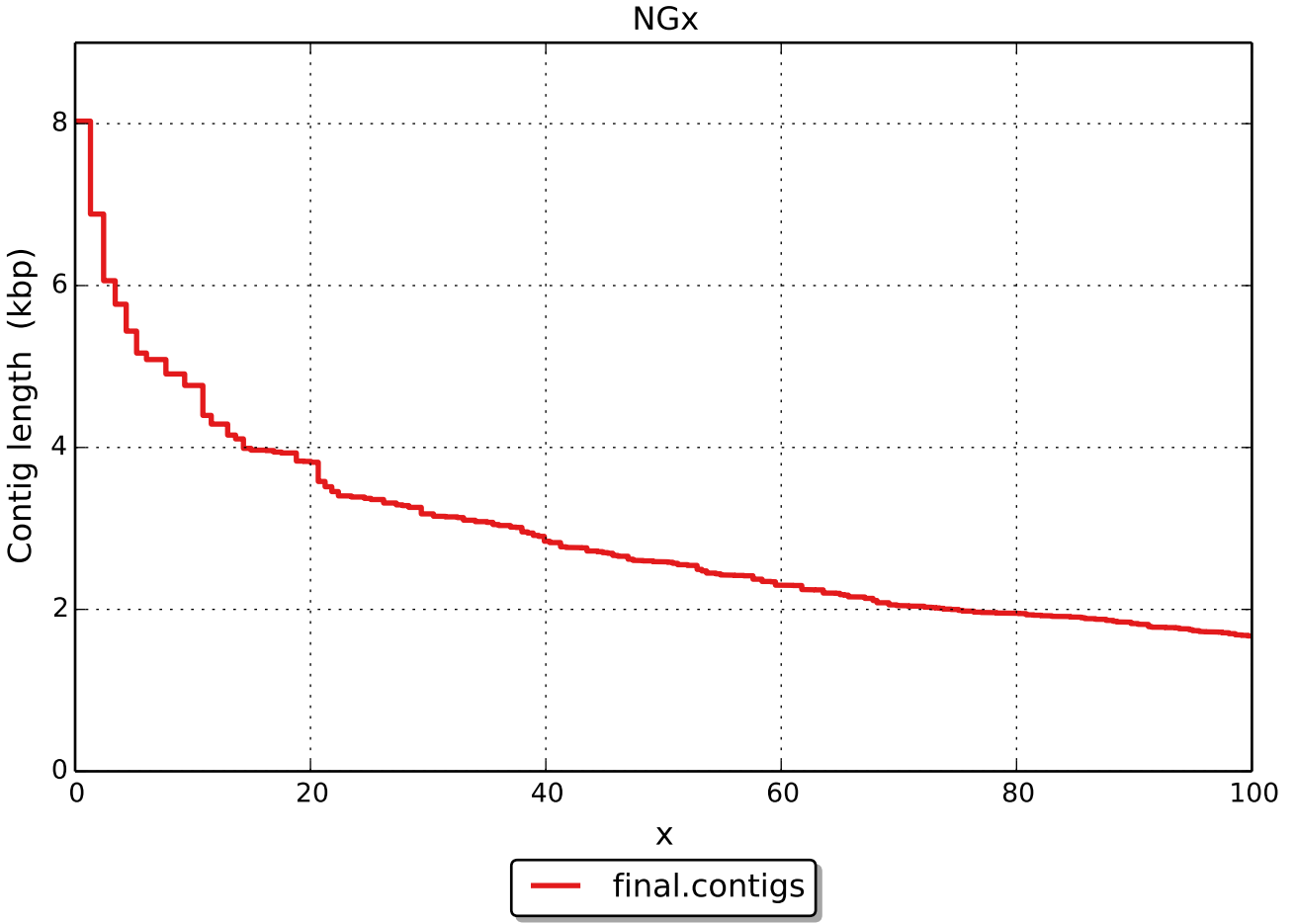
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	916
# N's	0

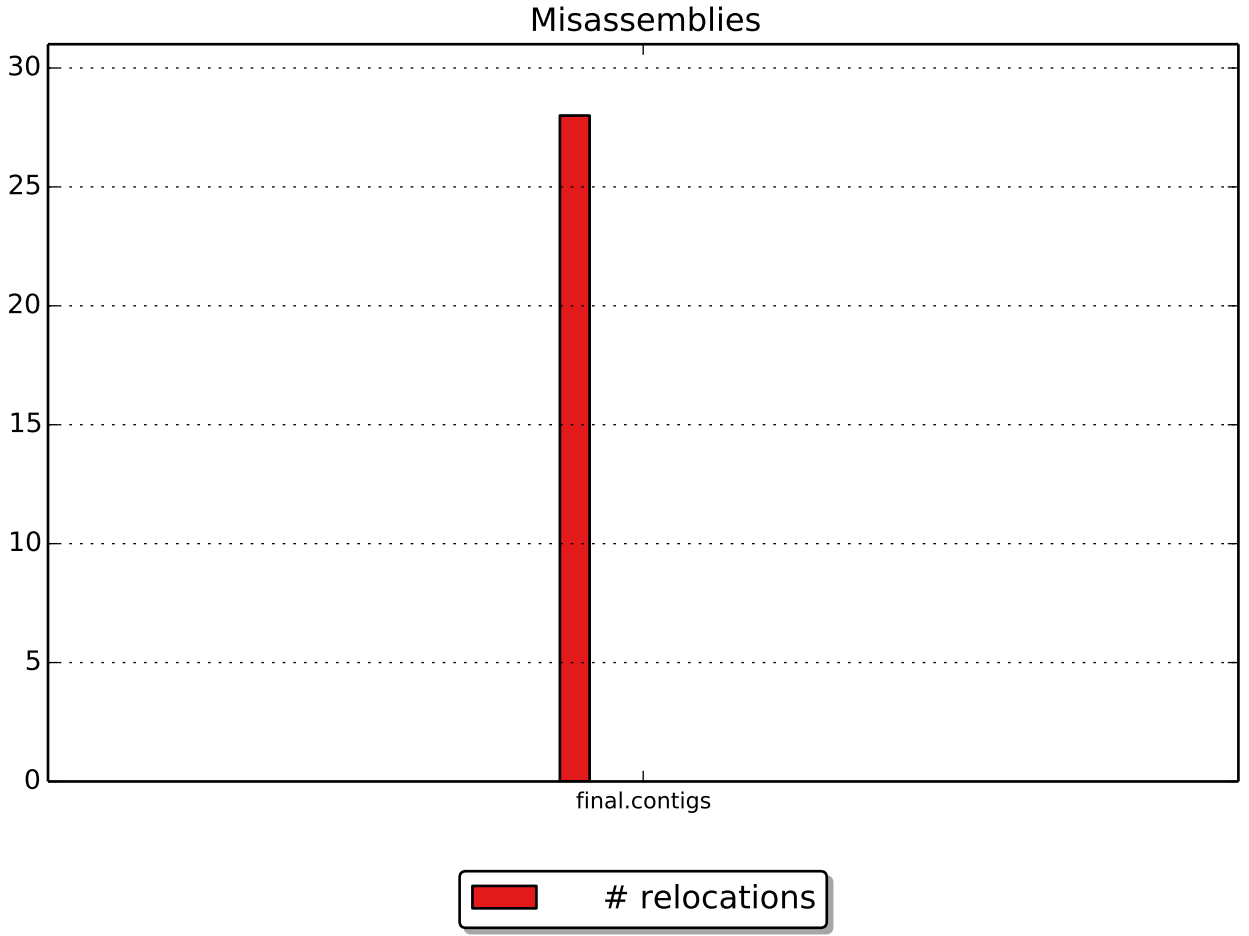
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

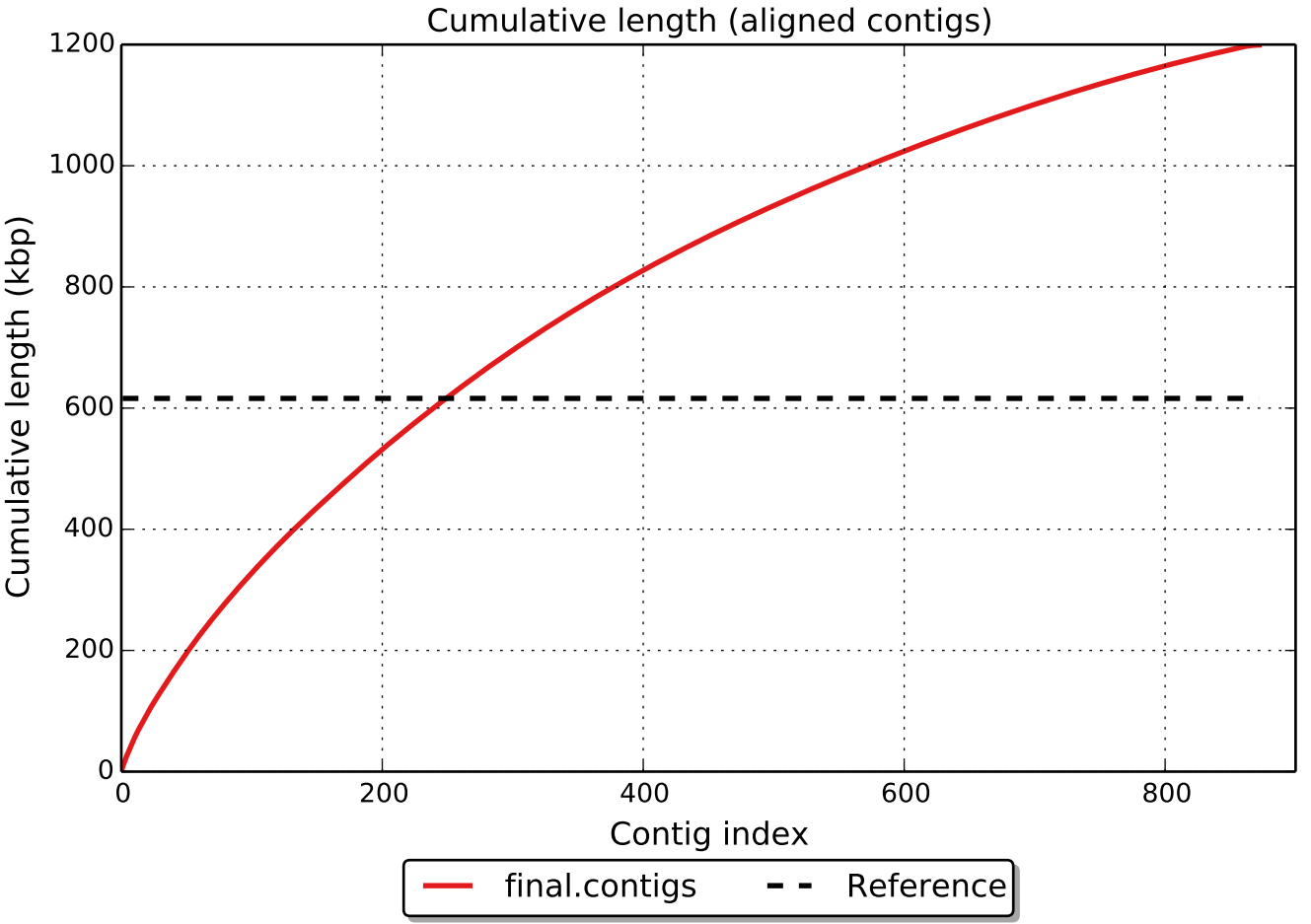

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
200
400
600
800
Contig index
final.contigs
Reference

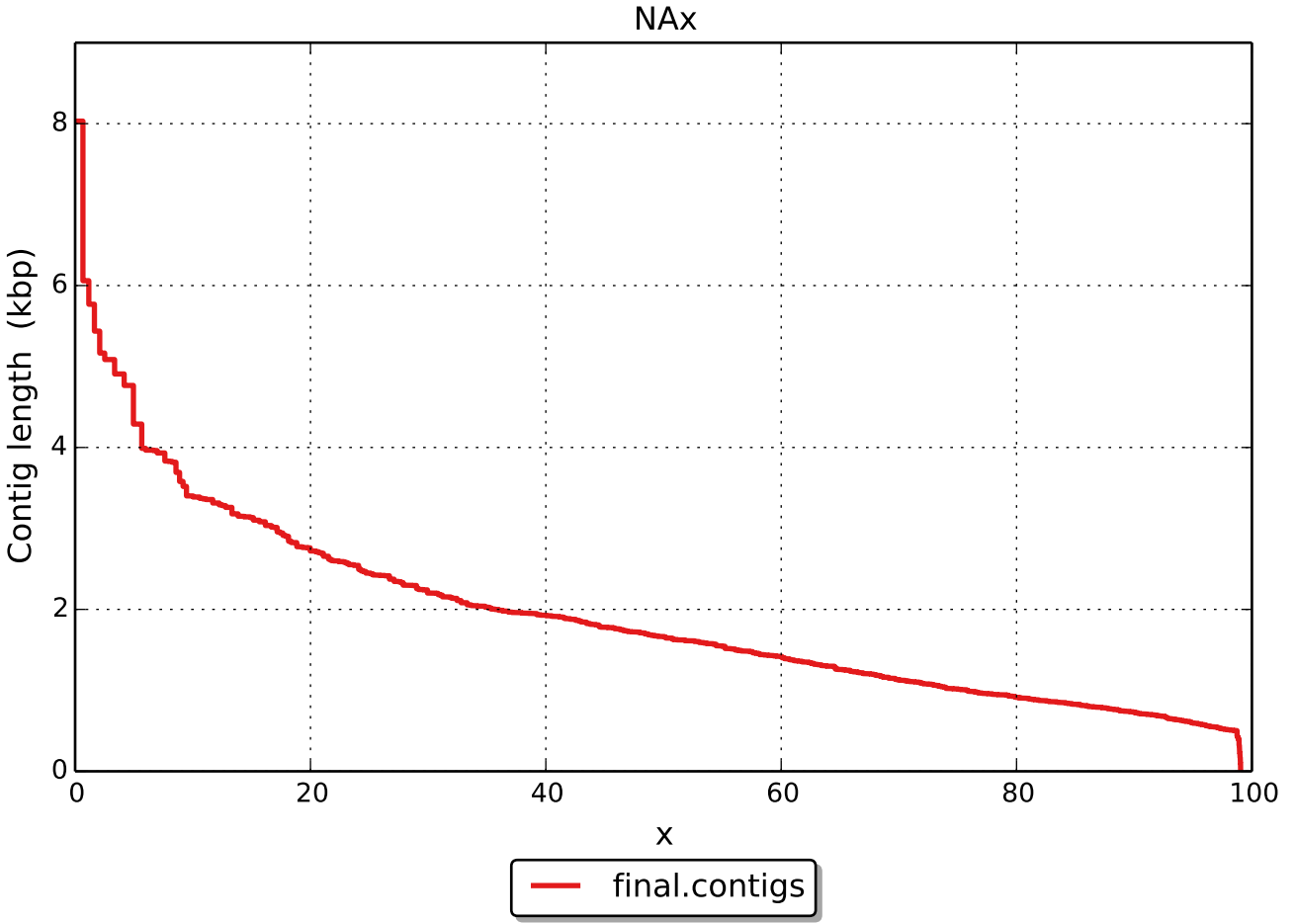

GC content
windows
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

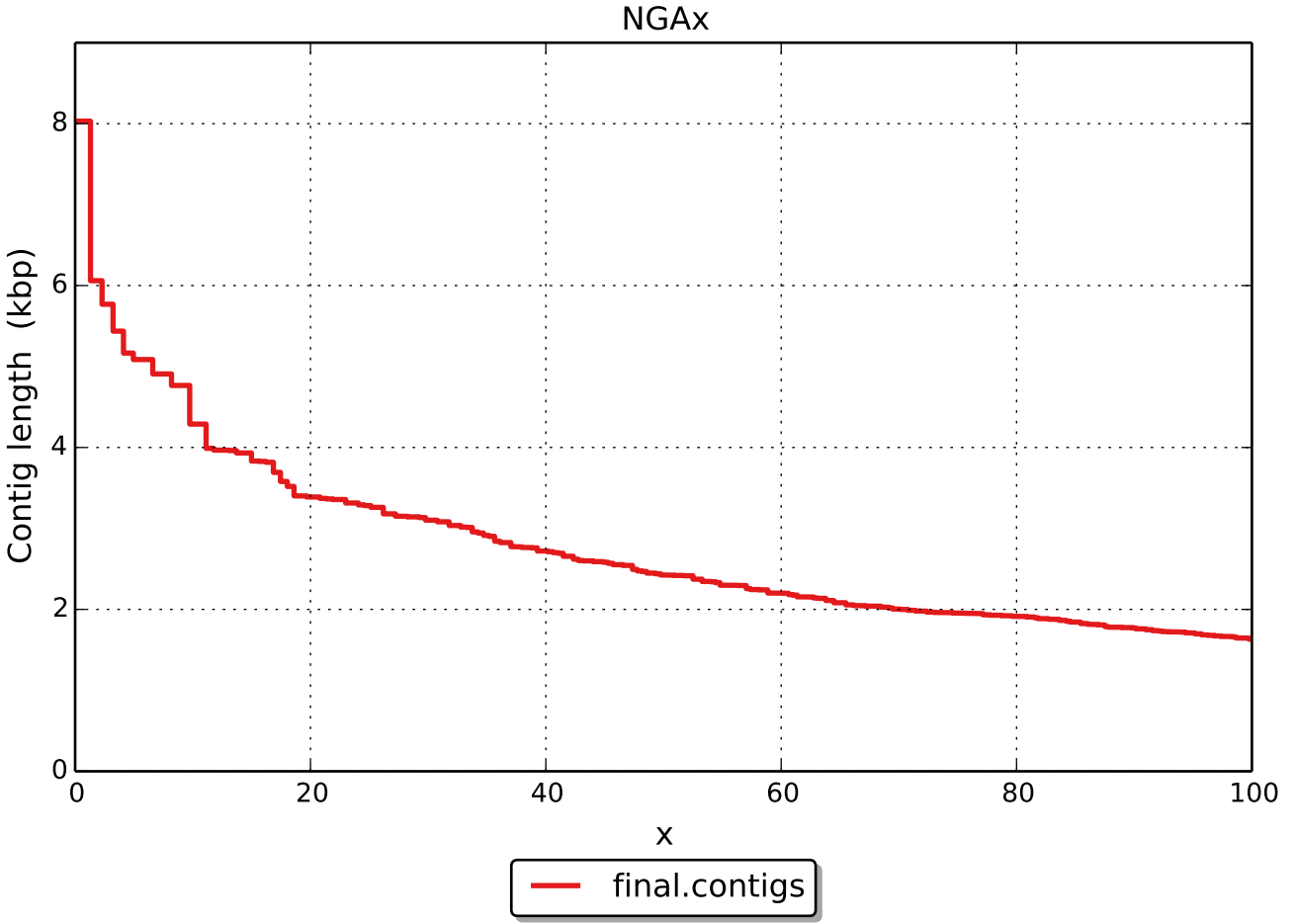

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
30
25
20
15
10
5
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
1200
1000
800
600
400
200
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