Report

	final.contigs
# contigs (>= 0 bp)	1378
# contigs (>= 1000 bp)	266
Total length (>= 0 bp)	1026645
Total length (>= 1000 bp)	436254
# contigs	826
Largest contig	5316
Total length	826744
Reference length	1283598
GC (%)	26.39
Reference GC (%)	26.30
N50	1045
NG50	698
N75	733
L50	244
LG50	514
L75	484
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.447
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	487.75
# indels per 100 kbp	0.37
Largest alignment	5316
NA50	1045
NGA50	698
NA75	733
LA50	244
LGA50	514
LA75	484

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

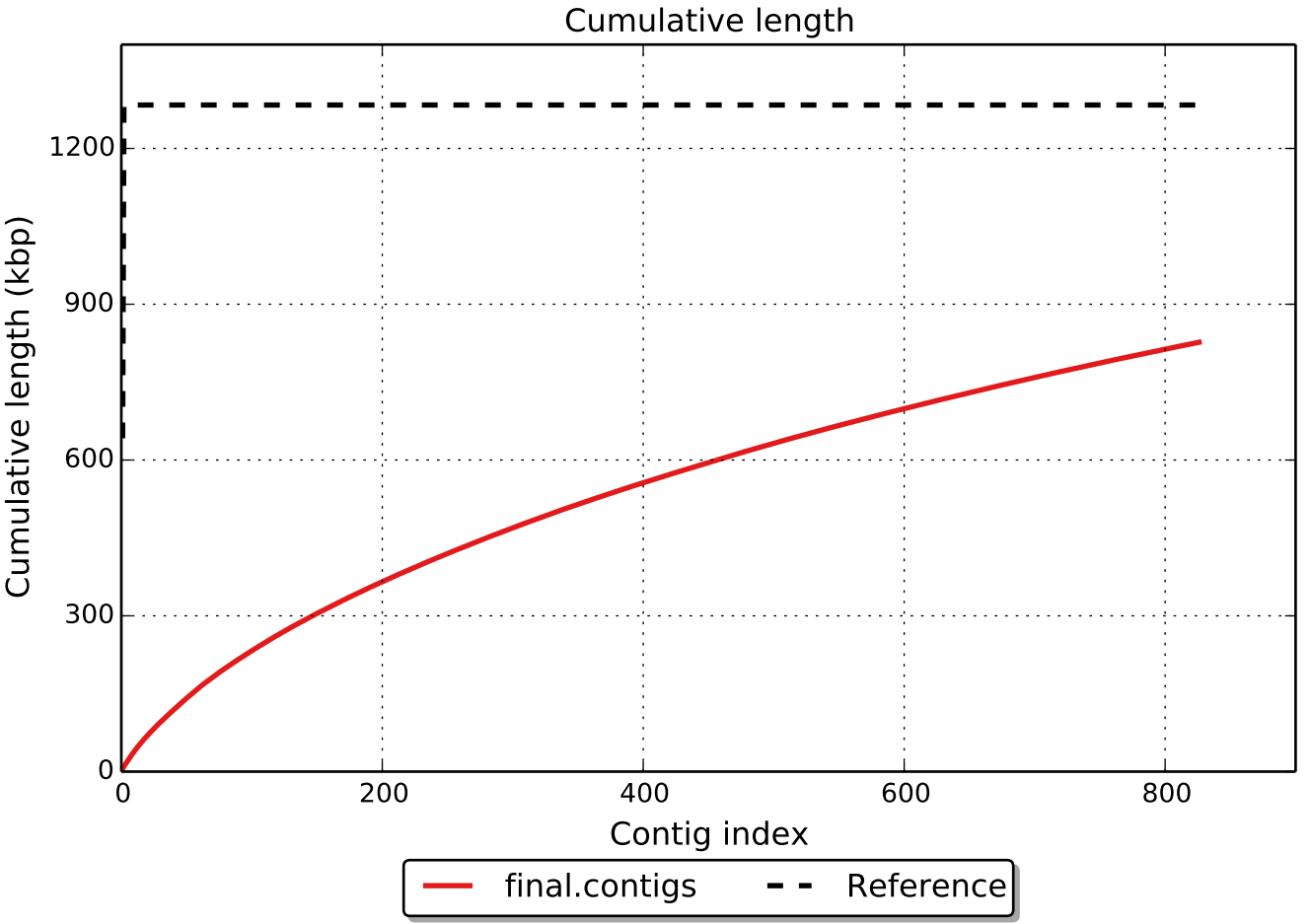
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	5287
# indels	4
# short indels	4
# long indels	0
Indels length	4

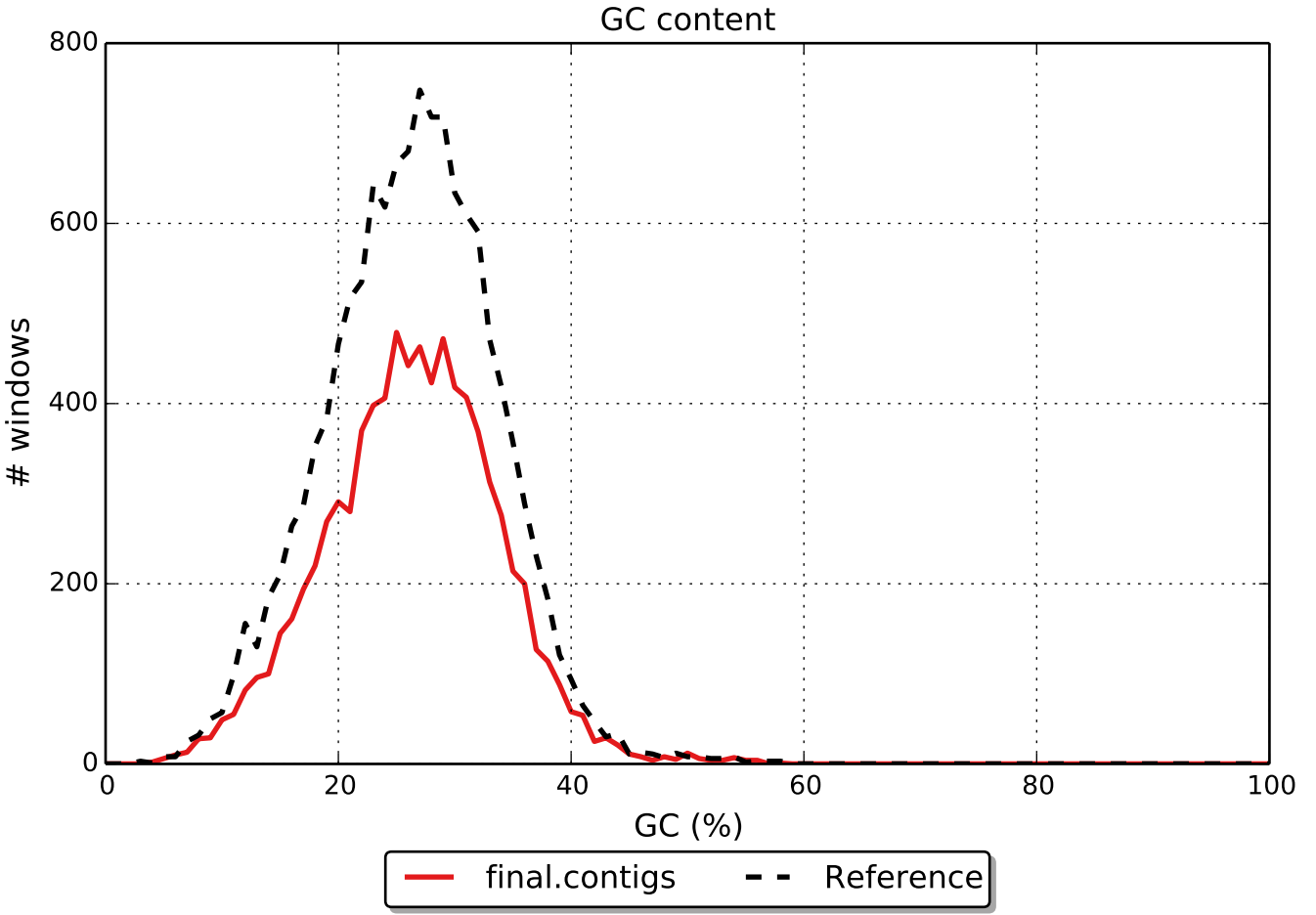
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

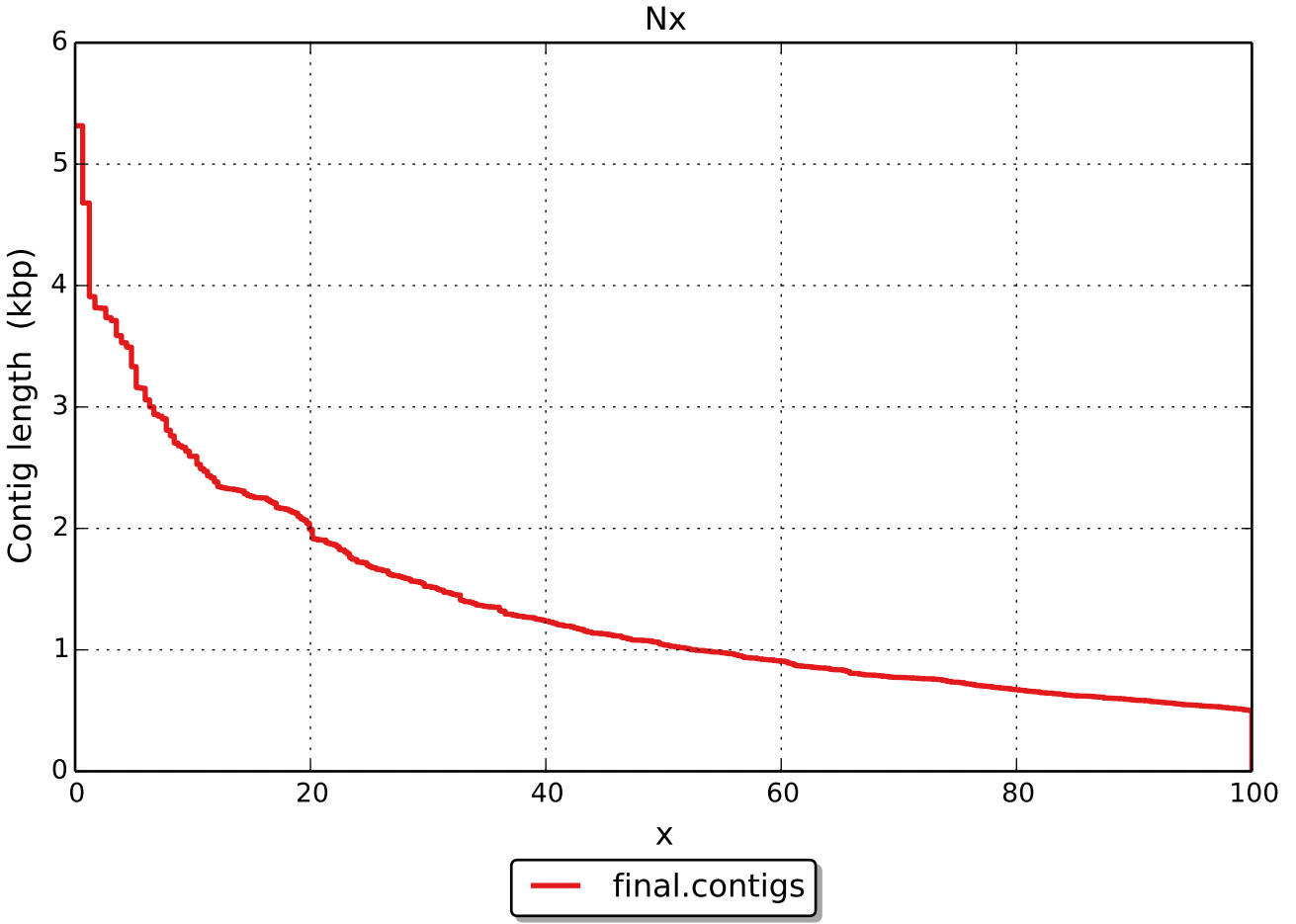
Unaligned report

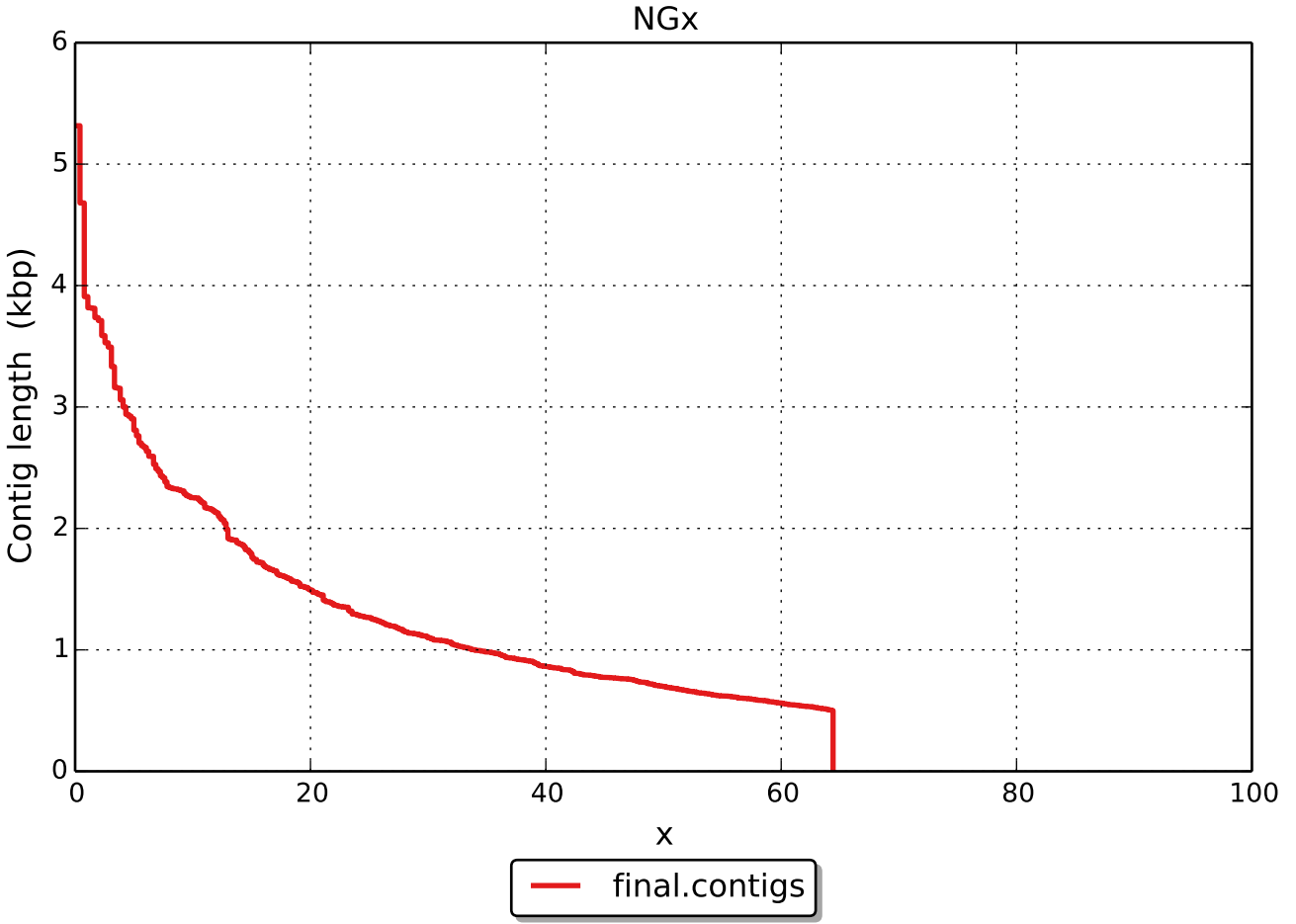
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

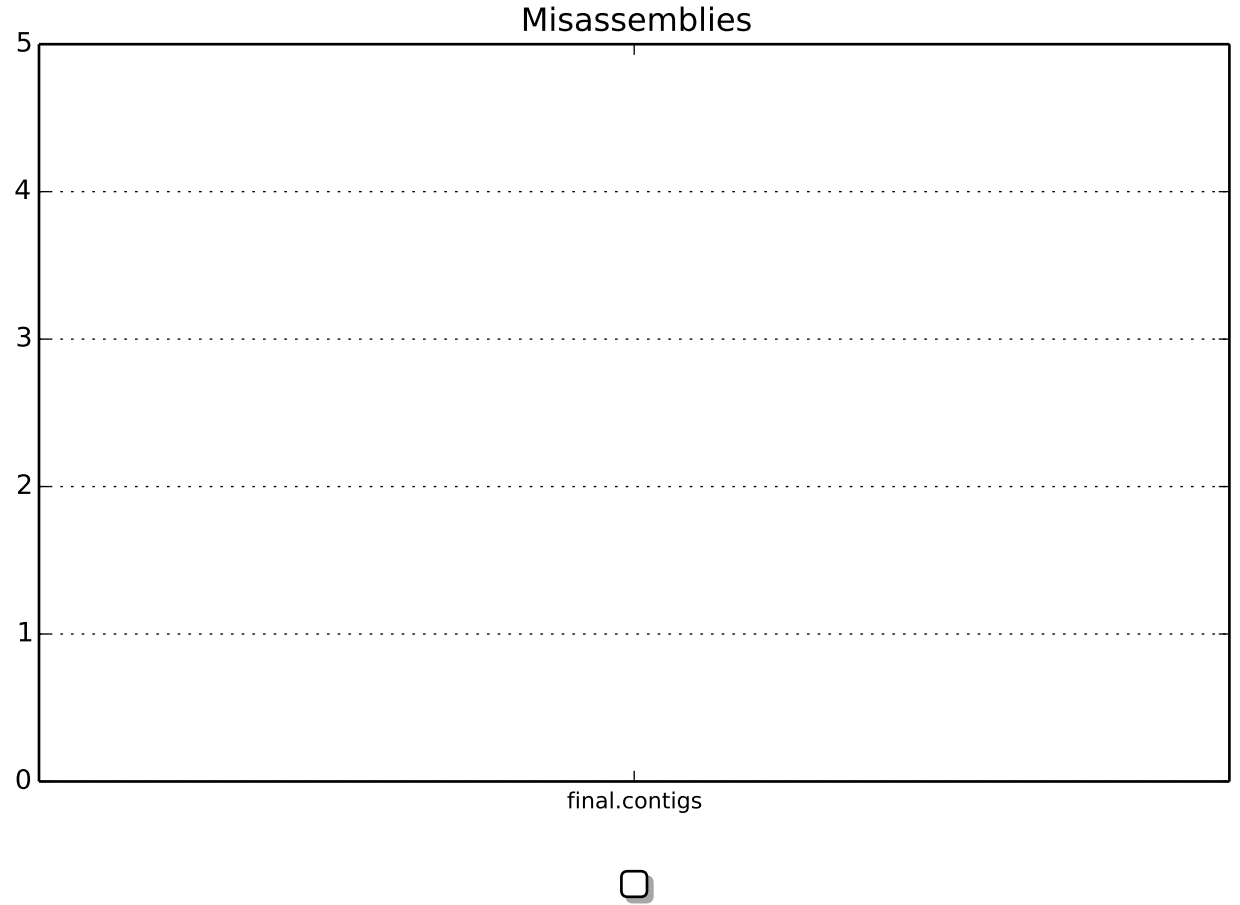
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

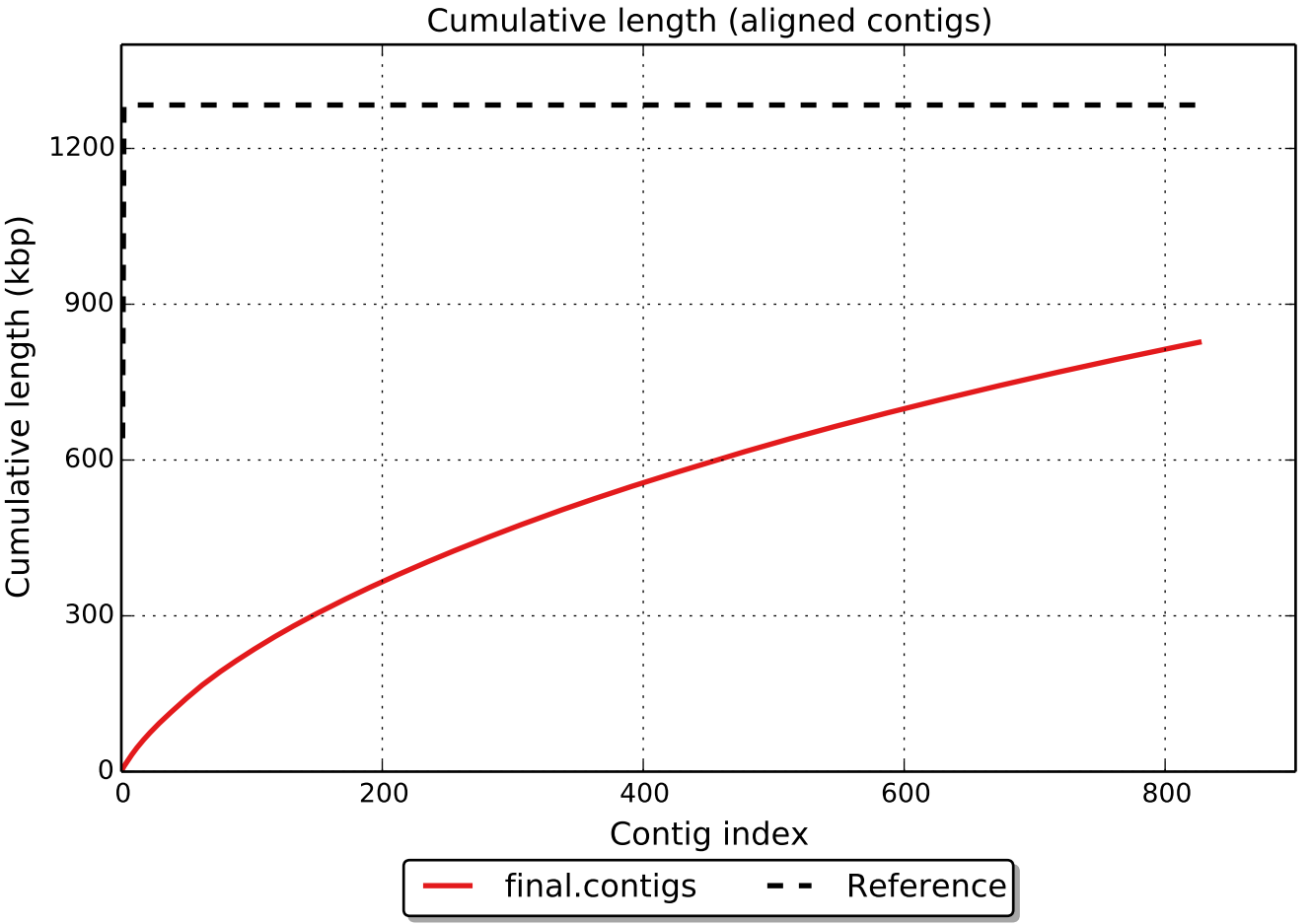

Cumulative length
Cumulative length (kbp)
1200
900
600
300
0
0
200
400
600
800
Contig index
final.contigs
Reference

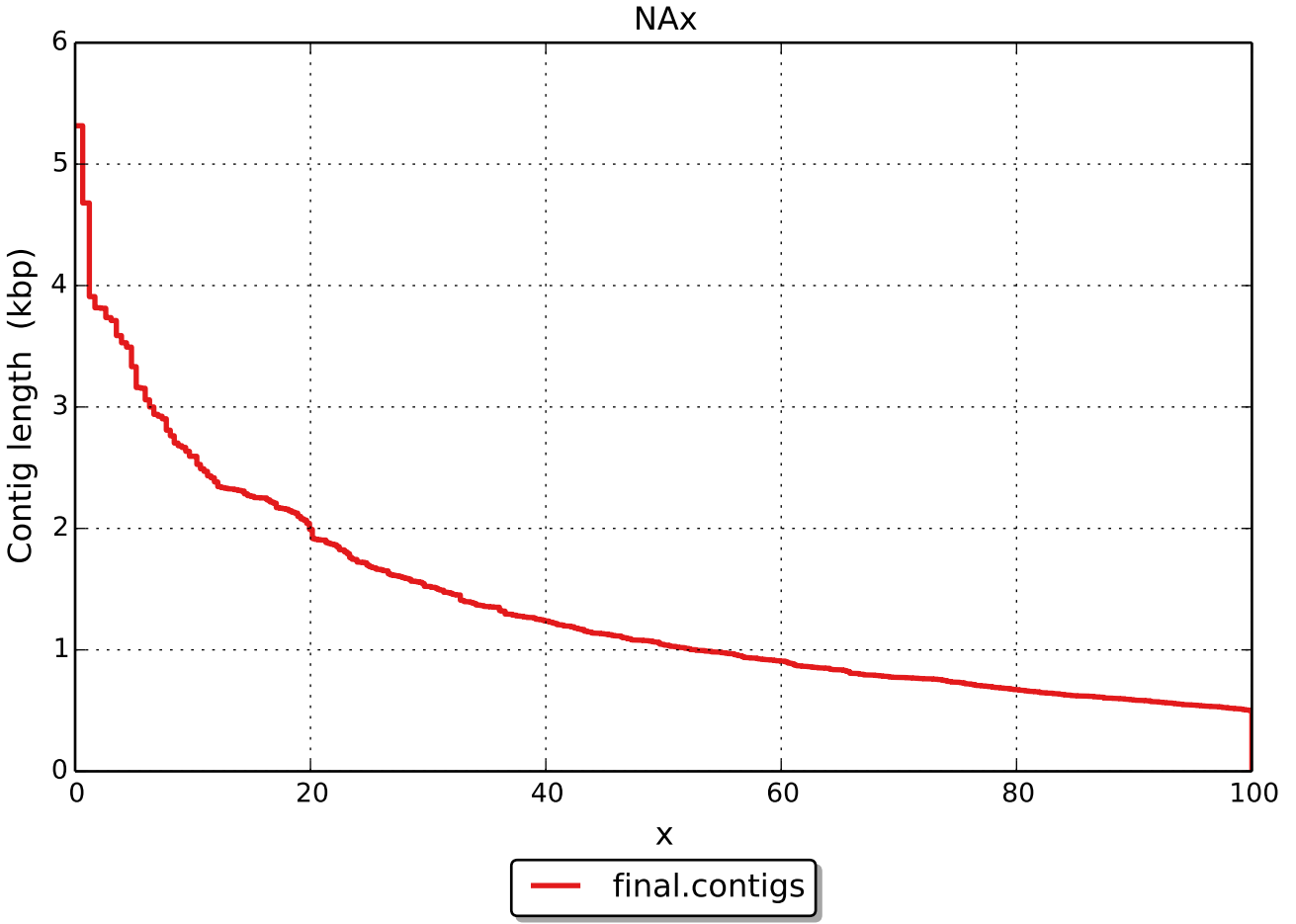

GC content
800
600
400
200
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

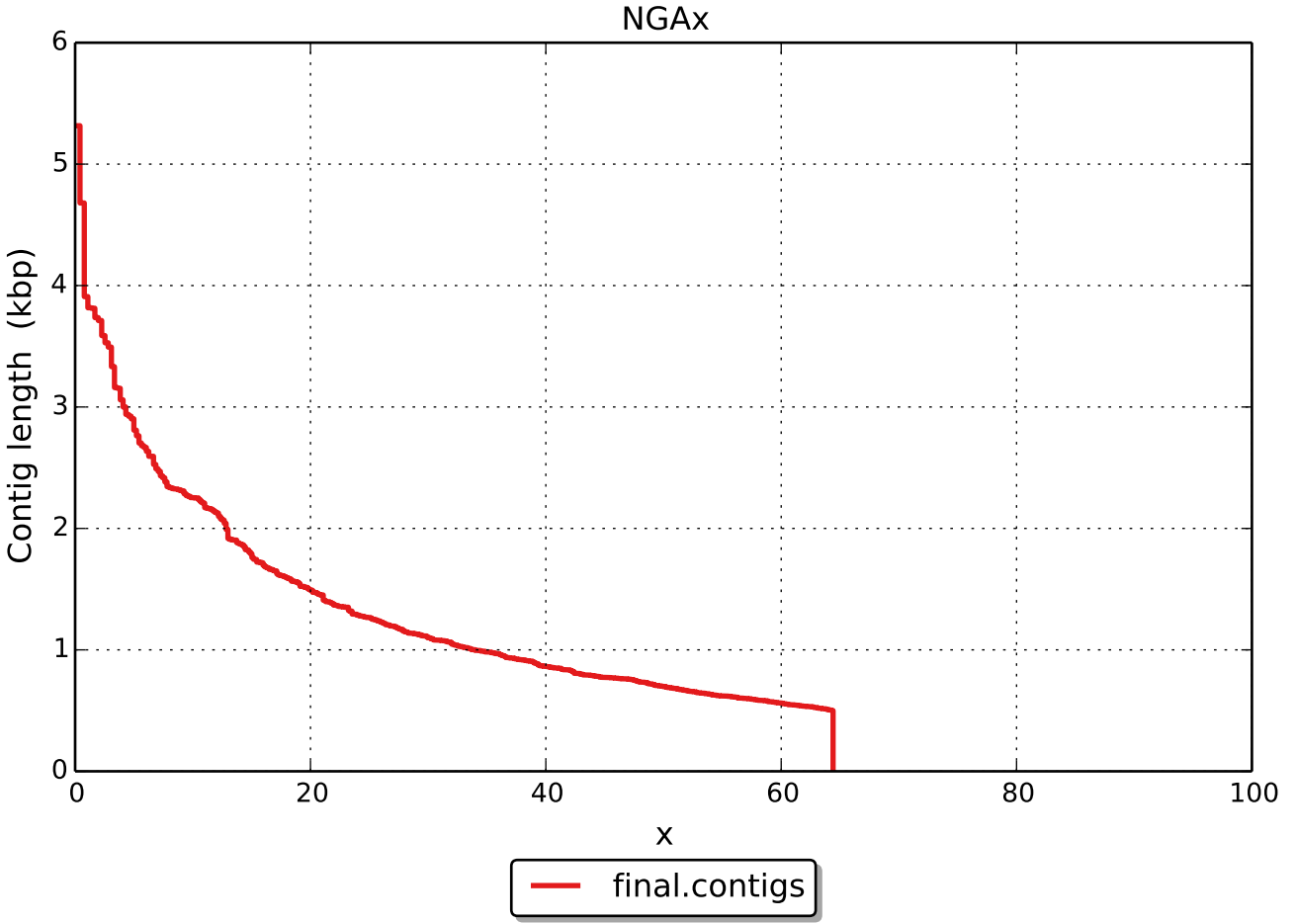

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
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
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