Report

	final.contigs
# contigs (>= 0 bp)	1190
# contigs (>= 1000 bp)	388
Total length (>= 0 bp)	1100318
Total length (>= 1000 bp)	532162
# contigs	1190
Largest contig	3516
Total length	1100318
Reference length	615980
GC (%)	25.32
Reference GC (%)	25.35
N50	979
NG50	1257
N75	728
NG75	1055
L50	407
LG50	186
L75	735
LG75	320
# misassemblies	20
# misassembled contigs	20
Misassembled contigs length	21819
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.169
Duplication ratio	1.981
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1278.49
# indels per 100 kbp	0.72
Largest alignment	3360
NA50	910
NGA50	1195
NA75	642
NGA75	1008
LA50	428
LGA50	194
LA75	787
LGA75	336

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

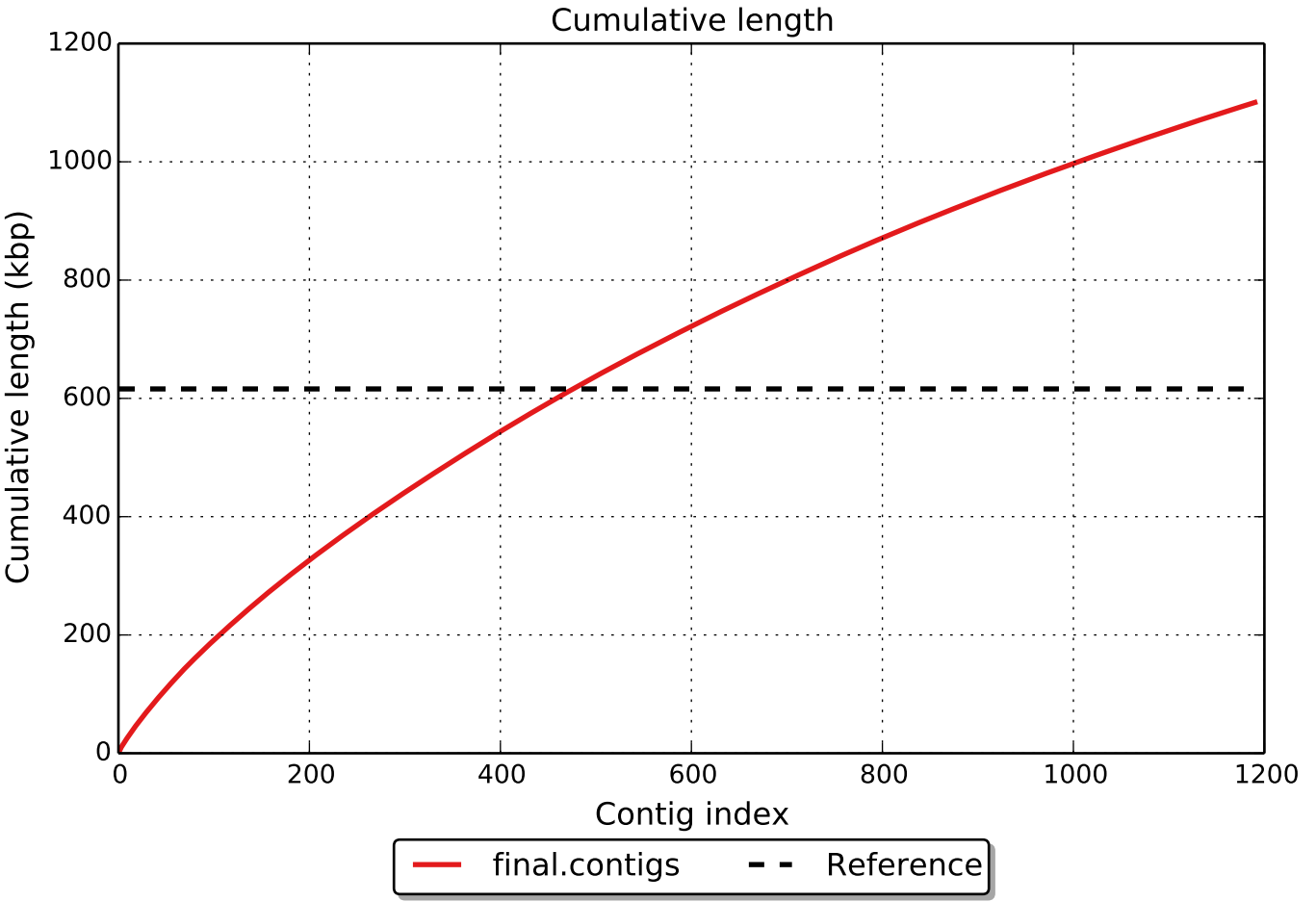
	final.contigs
# misassemblies	20
# relocations	20
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	20
Misassembled contigs length	21819
# local misassemblies	0
# mismatches	7101
# indels	4
# short indels	4
# long indels	0
Indels length	4

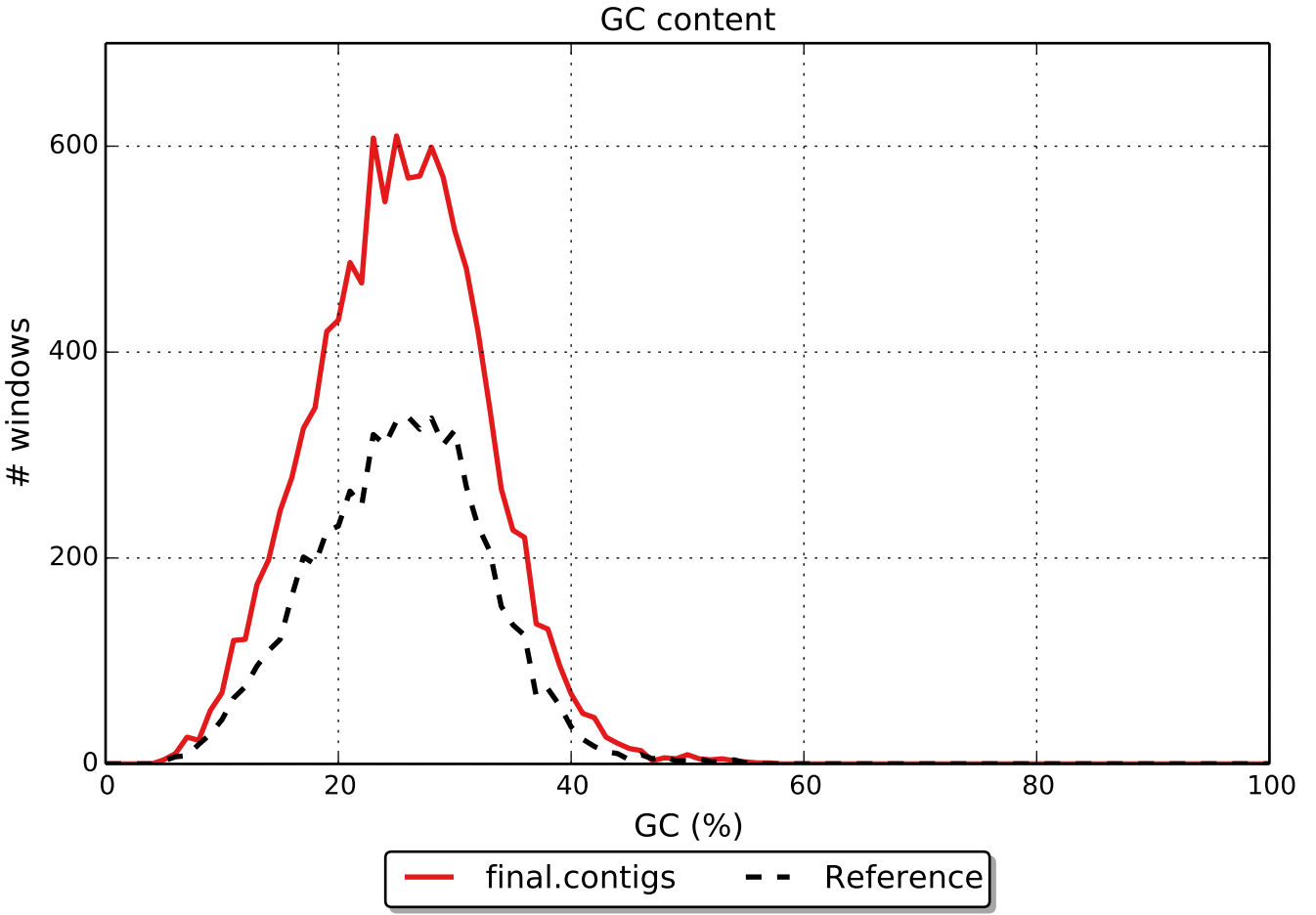
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

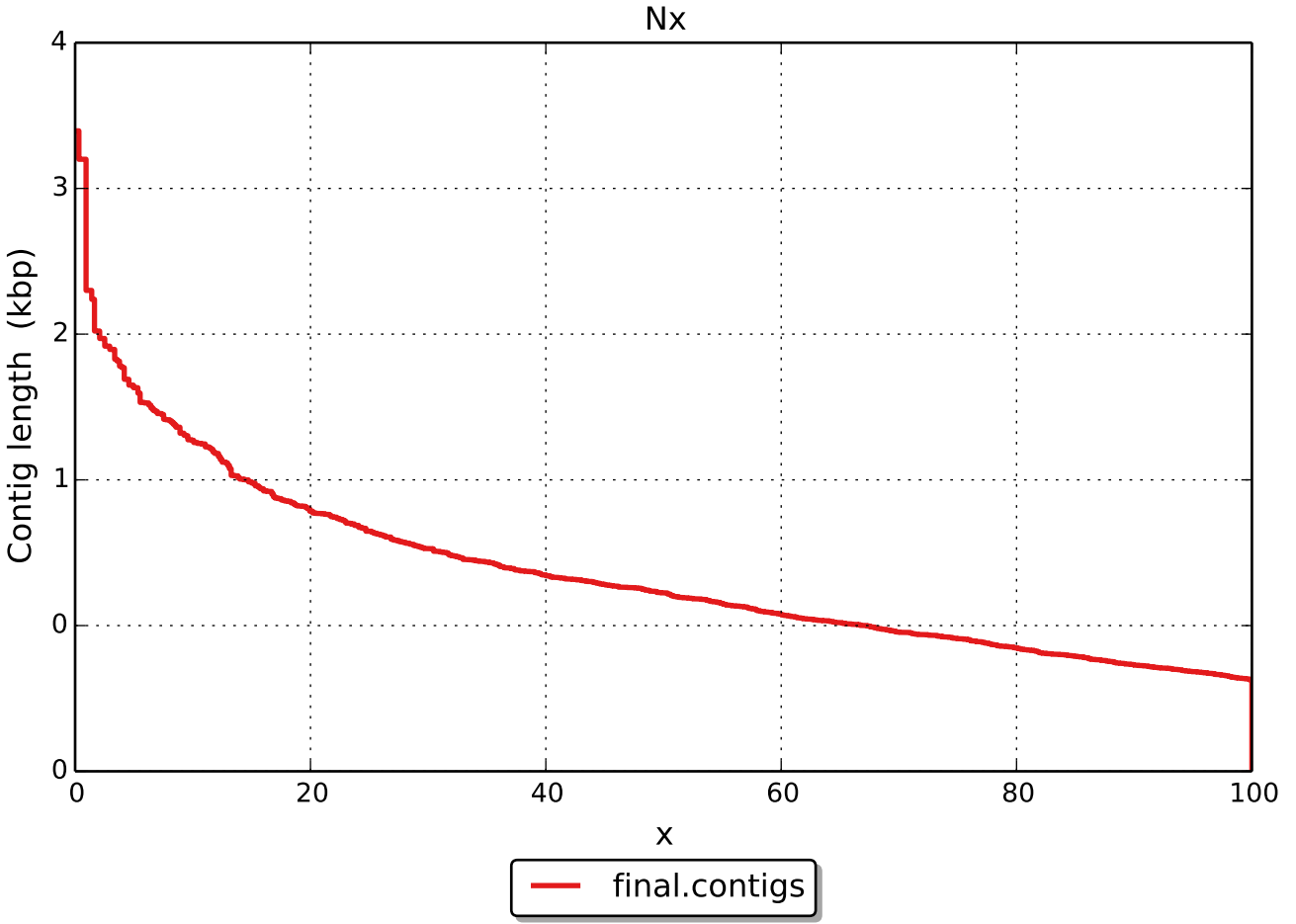
Unaligned report

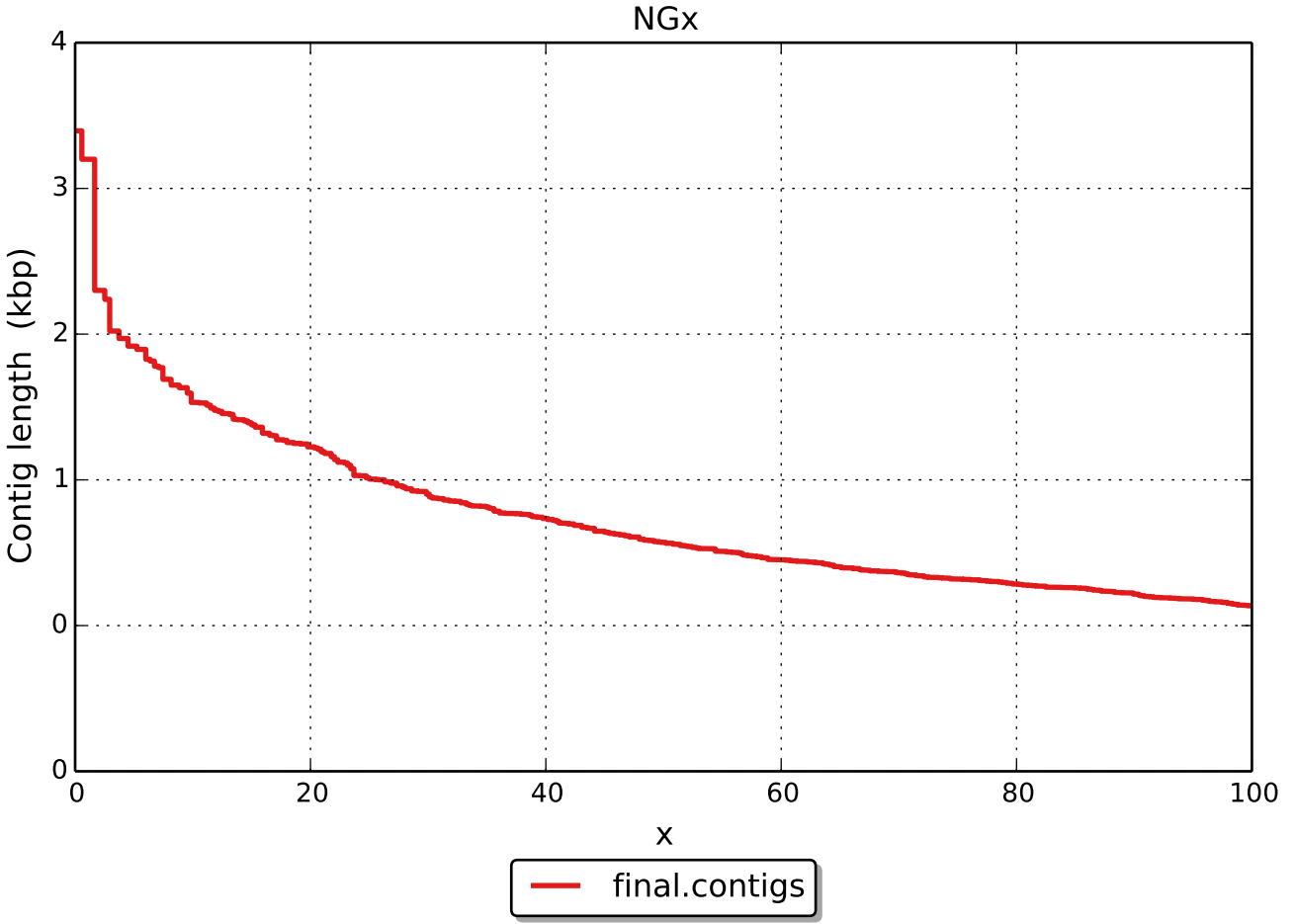
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

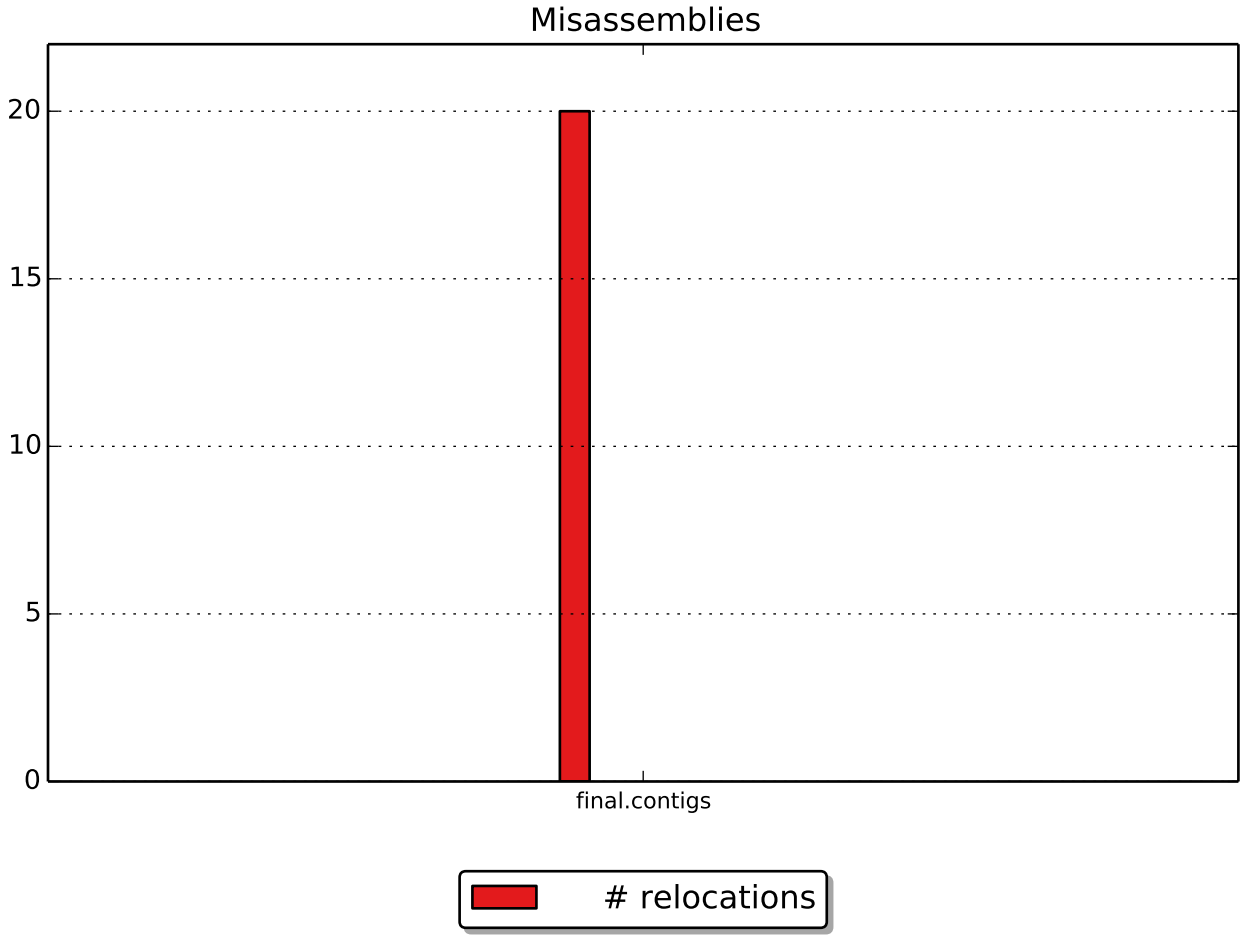
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

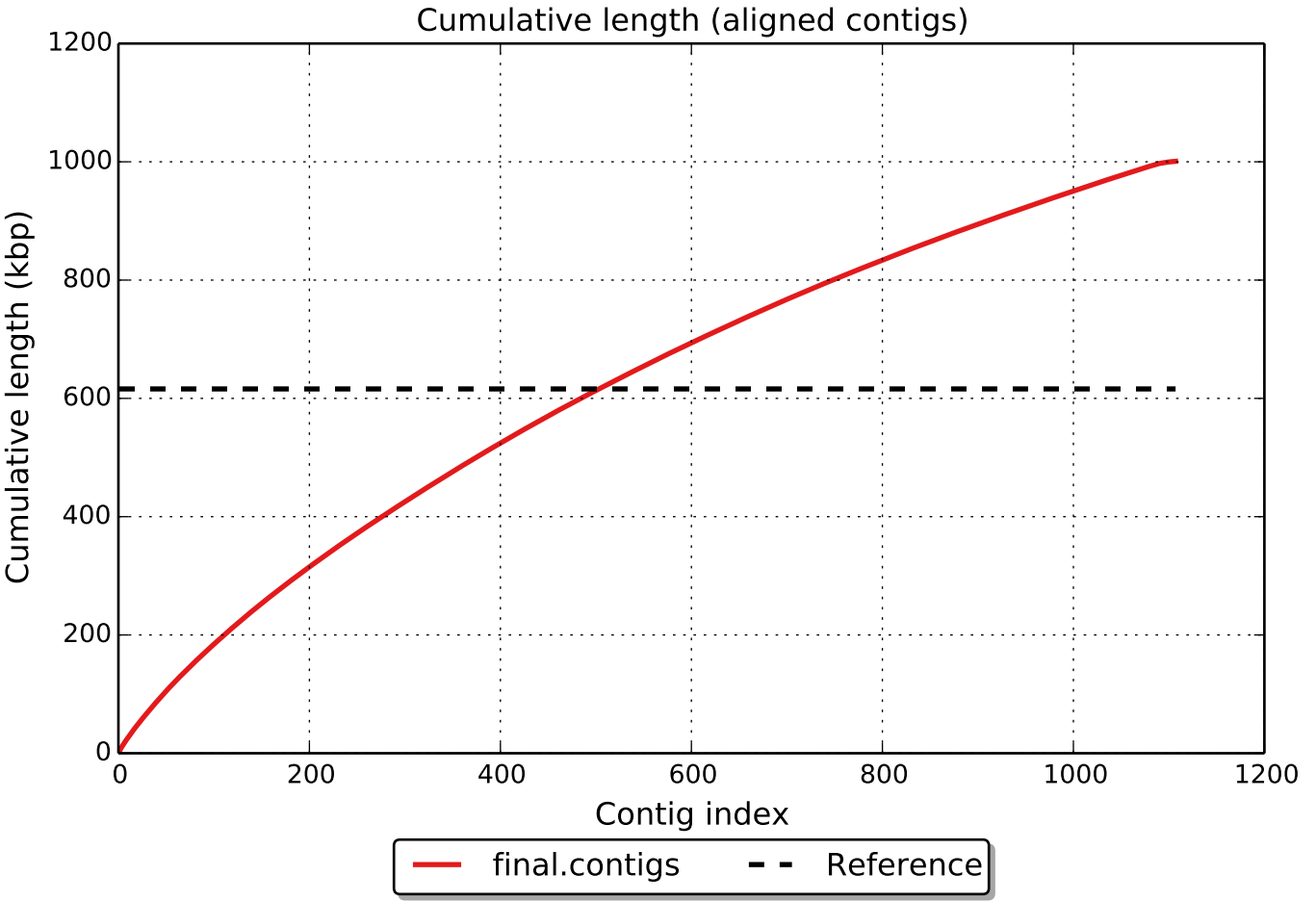

Cumulative length
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference

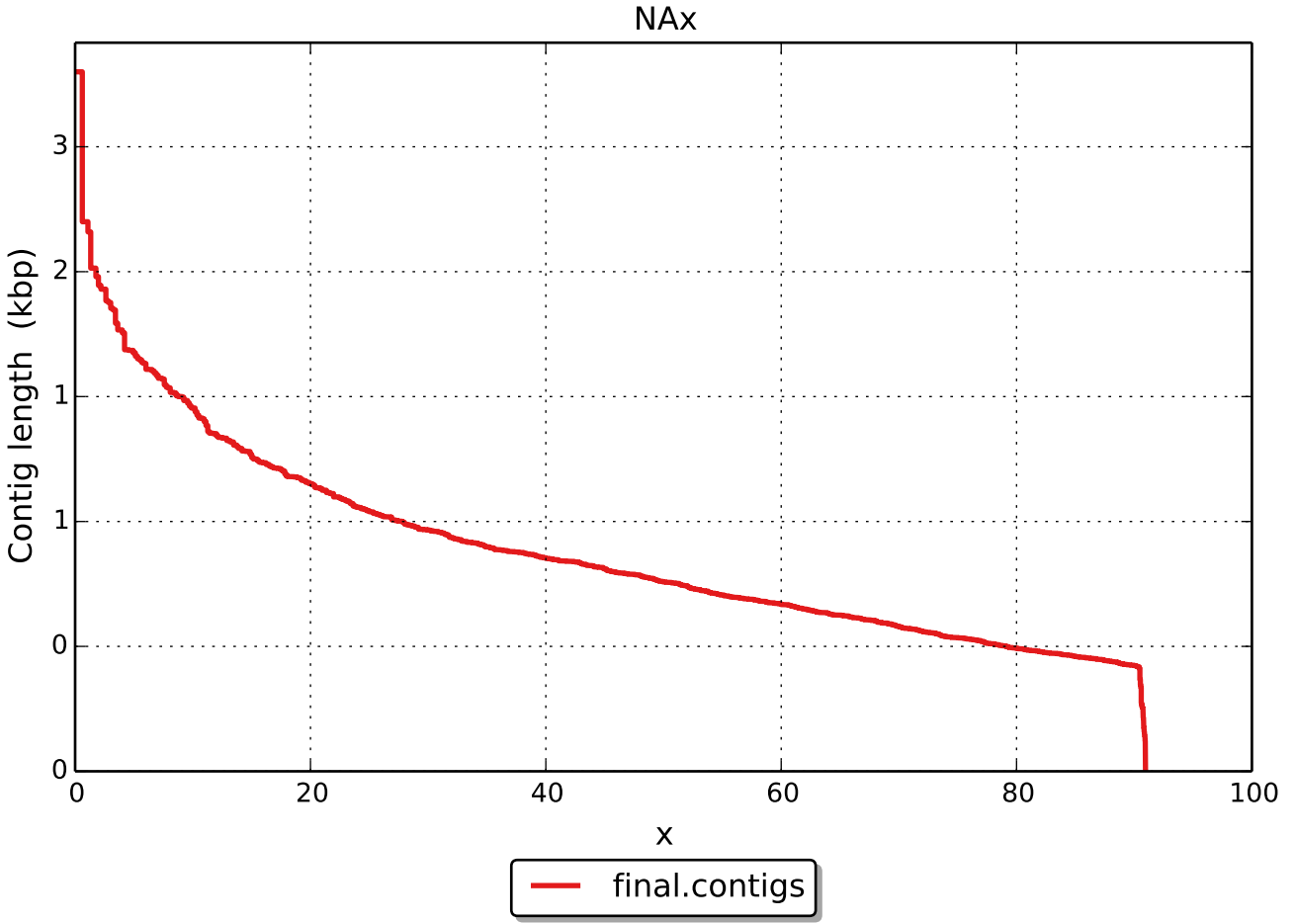

GC content
windows
600
400
200
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

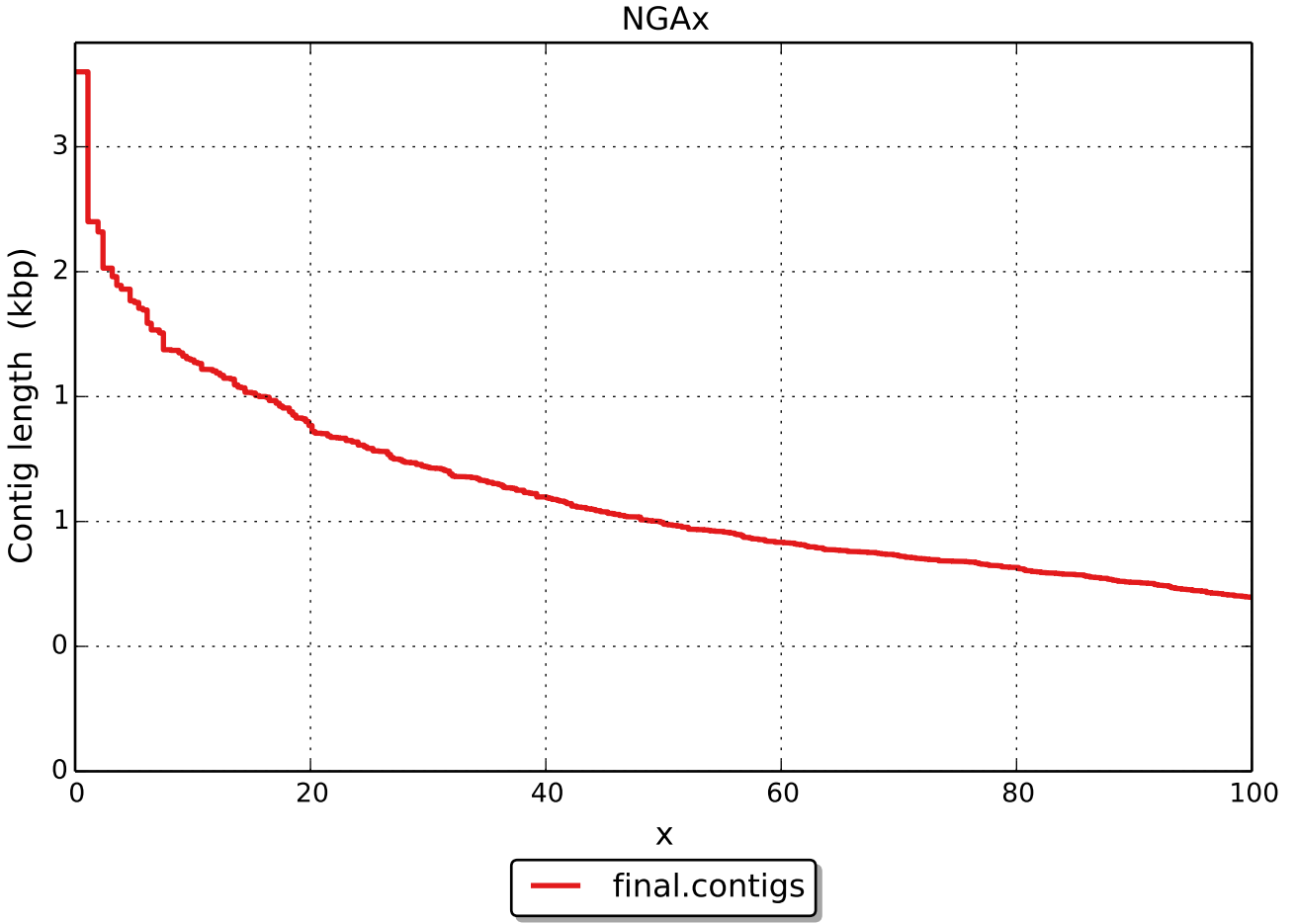

Nx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
20
15
10
5
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
Contig index
0
200
400
600
800
1000
1200
final.contigs
Reference


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


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