Report

	final.contigs
# contigs (>= 0 bp)	1551
# contigs (>= 1000 bp)	401
Total length (>= 0 bp)	1257889
Total length (>= 1000 bp)	598099
# contigs	1082
Largest contig	4336
Total length	1083010
Reference length	1231960
GC (%)	25.43
Reference GC (%)	25.35
N50	1053
NG50	983
N75	760
NG75	650
L50	346
LG50	420
L75	645
LG75	804
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.284
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	98.31
# indels per 100 kbp	0.00
Largest alignment	4336
NA50	1052
NGA50	983
NA75	760
NGA75	650
LA50	346
LGA50	420
LA75	645
LGA75	804

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

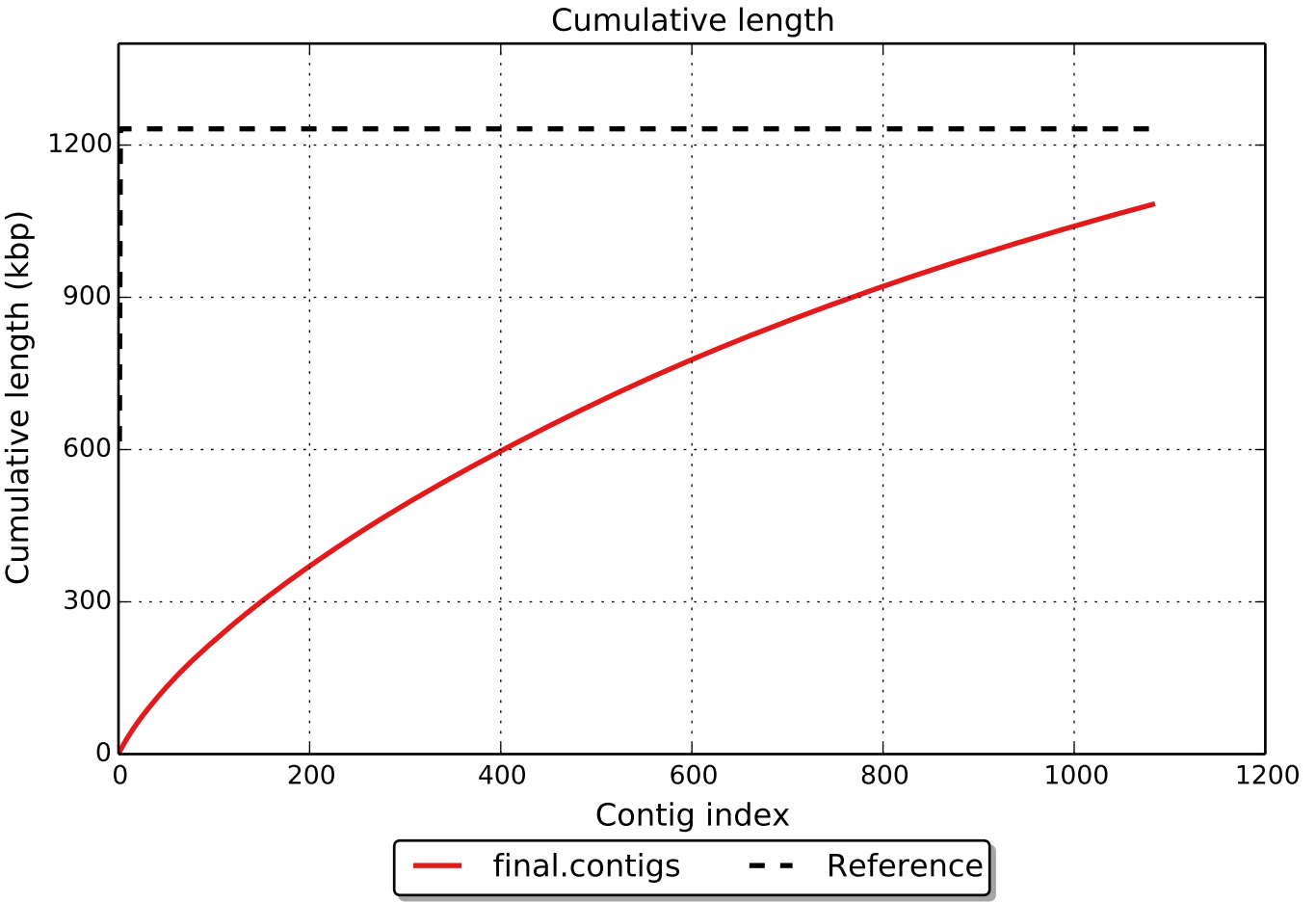
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1045
# indels	0
# short indels	0
# long indels	0
Indels length	0

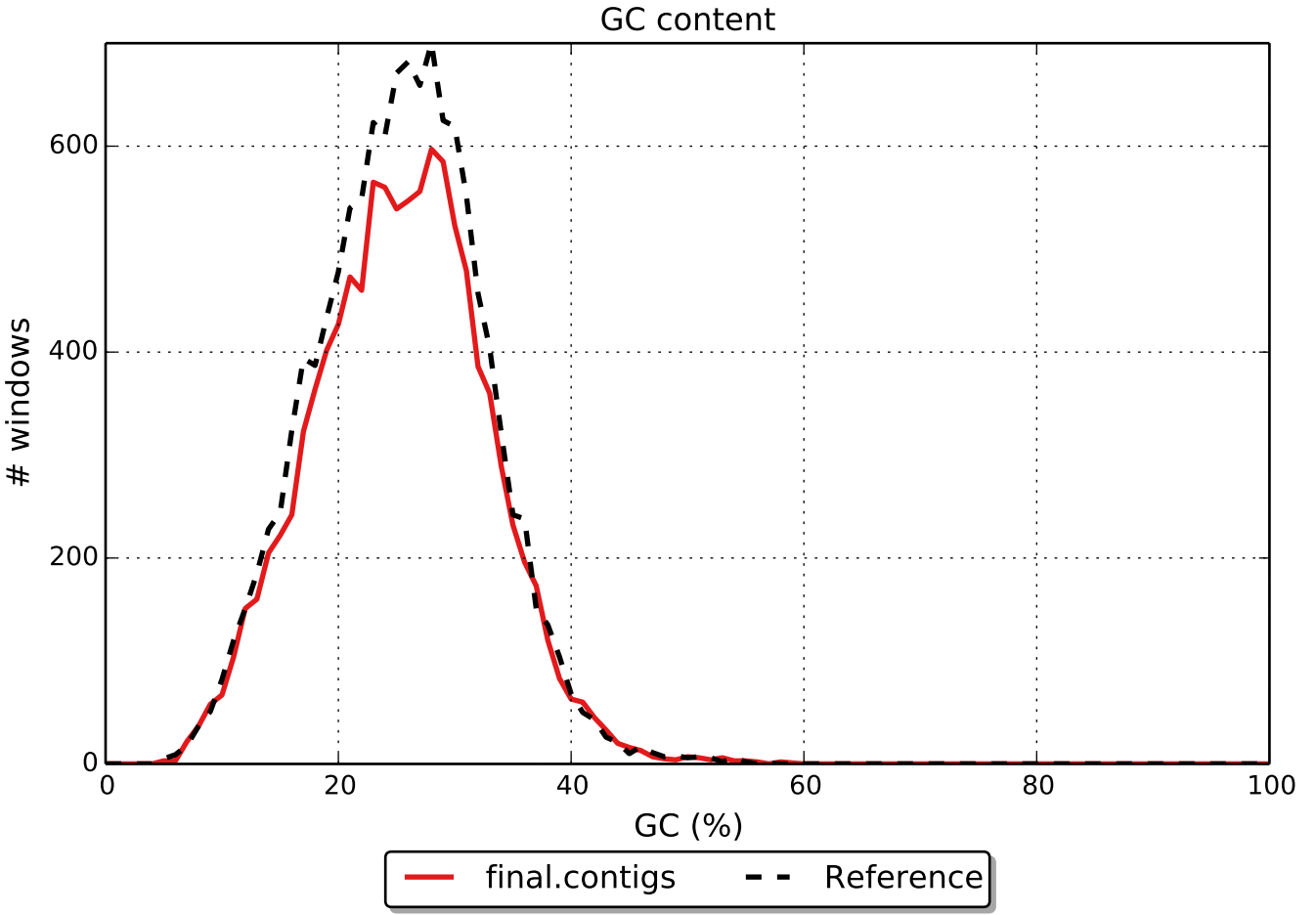
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

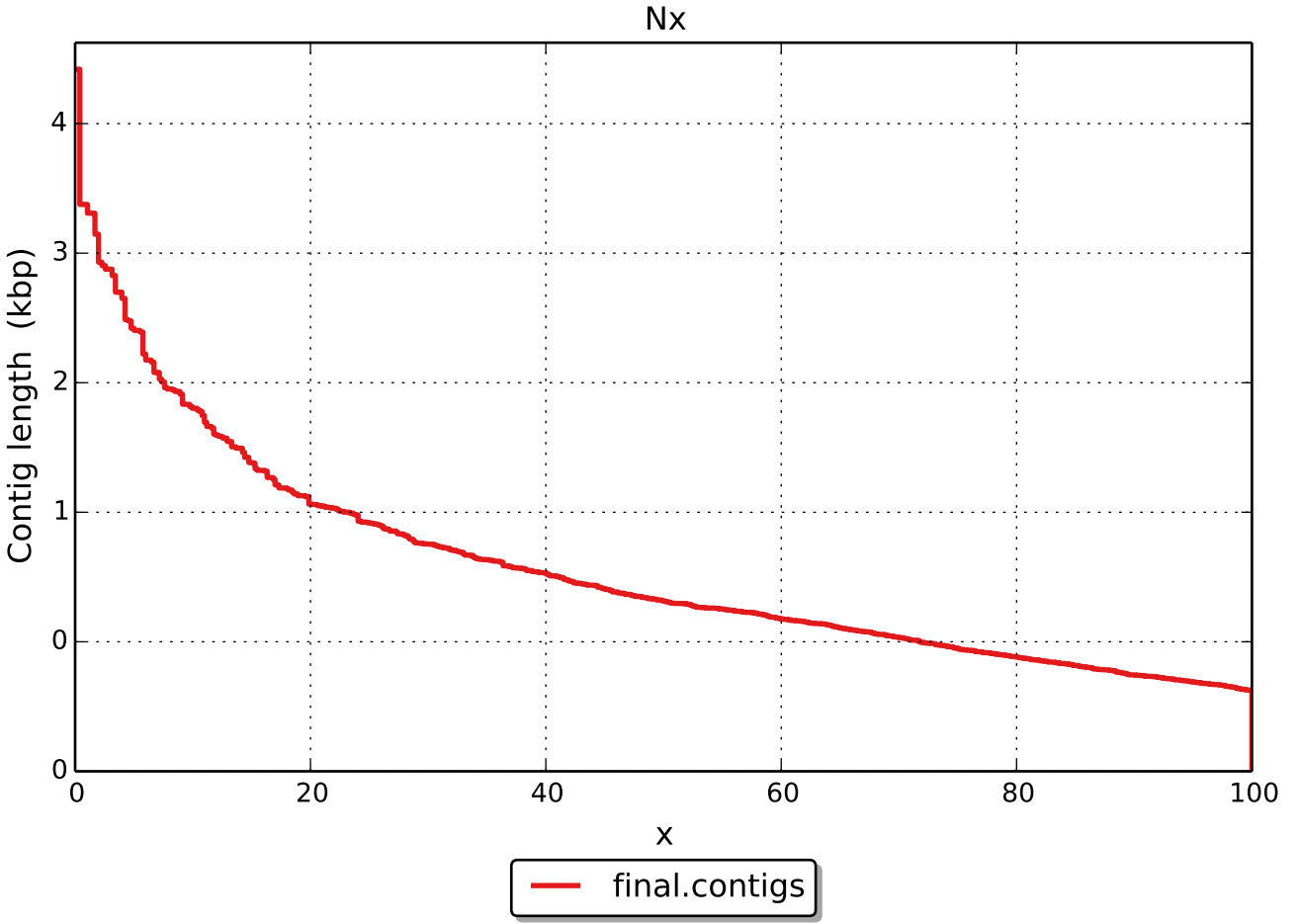
Unaligned report

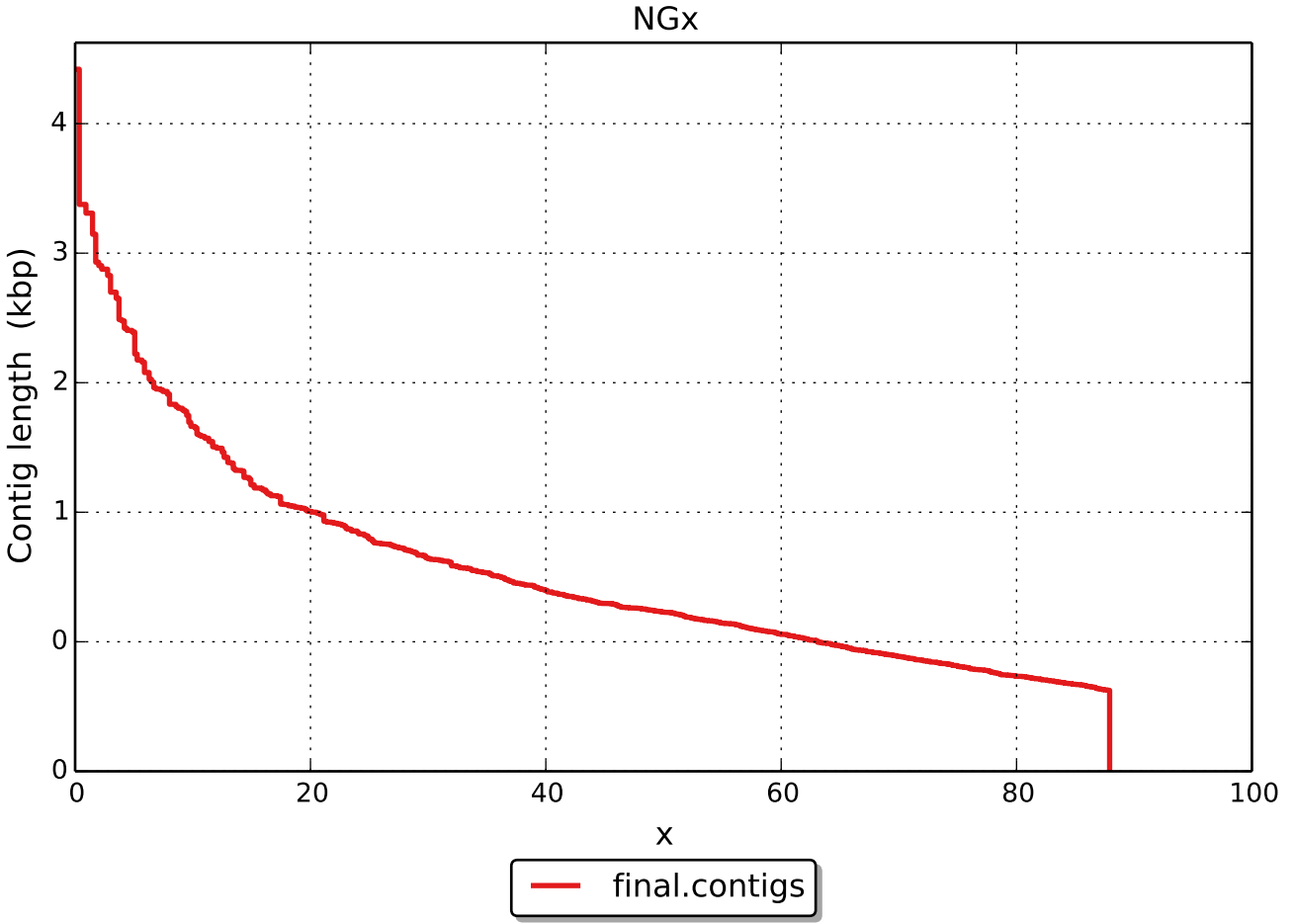
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

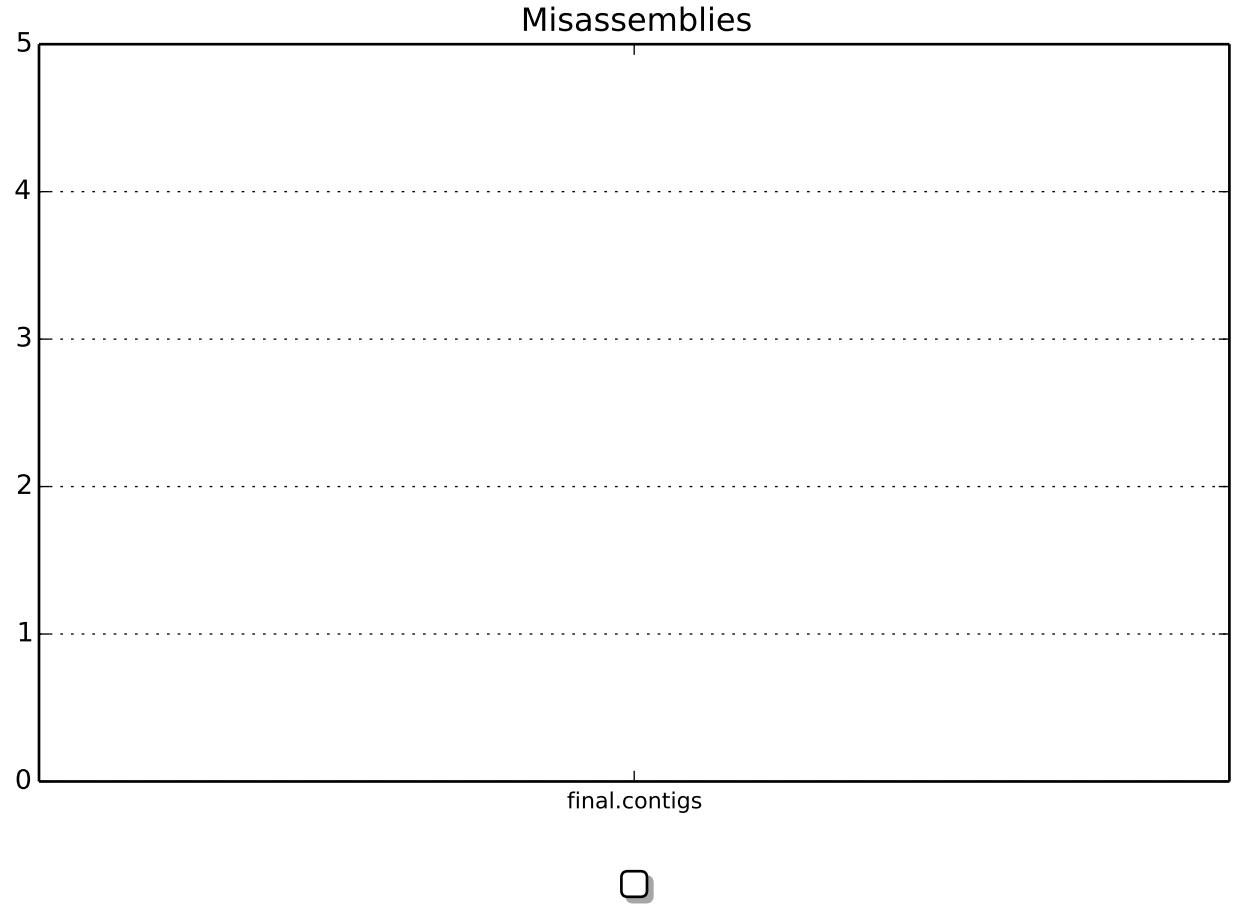
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

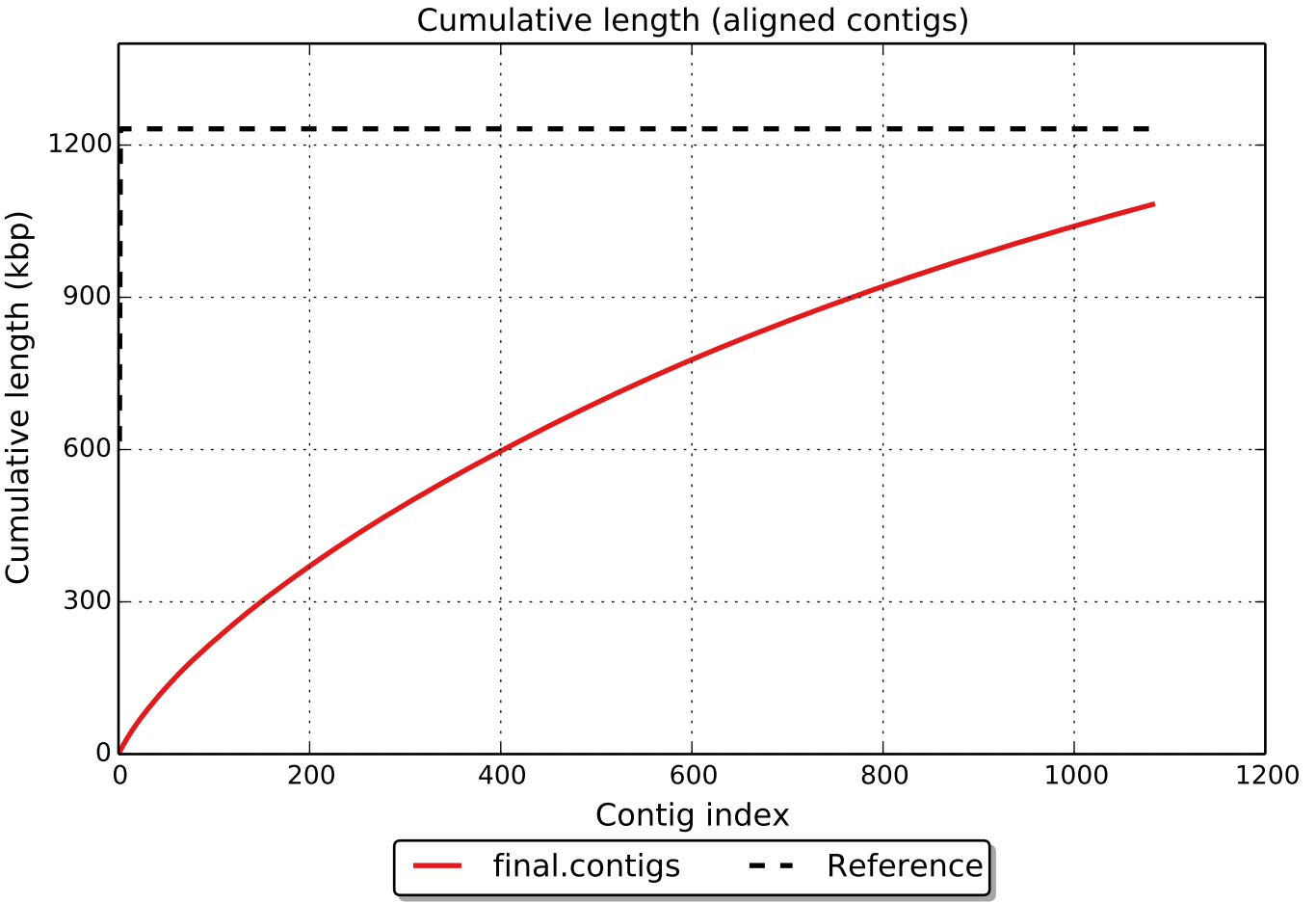

Cumulative length
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference

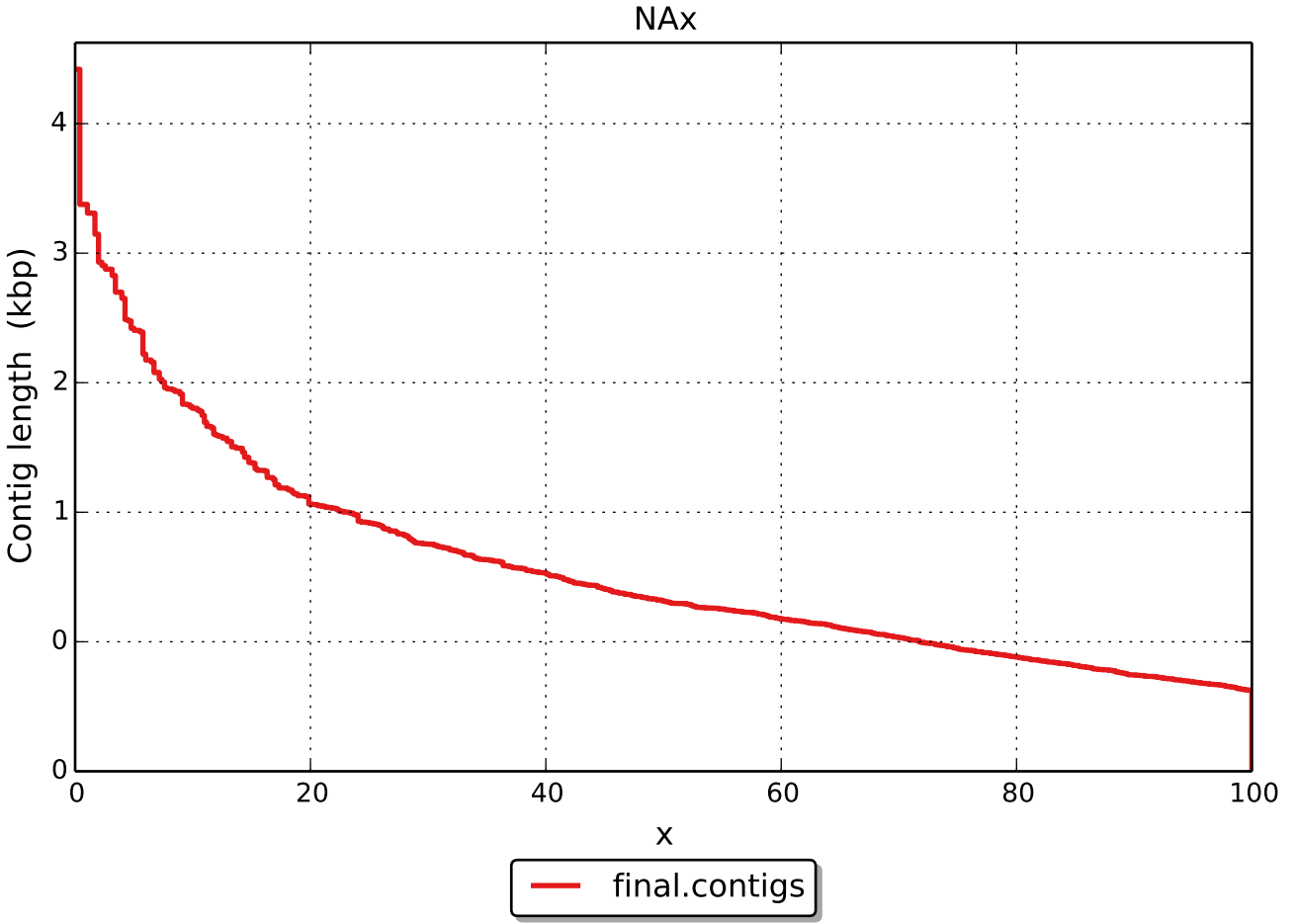

GC content
windows
GC (%)
0
200
400
600
0
20
40
60
80
100
final.contigs
Reference

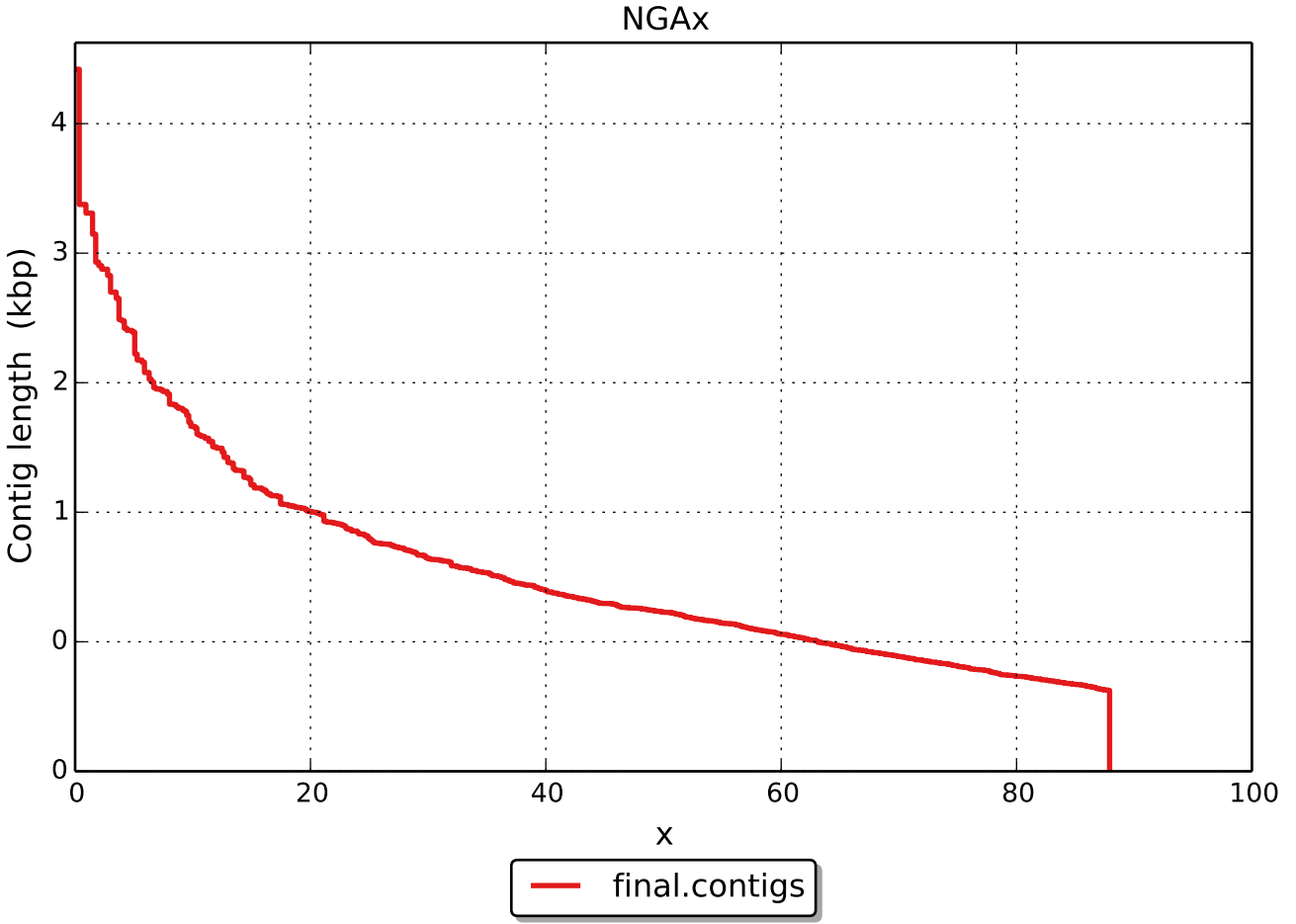

Nx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
300
600
900
1200
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


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


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