Report

	final.contigs
# contigs (>= 0 bp)	737
# contigs (>= 1000 bp)	594
Total length (>= 0 bp)	5232056
Total length (>= 1000 bp)	5132097
# contigs	737
Largest contig	62567
Total length	5232056
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	15011
NG50	13440
N75	7162
NG75	6357
L50	104
LG50	112
L75	232
LG75	259
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	50
Genome fraction (%)	94.702
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.26
# indels per 100 kbp	0.04
Largest alignment	62567
NA50	15011
NGA50	13440
NA75	7162
NGA75	6357
LA50	104
LGA50	112
LA75	232
LGA75	259

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

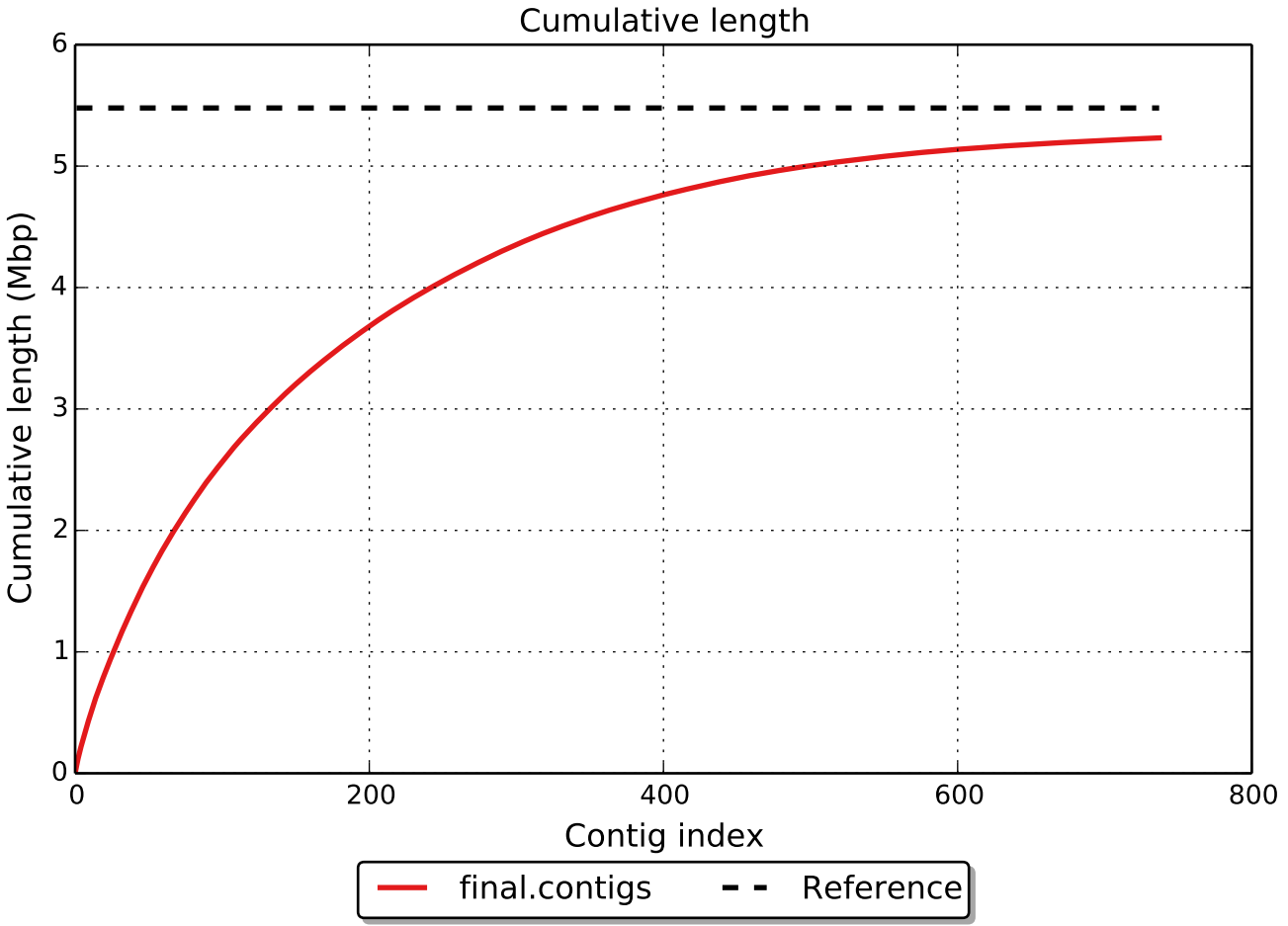
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	169
# indels	2
# short indels	0
# long indels	2
Indels length	24

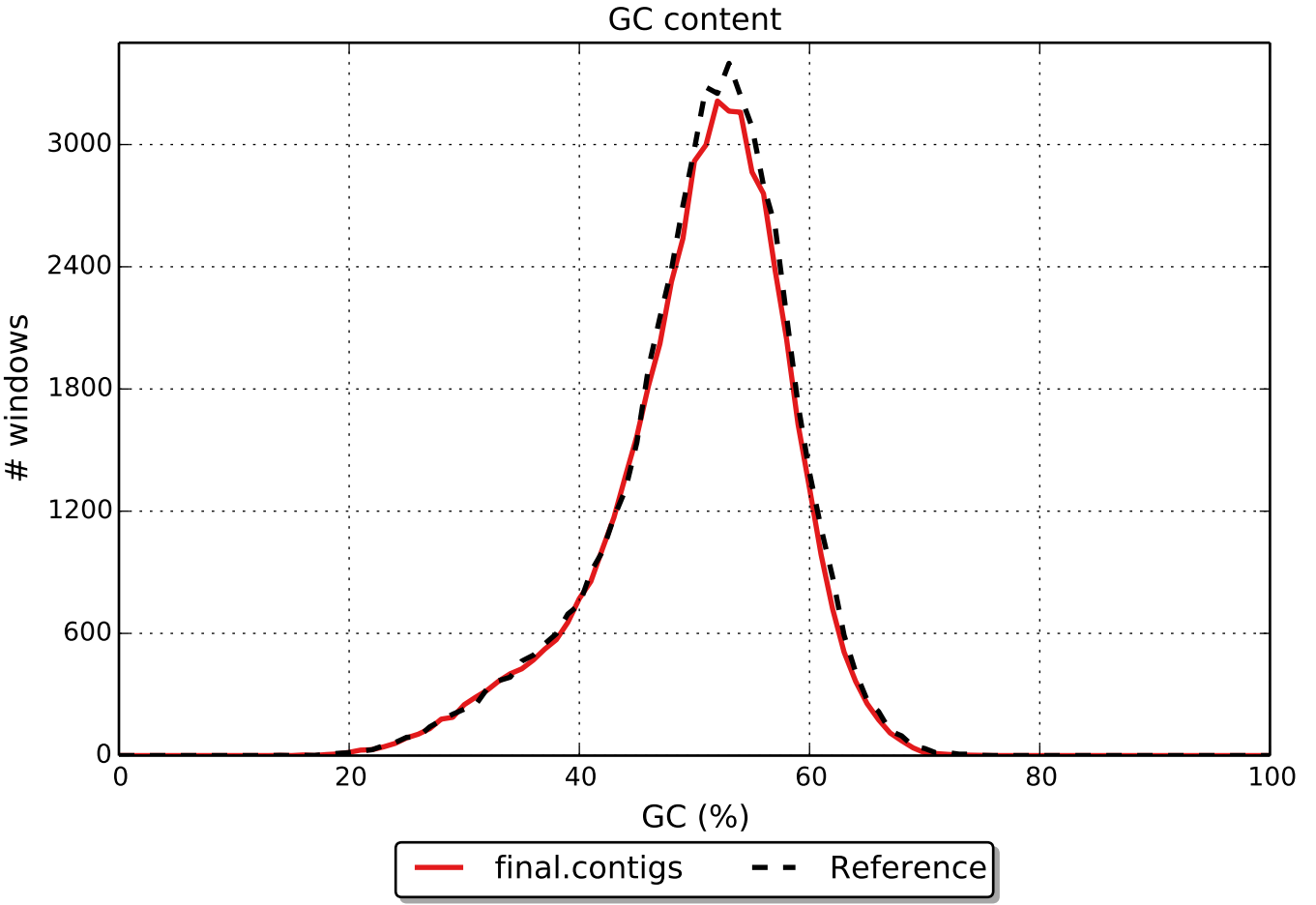
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

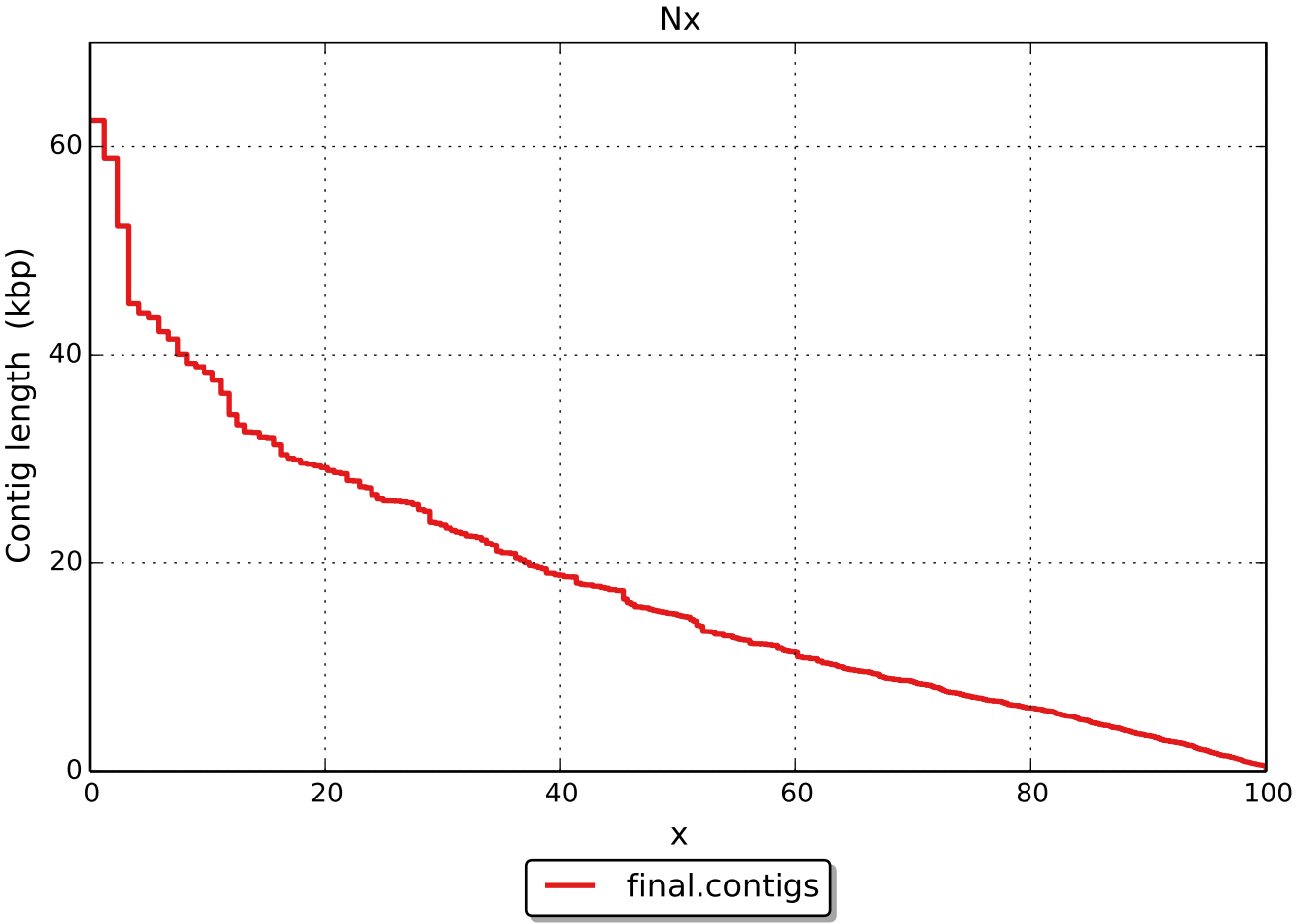
Unaligned report

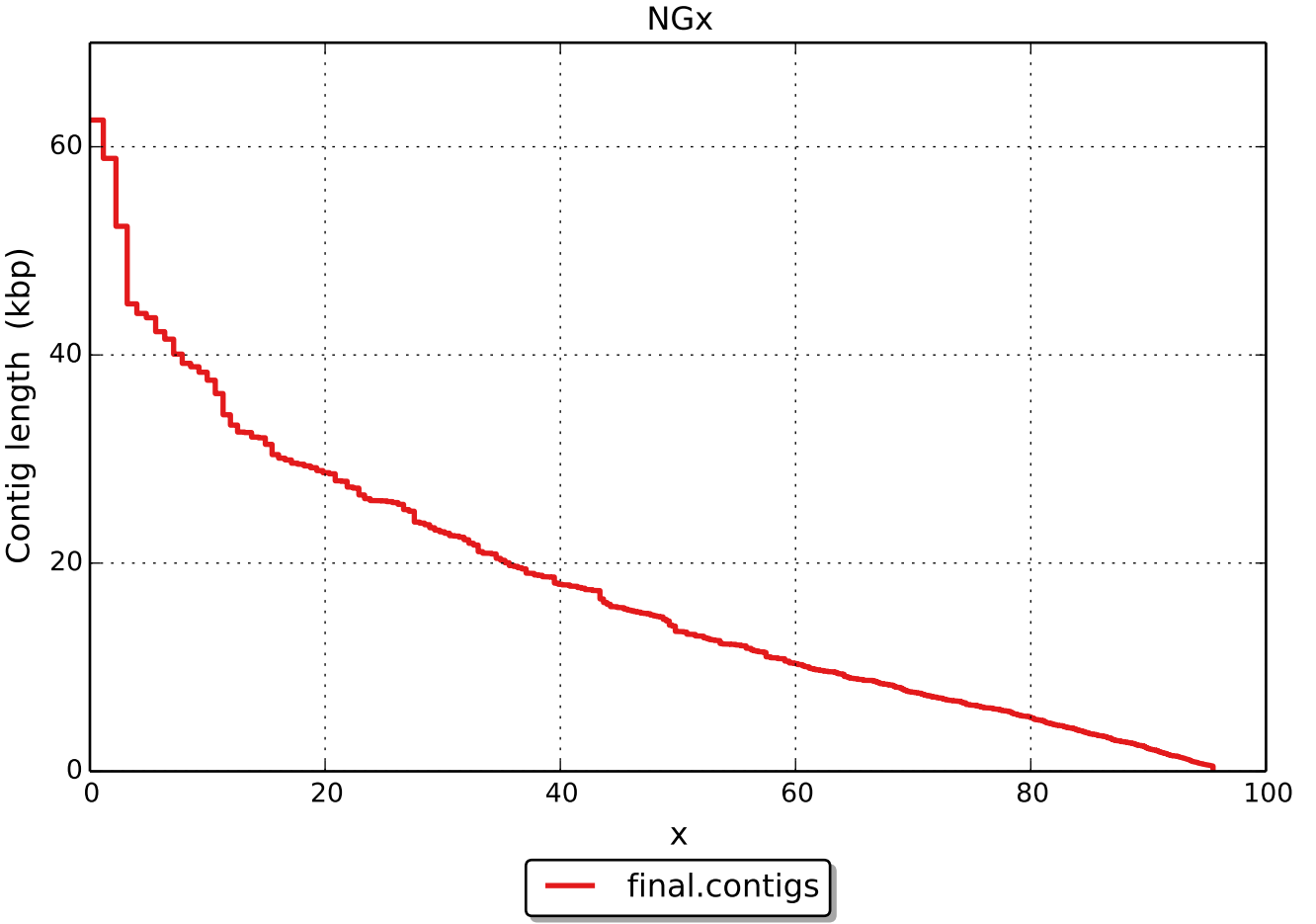
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	50
# N's	0

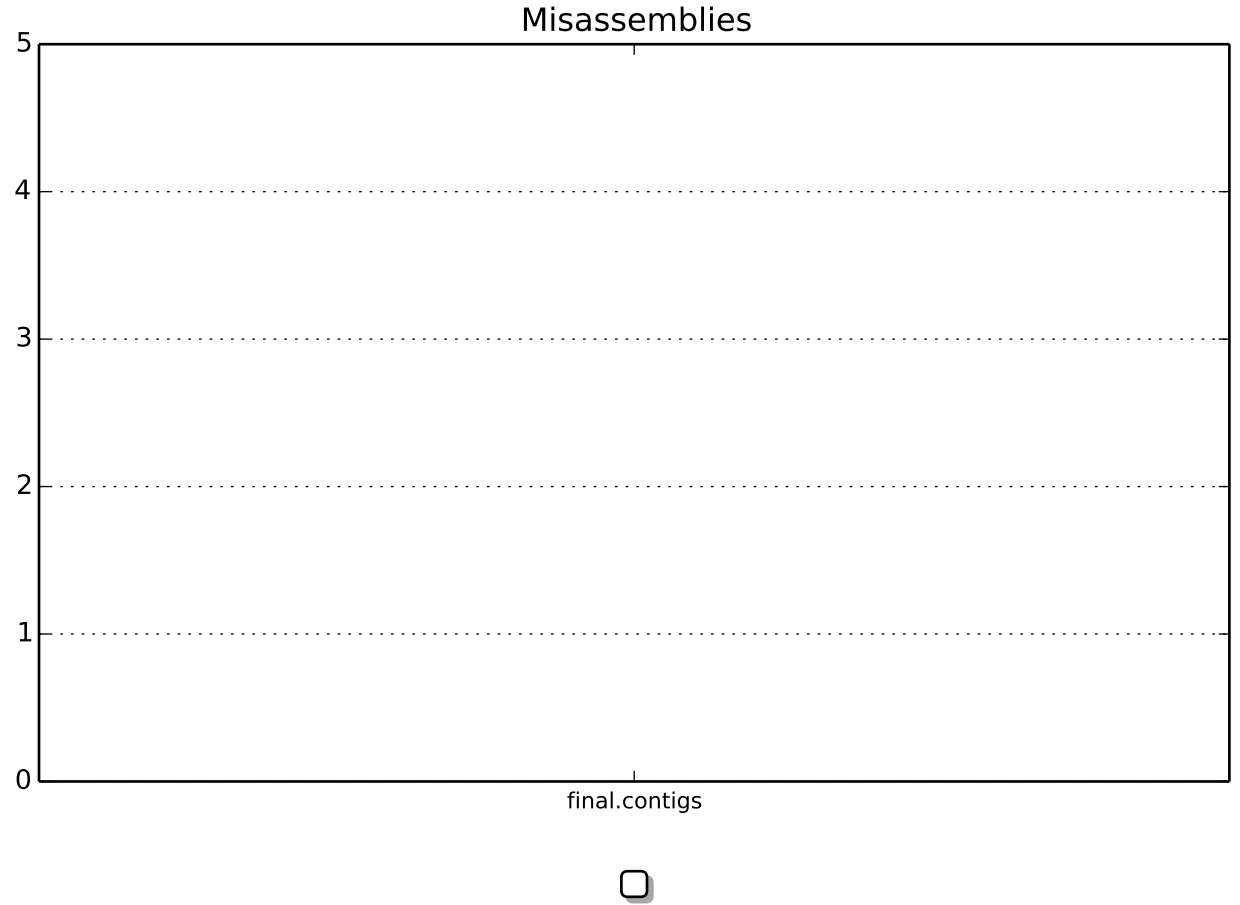
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

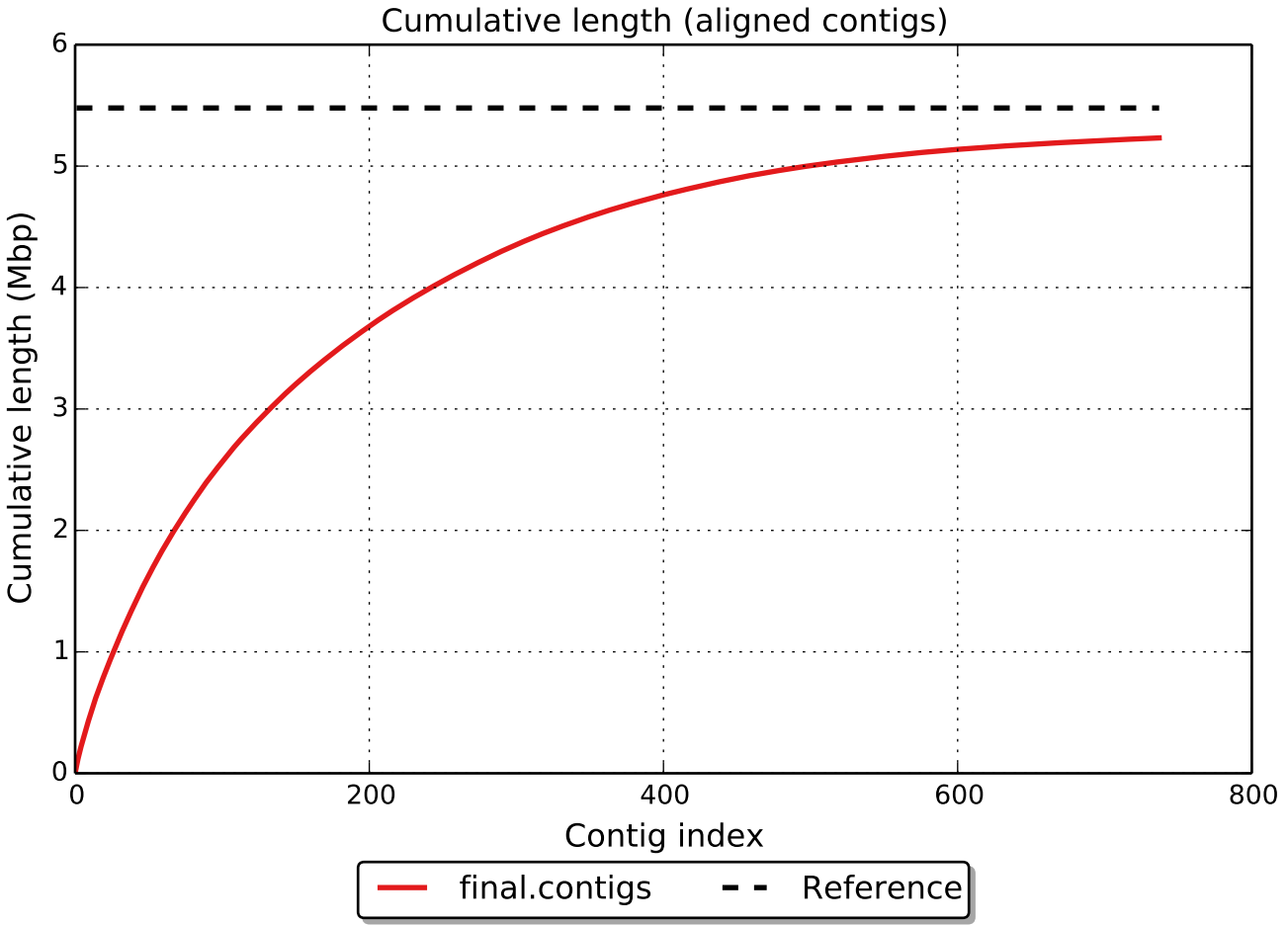

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
800
Contig index
final.contigs
Reference

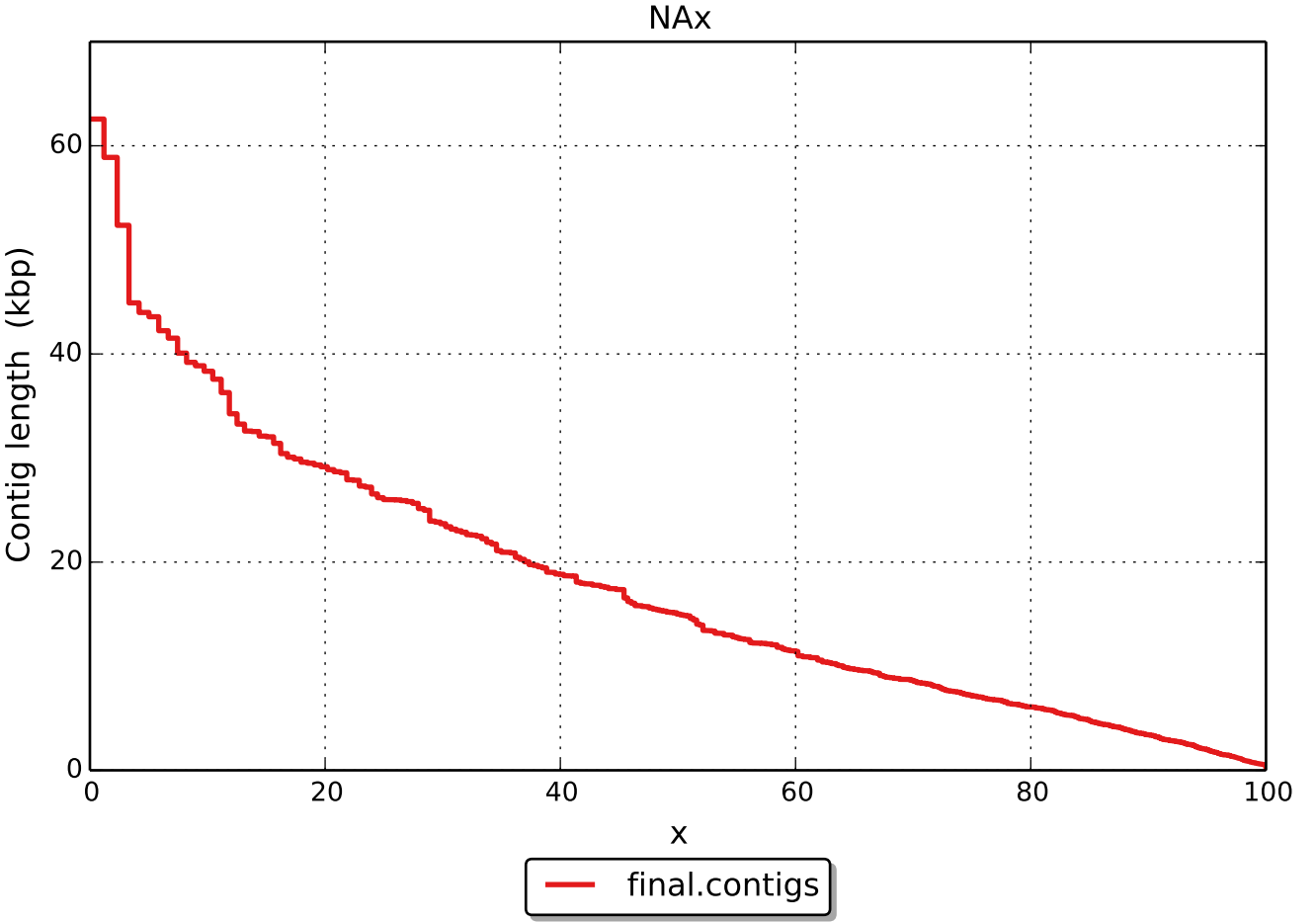

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

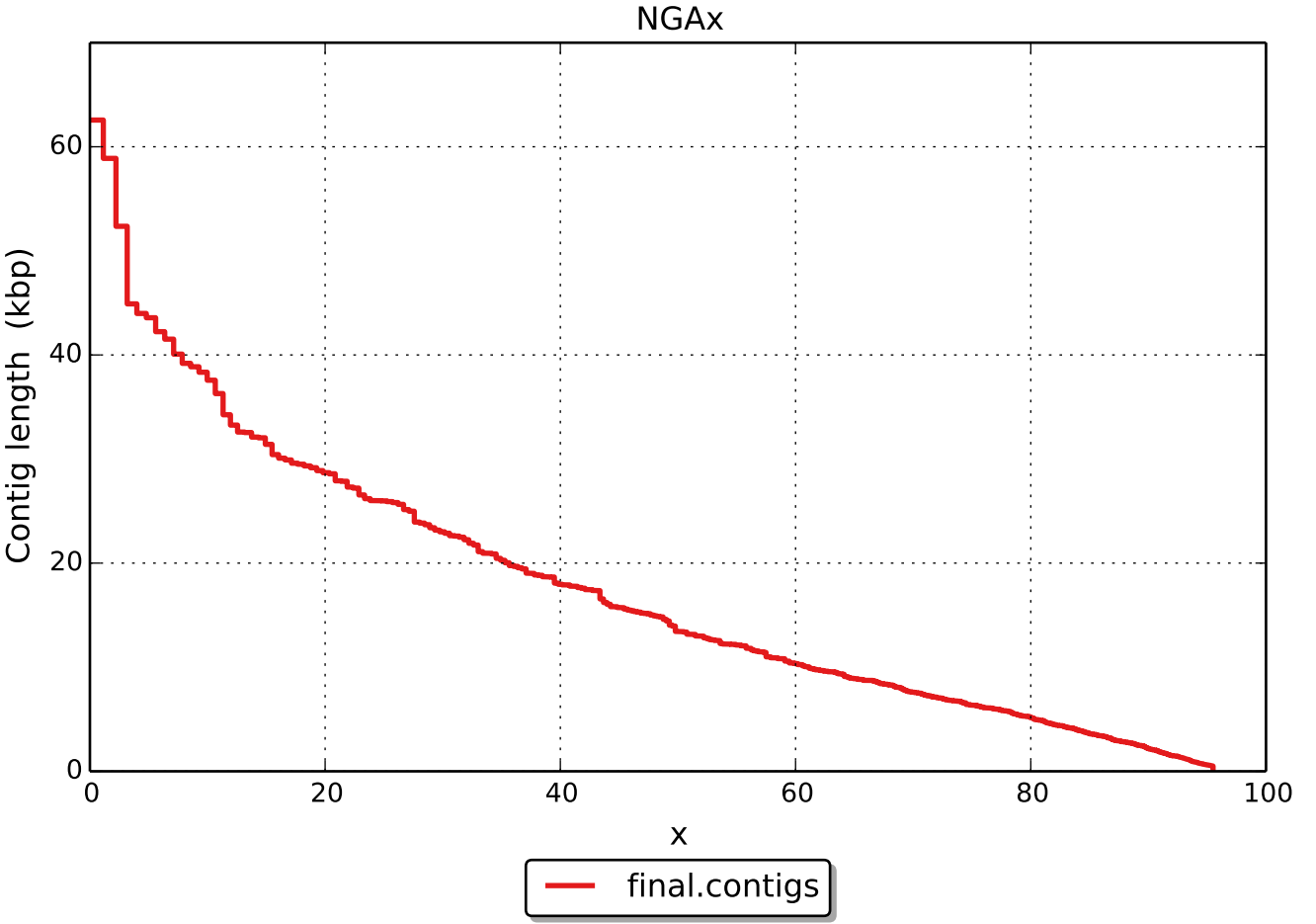

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
200
400
600
800
Contig index
final.contigs
Reference


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


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