Report

	final.contigs
# contigs (>= 0 bp)	3975
# contigs (>= 1000 bp)	2175
Total length (>= 0 bp)	5348965
Total length (>= 1000 bp)	4038399
# contigs	3975
Largest contig	6941
Total length	5348965
Reference length	5478683
GC (%)	50.47
Reference GC (%)	50.49
N50	1589
NG50	1557
N75	1015
NG75	973
L50	1095
LG50	1136
L75	2149
LG75	2247
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.046
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	54.69
# indels per 100 kbp	0.04
Largest alignment	6941
NA50	1589
NGA50	1557
NA75	1015
NGA75	973
LA50	1095
LGA50	1136
LA75	2149
LGA75	2247

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

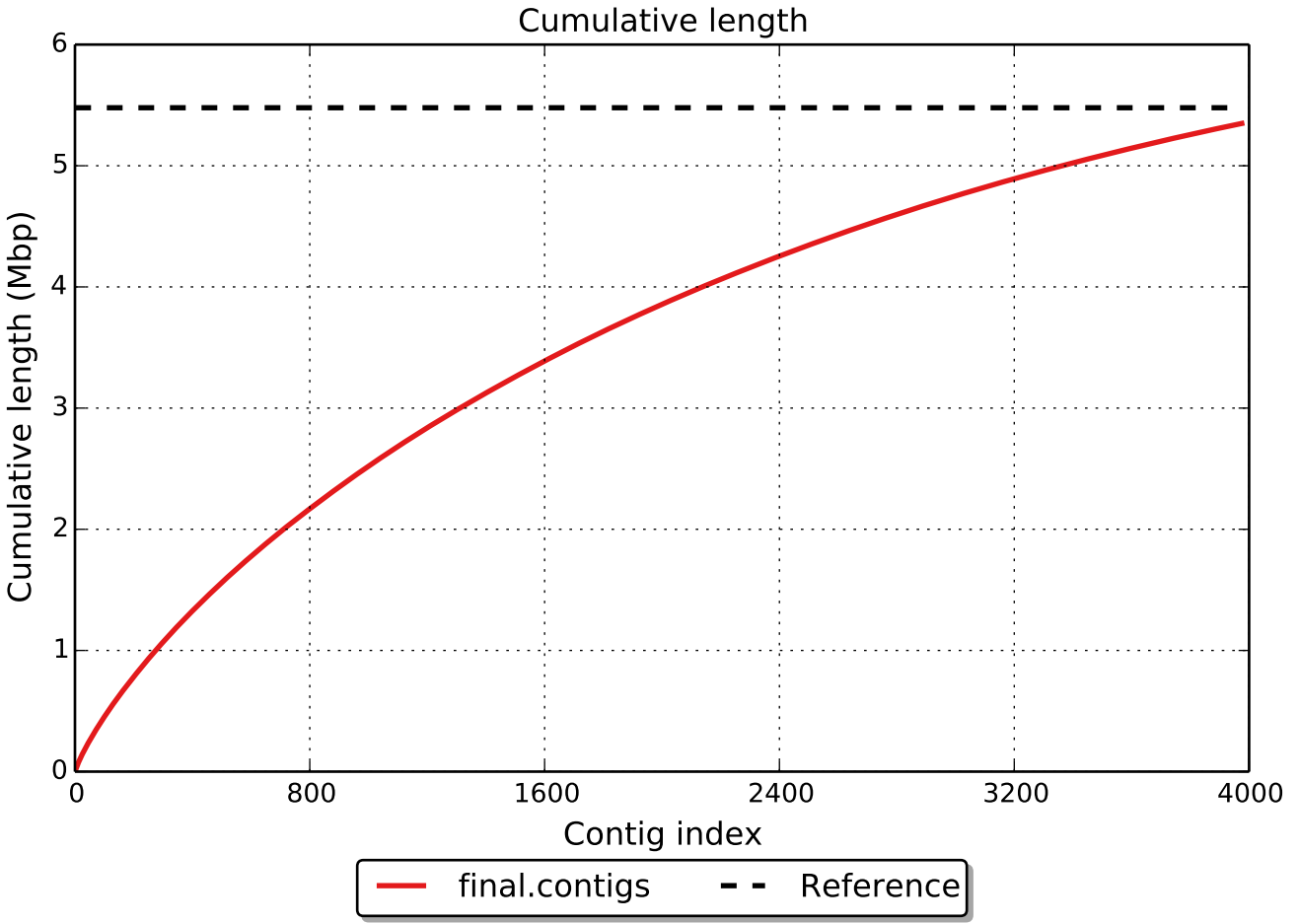
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2788
# indels	2
# short indels	2
# long indels	0
Indels length	2

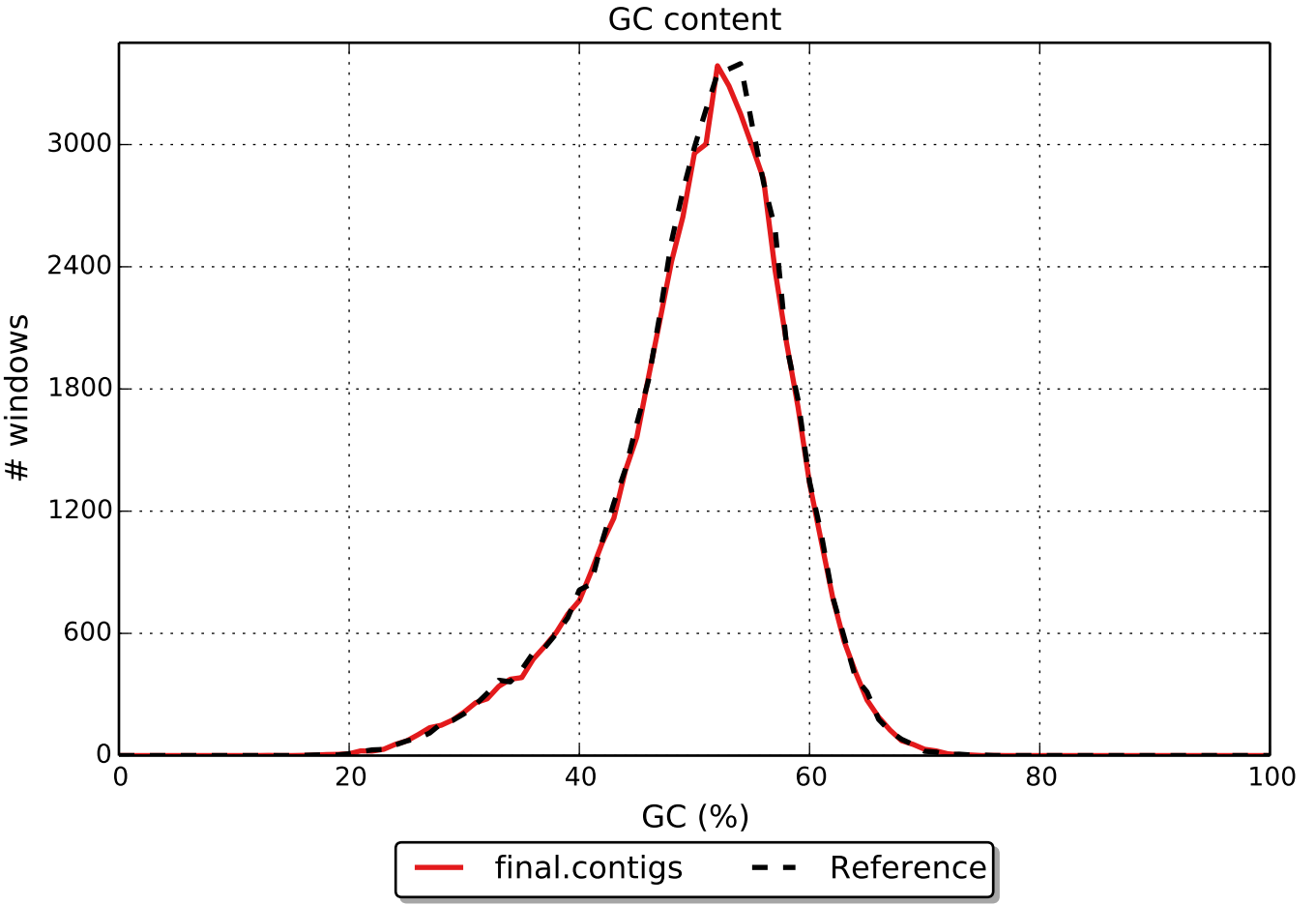
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

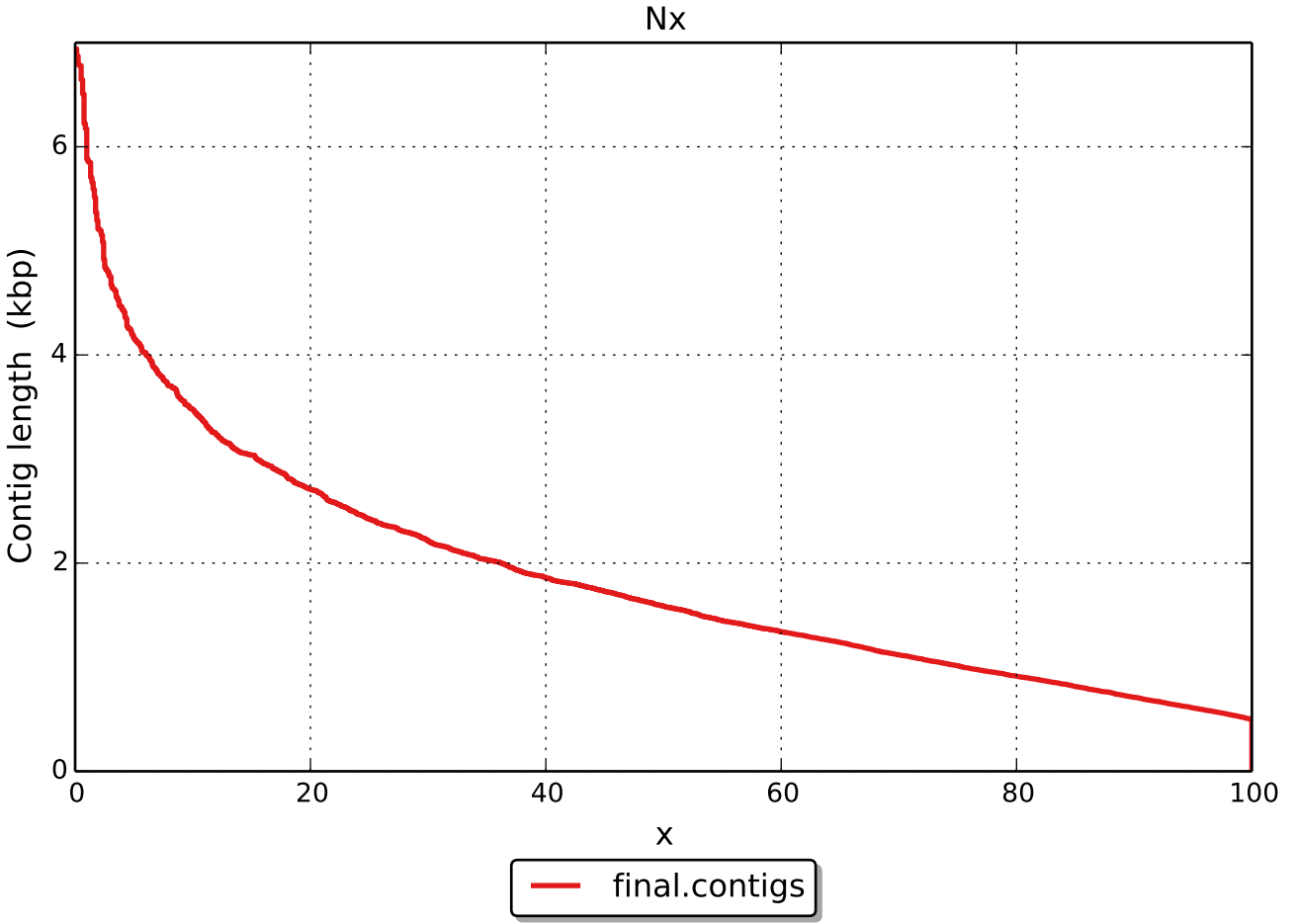
Unaligned report

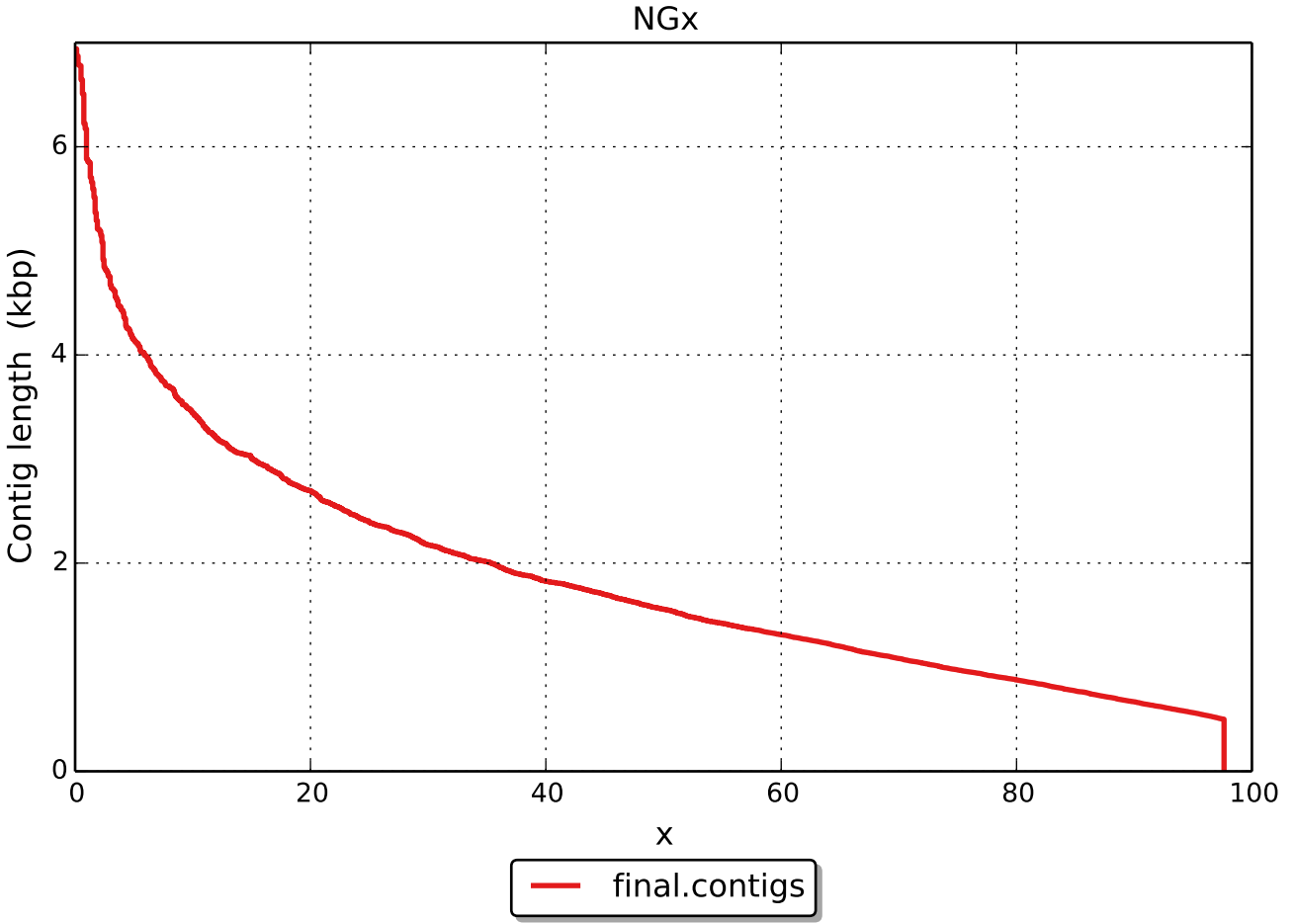
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

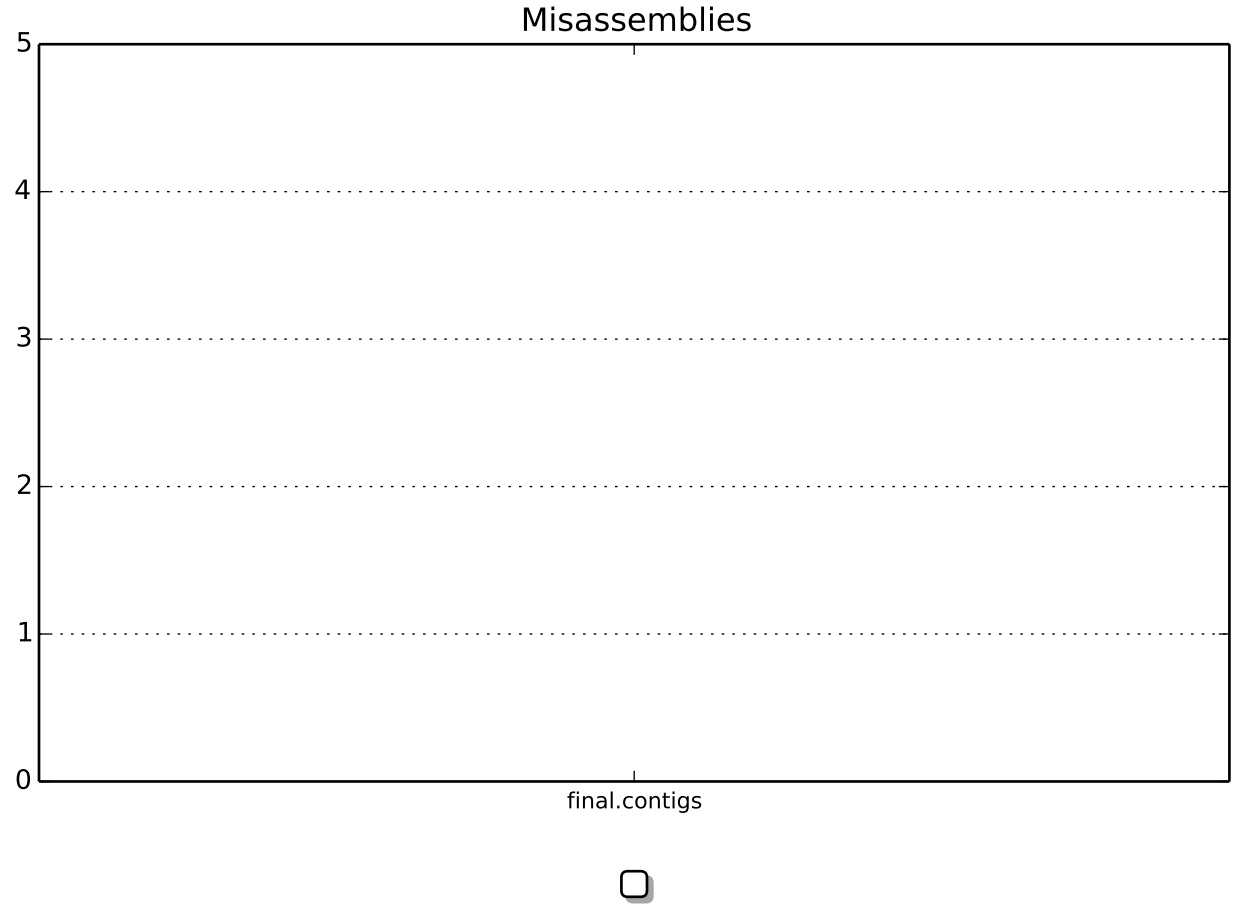
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

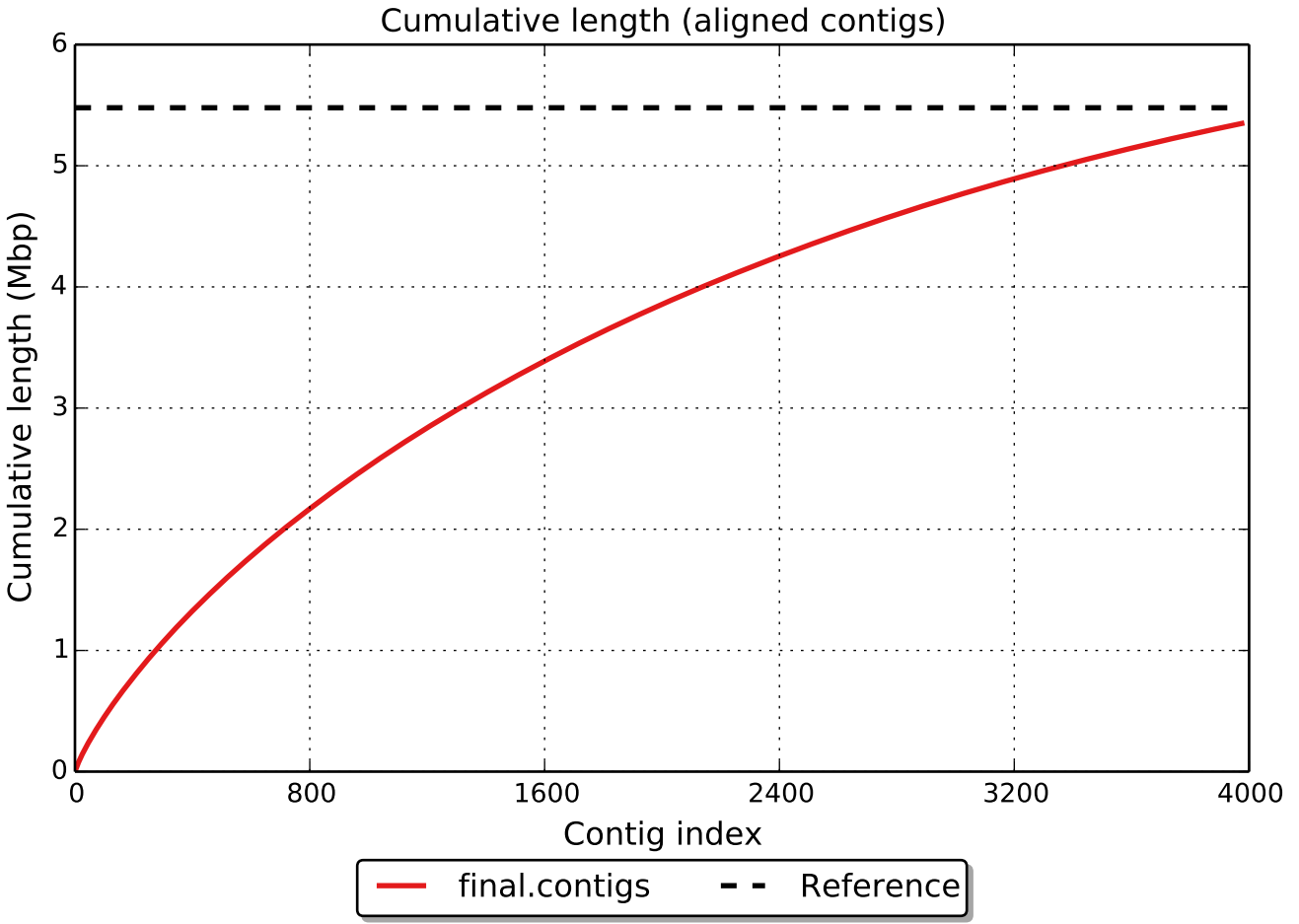

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference

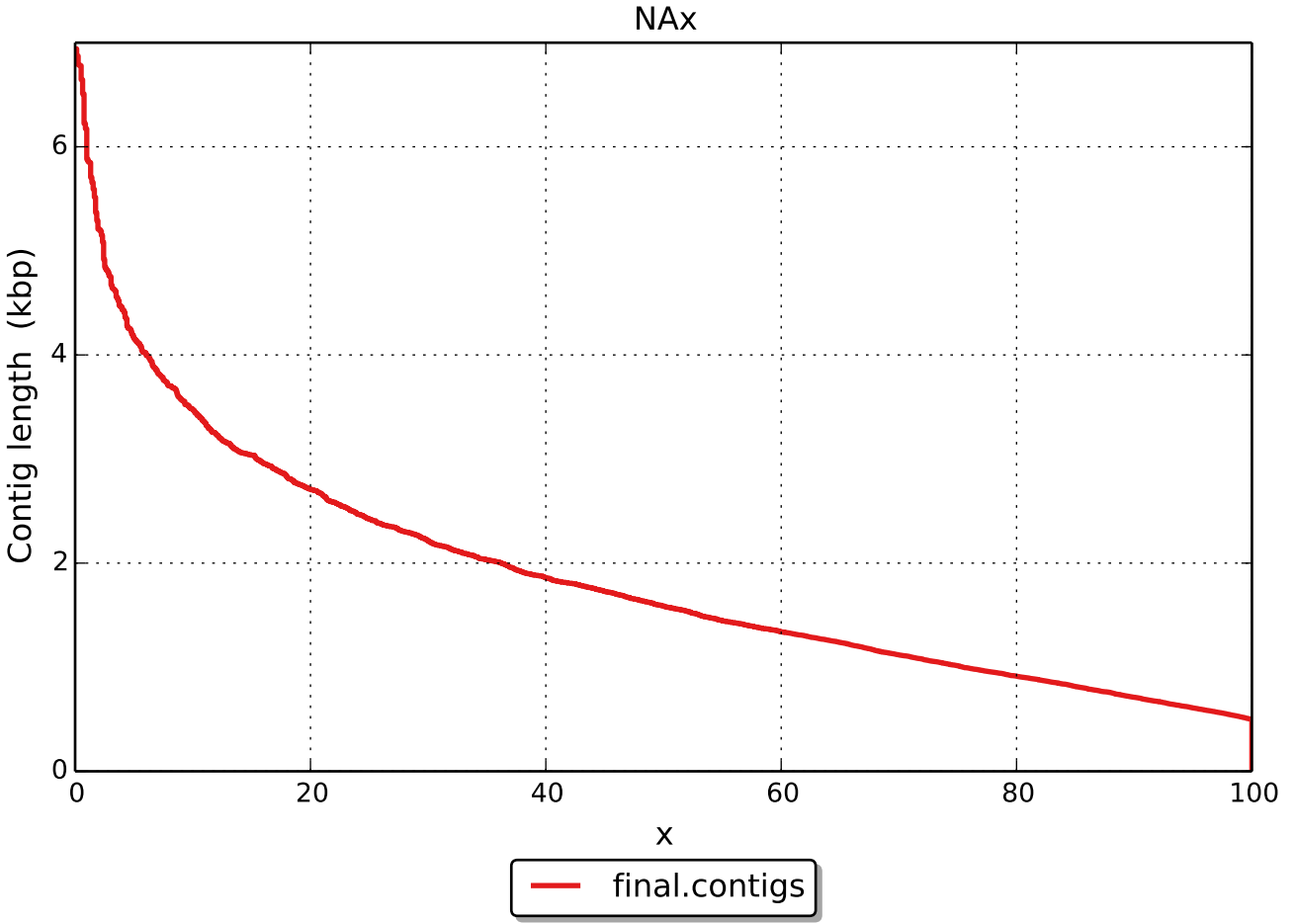

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

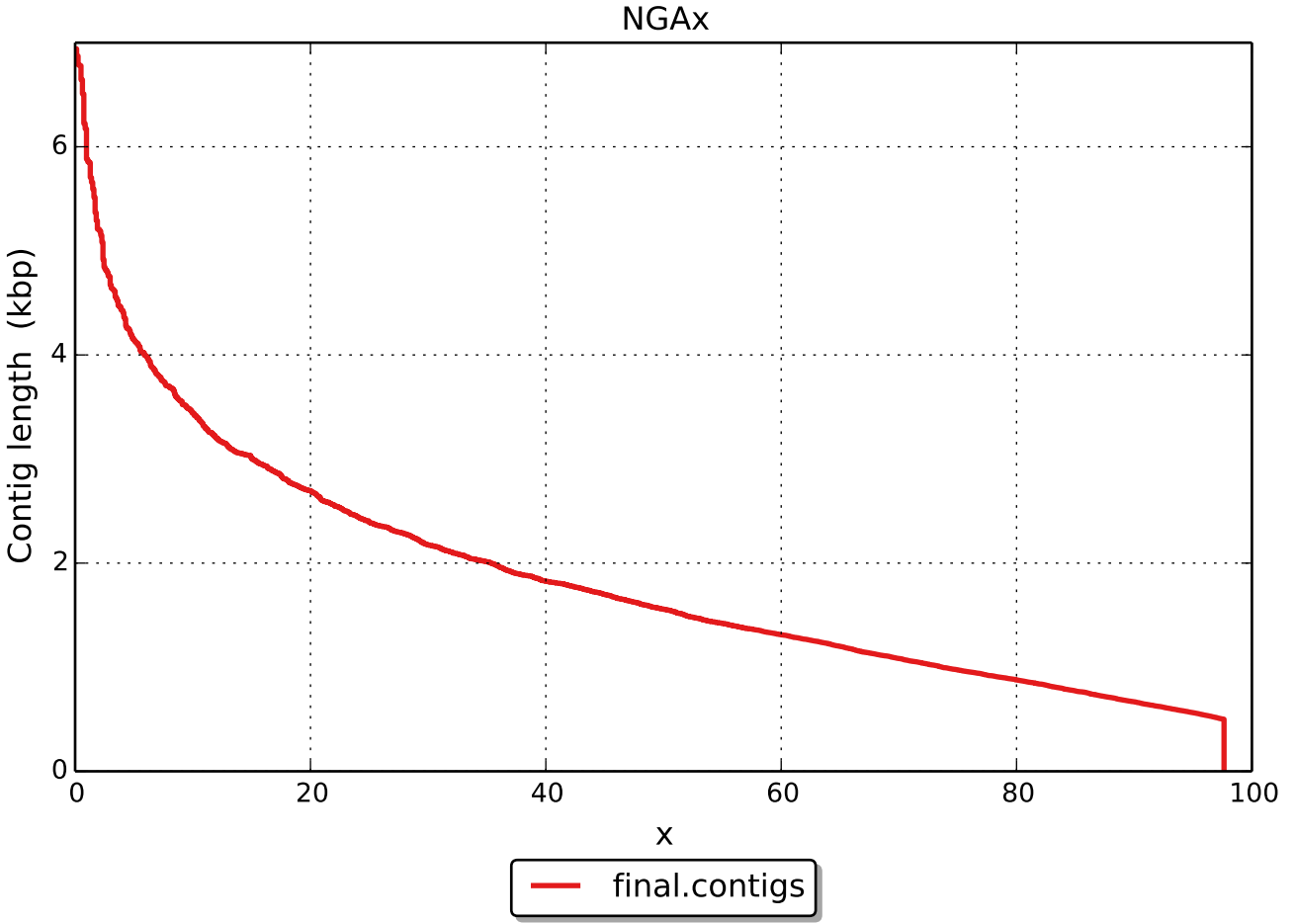

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
2
4
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 (Mbp)
0
1
2
3
4
5
6
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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


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