Report

	final.contigs
# contigs (>= 0 bp)	4575
# contigs (>= 1000 bp)	1999
Total length (>= 0 bp)	5120870
Total length (>= 1000 bp)	3262293
# contigs	4575
Largest contig	6941
Total length	5120870
Reference length	5478683
GC (%)	50.47
Reference GC (%)	50.49
N50	1236
NG50	1176
N75	839
NG75	769
L50	1368
LG50	1516
L75	2629
LG75	2963
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	88.859
Duplication ratio	1.052
# N's per 100 kbp	0.00
# mismatches per 100 kbp	77.85
# indels per 100 kbp	0.08
Largest alignment	6941
NA50	1236
NGA50	1176
NA75	839
NGA75	769
LA50	1368
LGA50	1516
LA75	2629
LGA75	2963

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

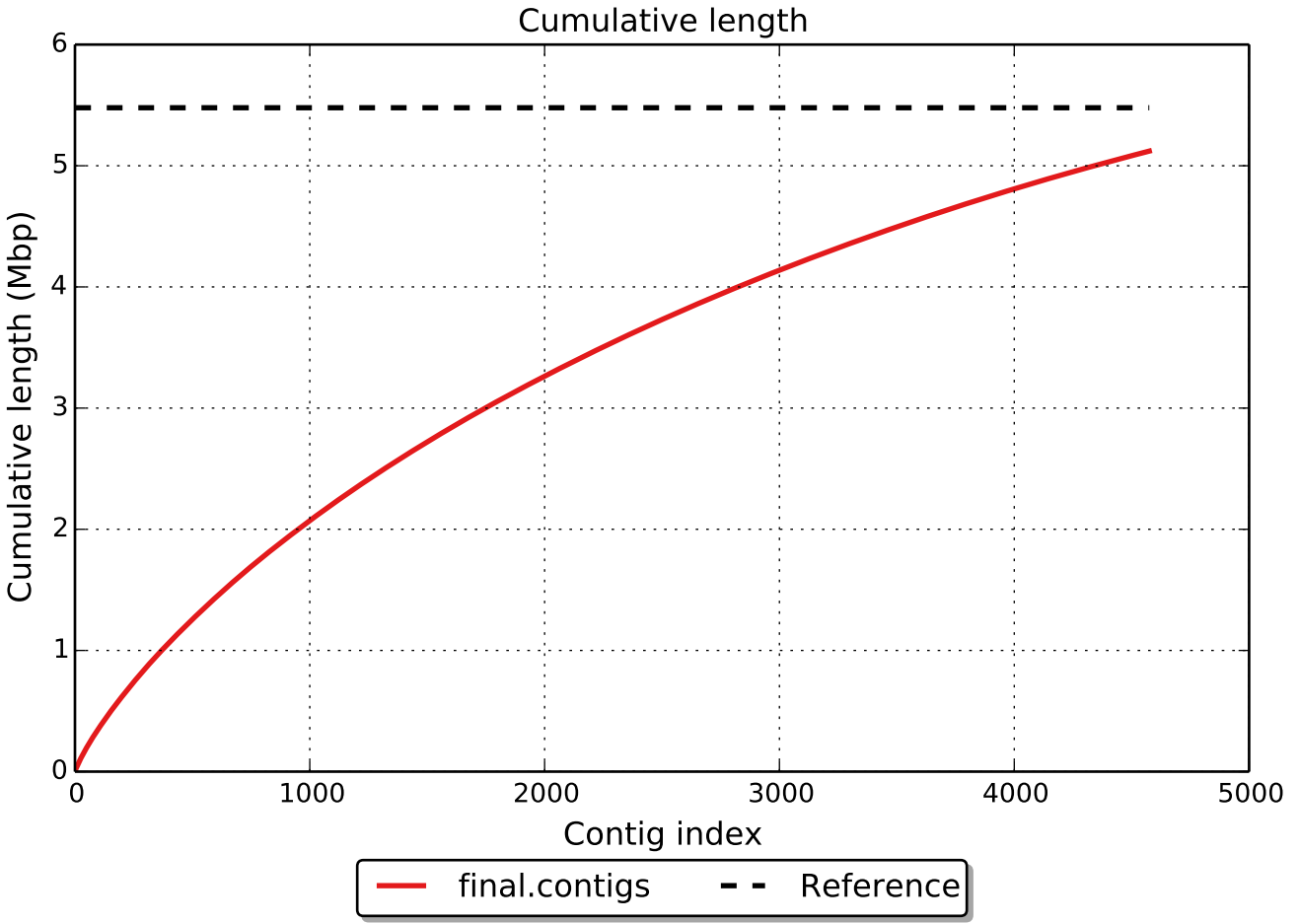
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3790
# indels	4
# short indels	2
# long indels	2
Indels length	32

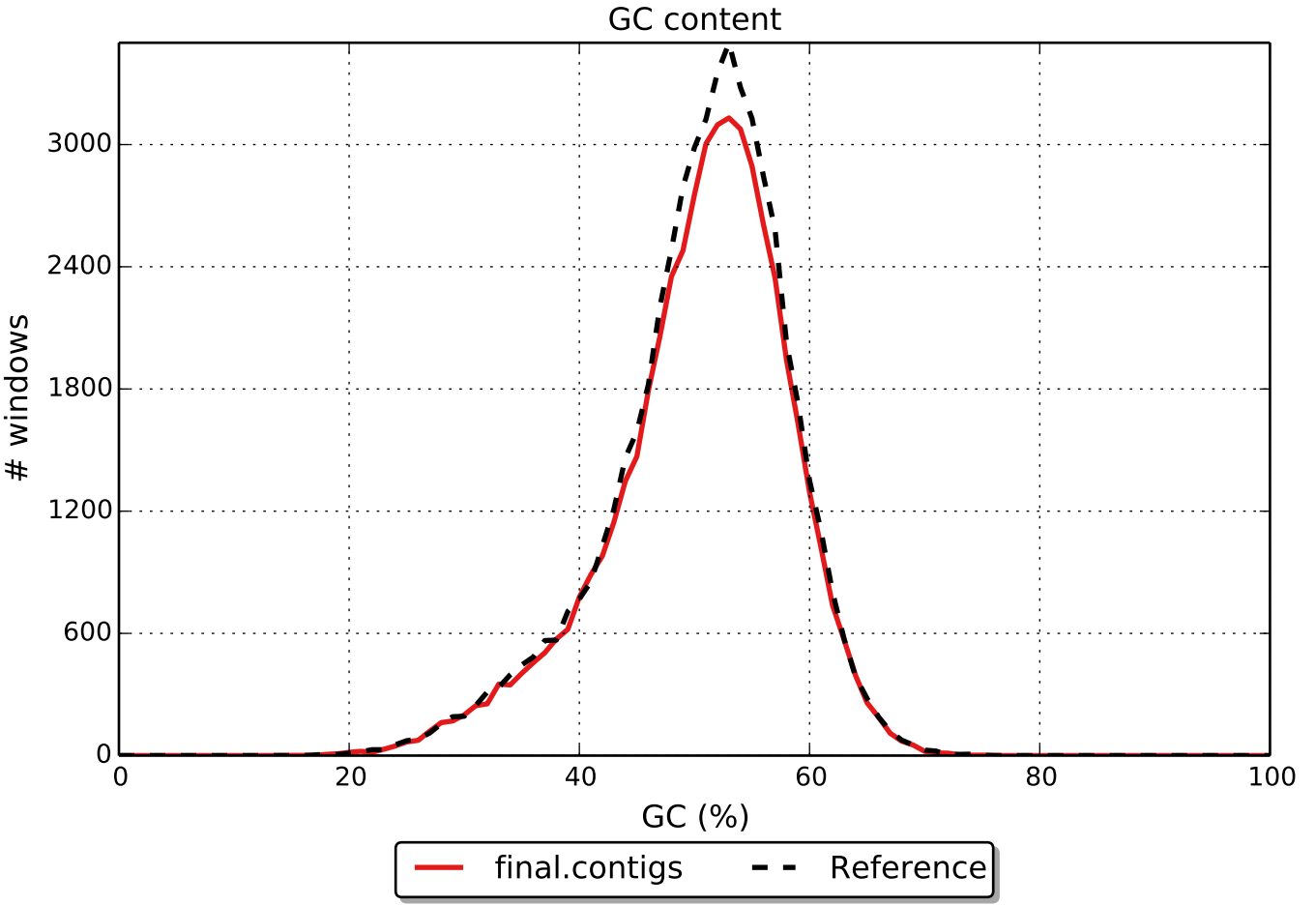
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

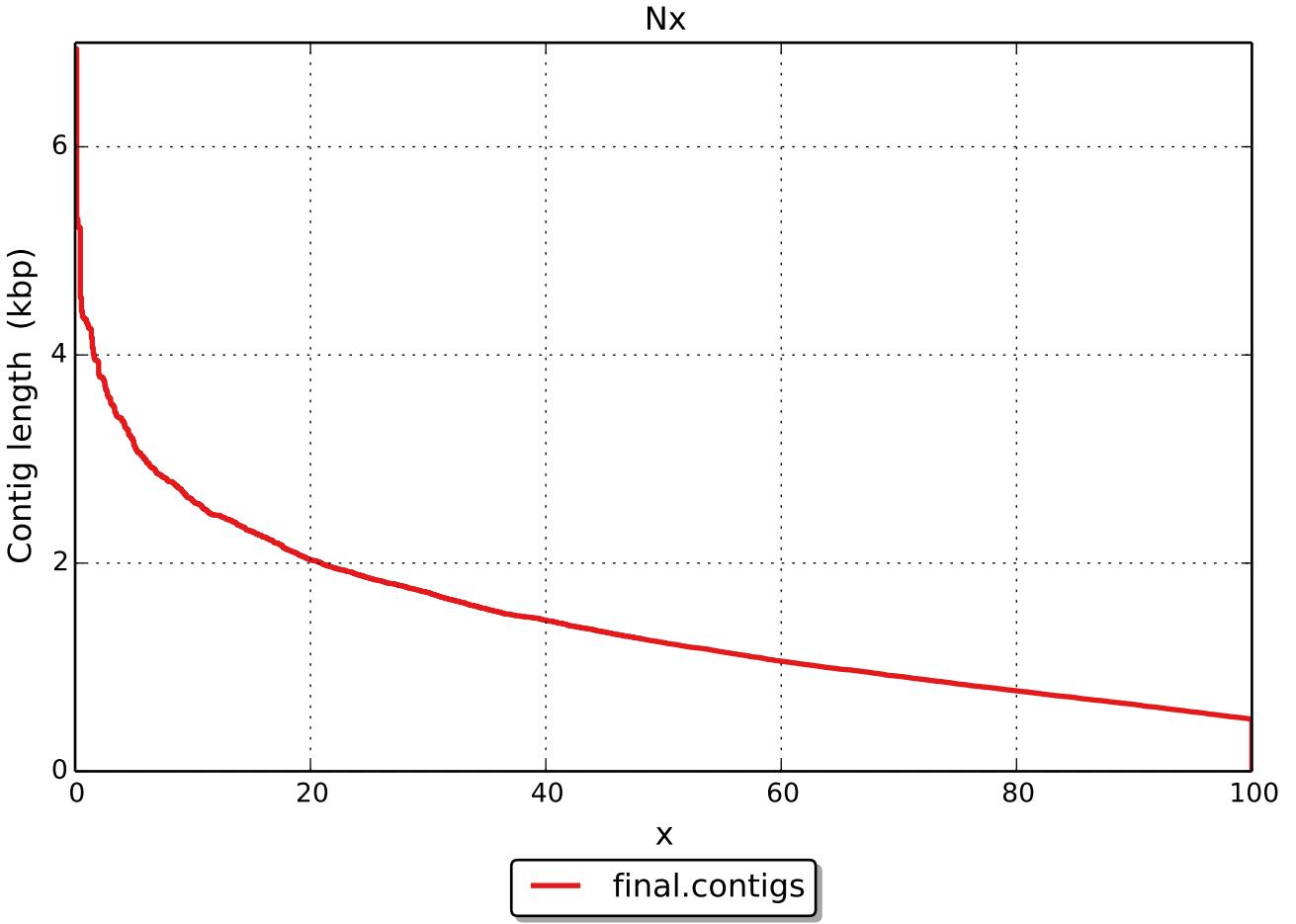
Unaligned report

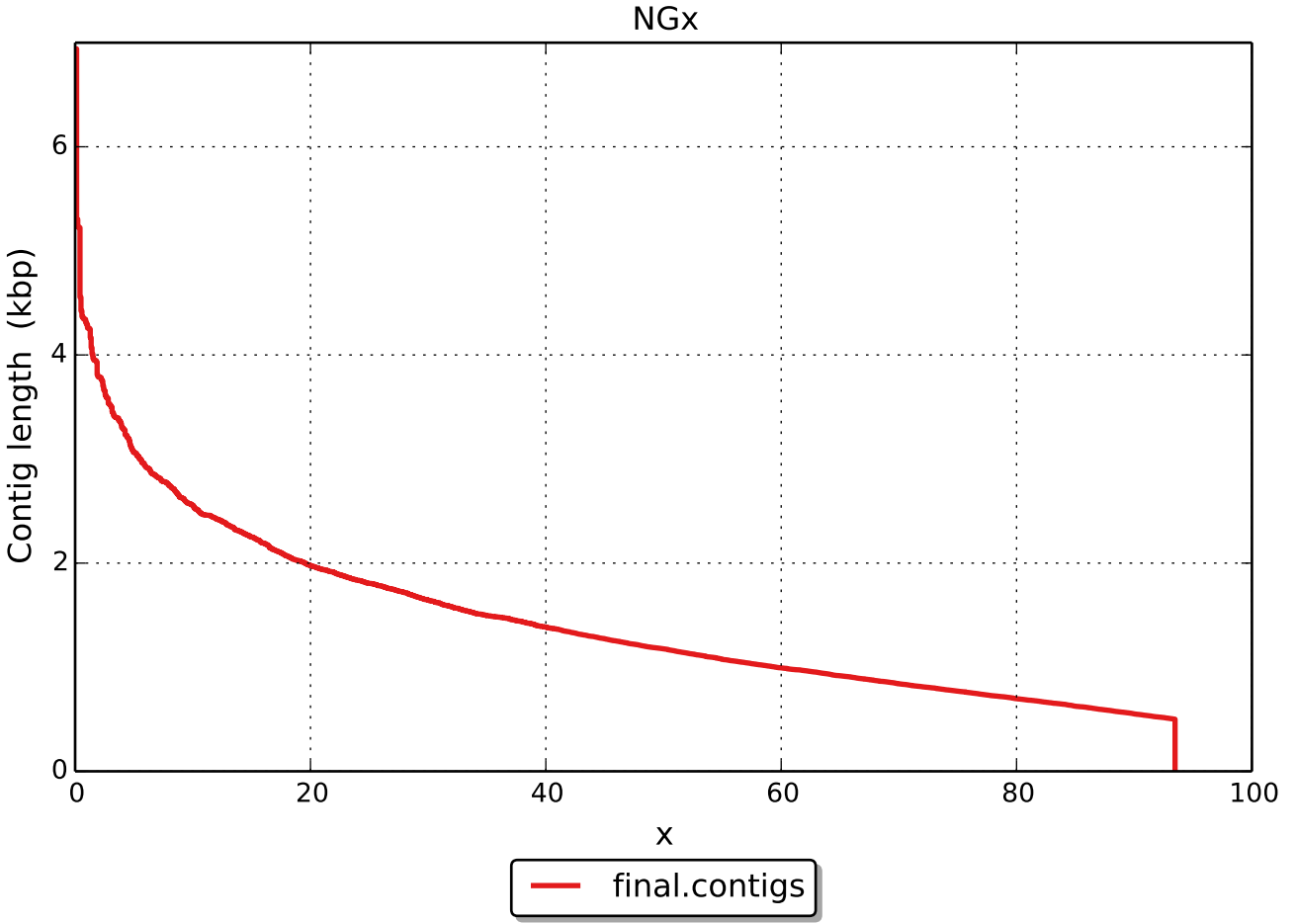
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

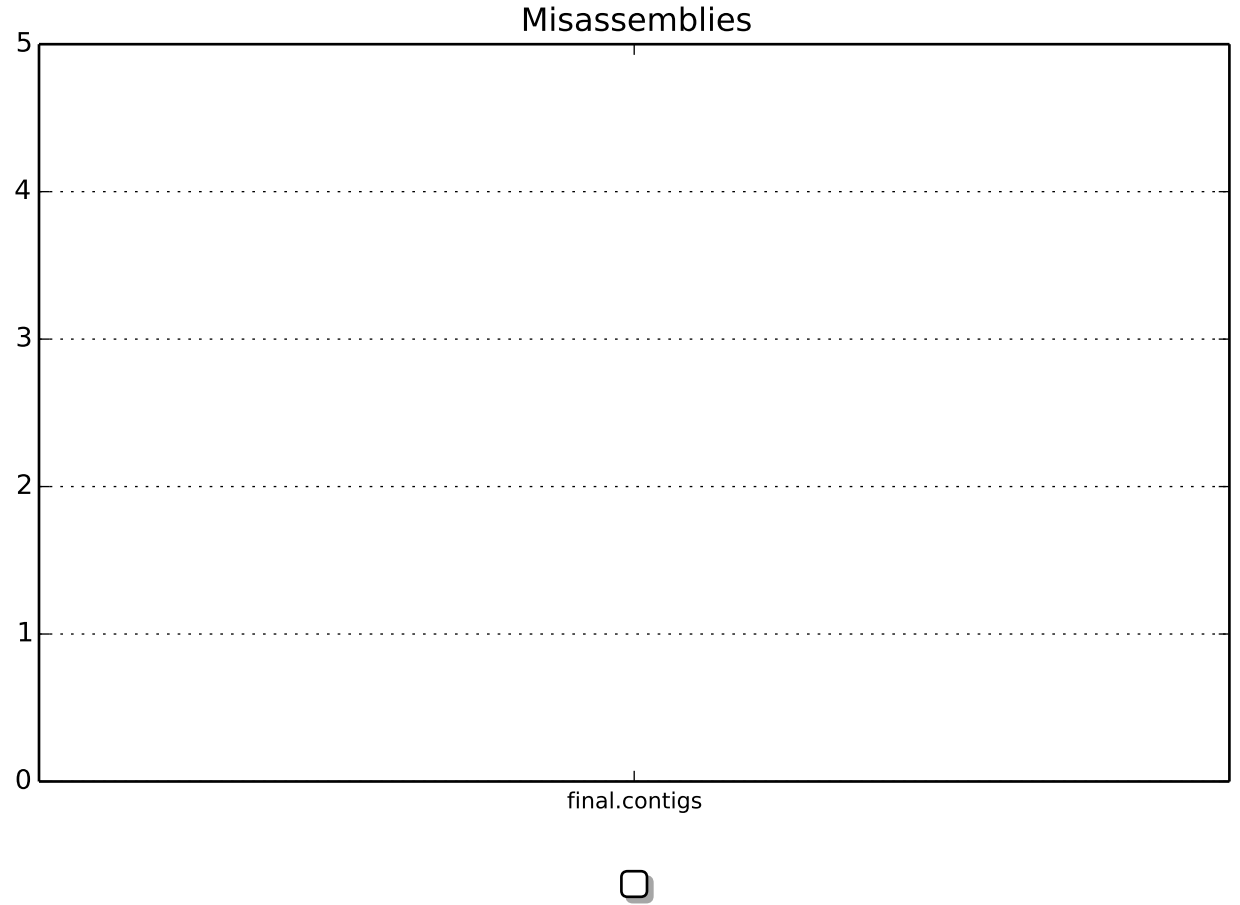
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

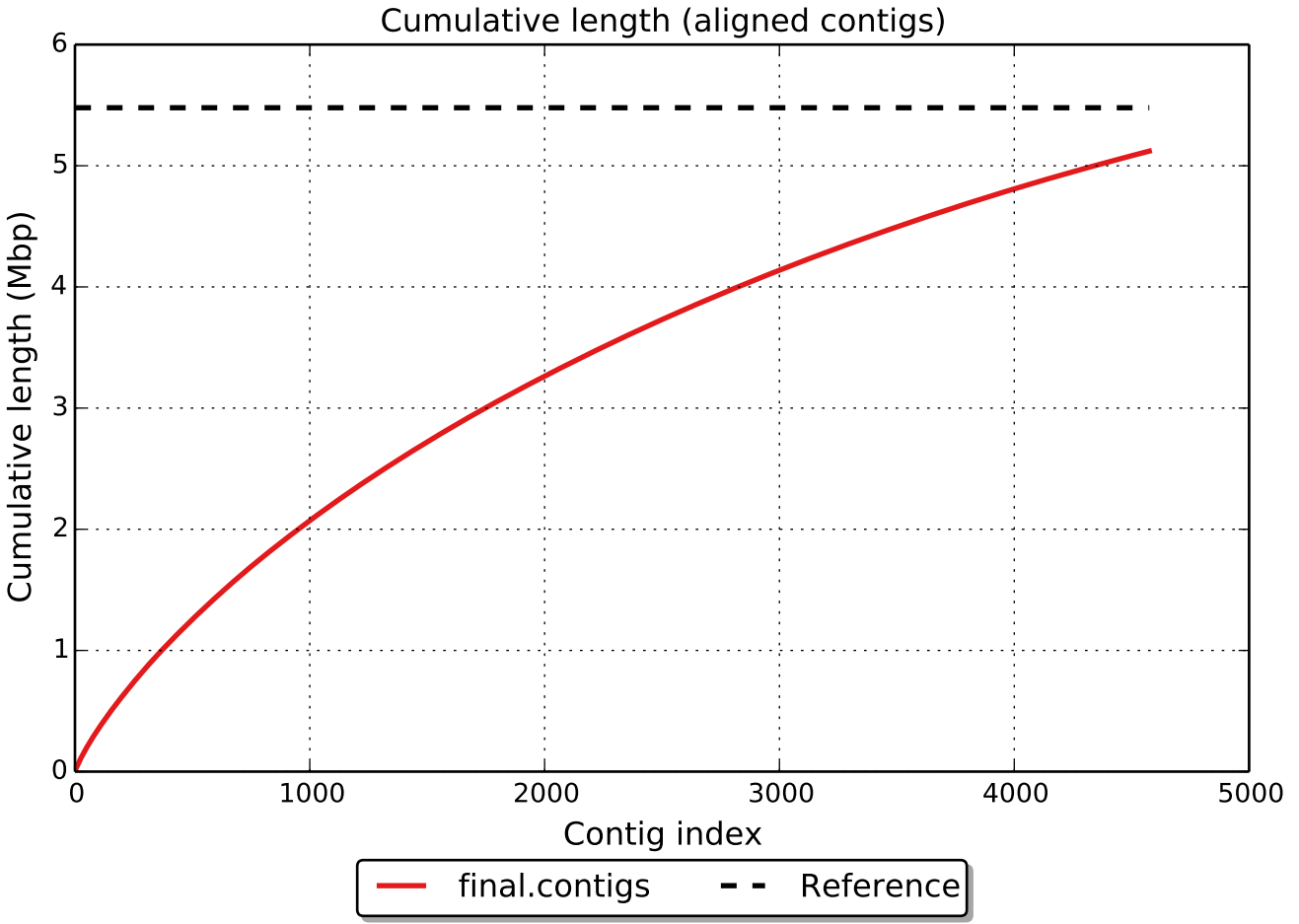

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
Contig index
final.contigs
Reference

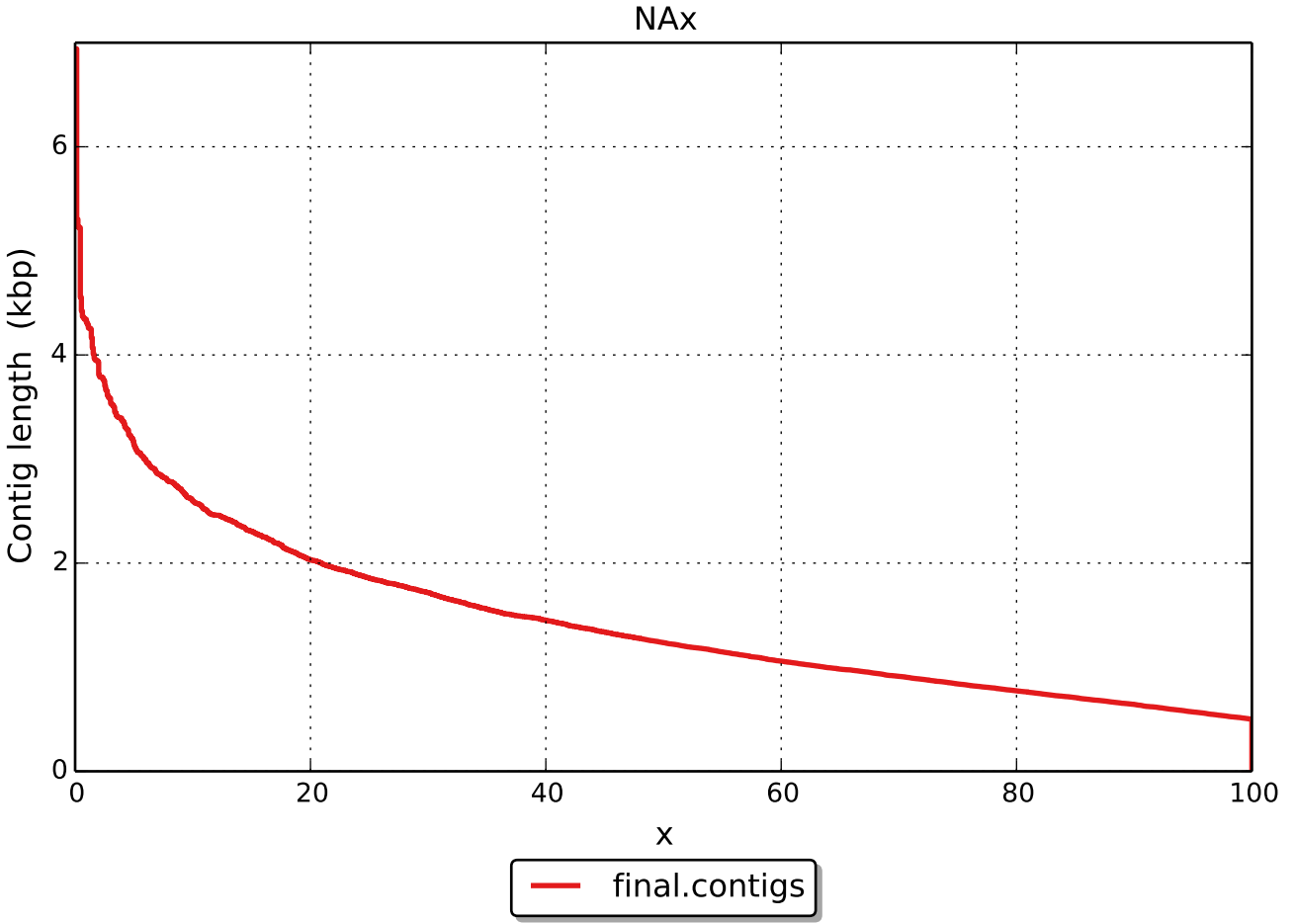

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

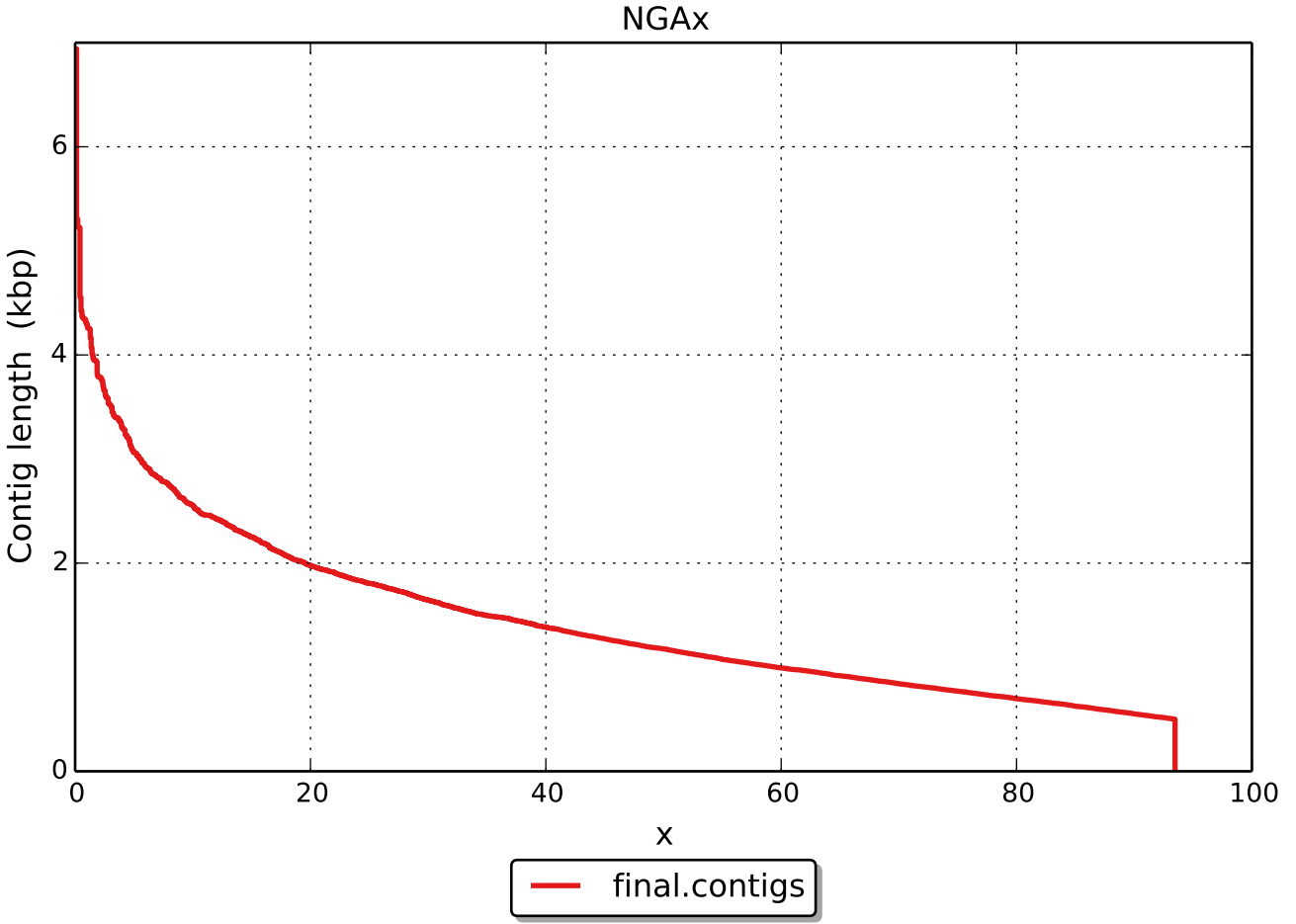

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs


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
1000
2000
3000
4000
5000
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