Report

	final.contigs
# contigs (>= 0 bp)	2134
# contigs (>= 1000 bp)	1618
Total length (>= 0 bp)	5216530
Total length (>= 1000 bp)	4840593
# contigs	2134
Largest contig	15765
Total length	5216530
Reference length	5478683
GC (%)	50.29
Reference GC (%)	50.49
N50	3469
NG50	3293
N75	1964
NG75	1755
L50	469
LG50	508
L75	968
LG75	1074
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	4159
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	2369
Genome fraction (%)	92.488
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	19.56
# indels per 100 kbp	0.10
Largest alignment	15765
NA50	3457
NGA50	3280
NA75	1963
NGA75	1755
LA50	470
LGA50	509
LA75	969
LGA75	1075

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

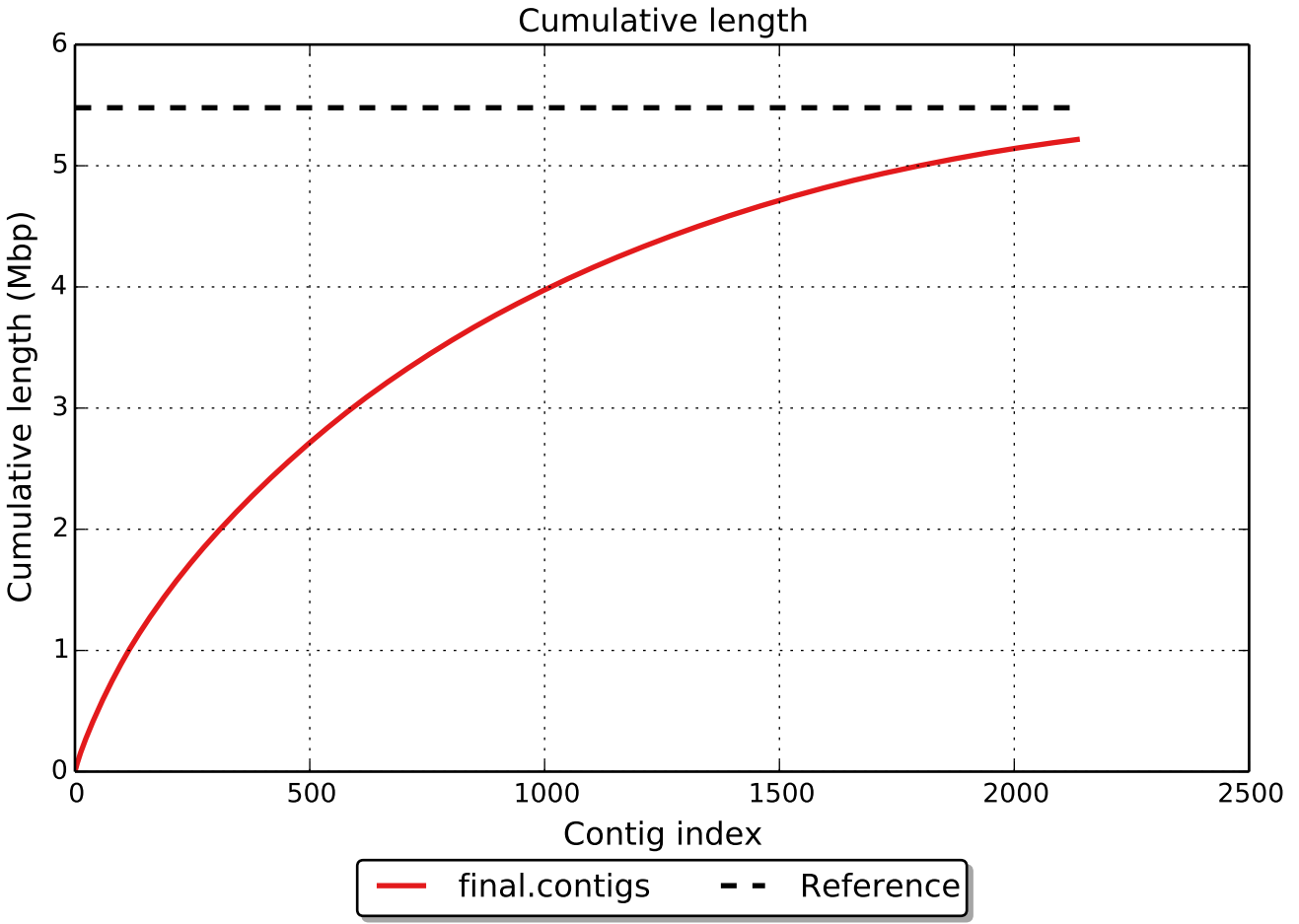
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	1
Misassembled contigs length	4159
# local misassemblies	0
# mismatches	991
# indels	5
# short indels	3
# long indels	2
Indels length	28

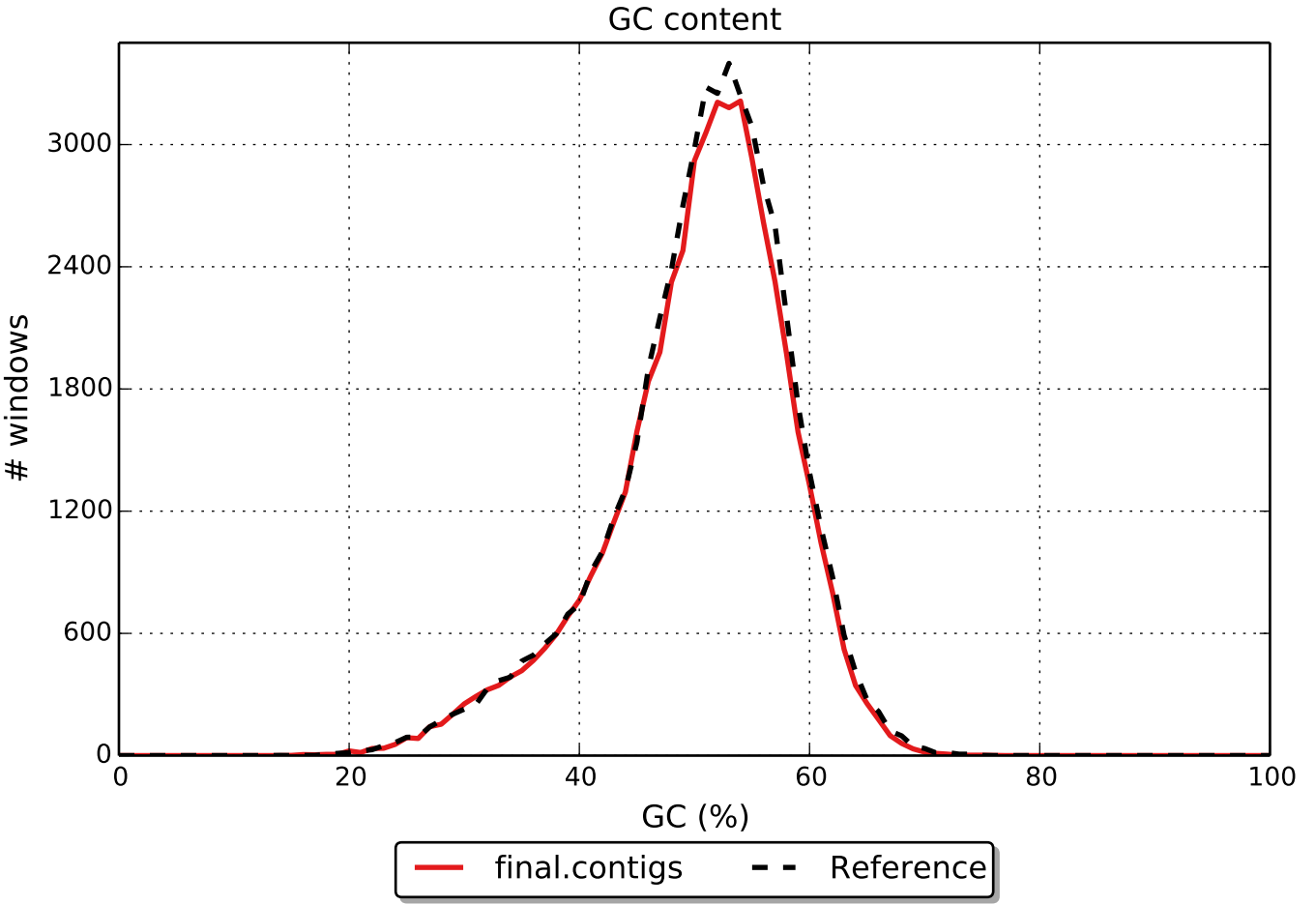
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

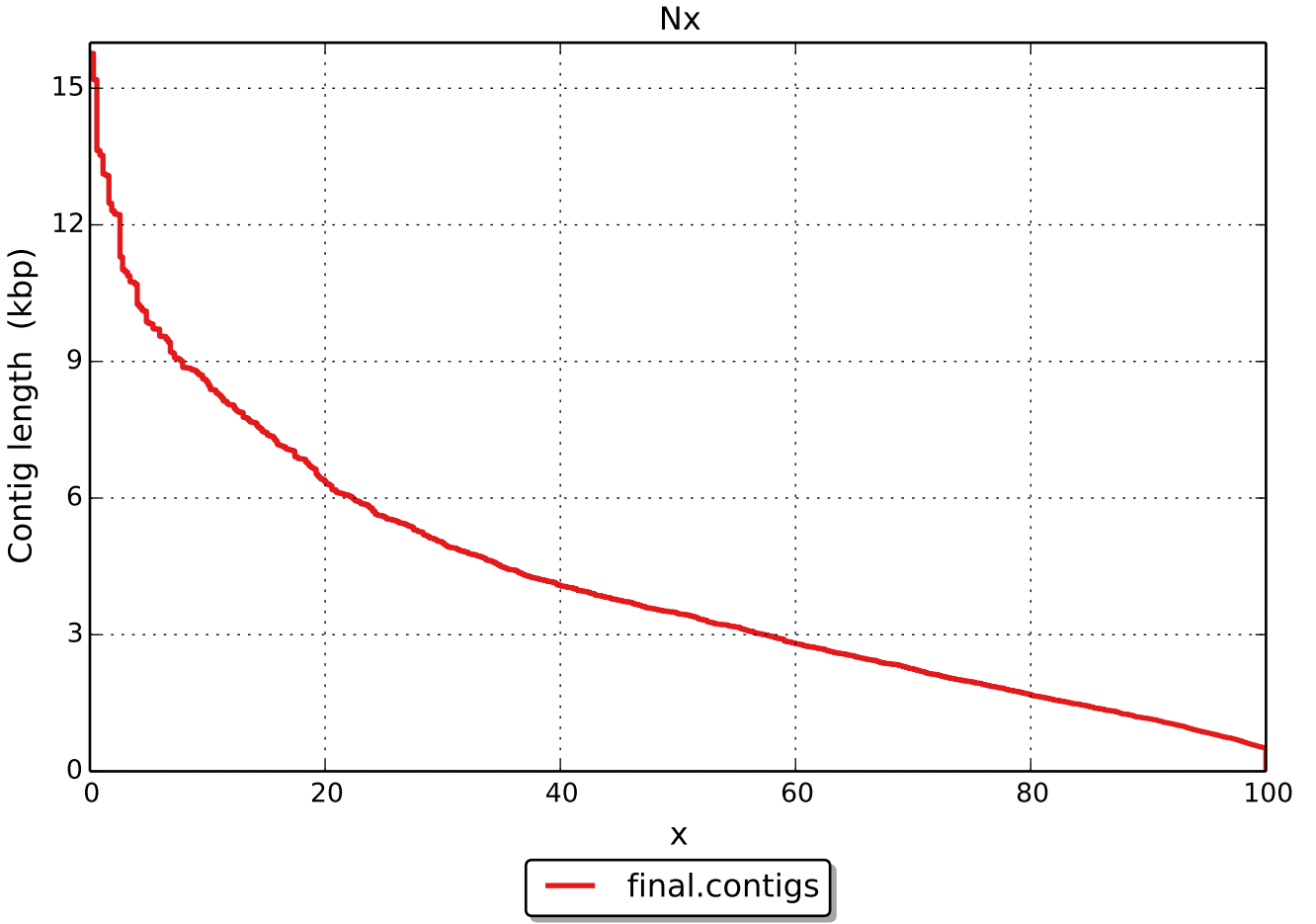
Unaligned report

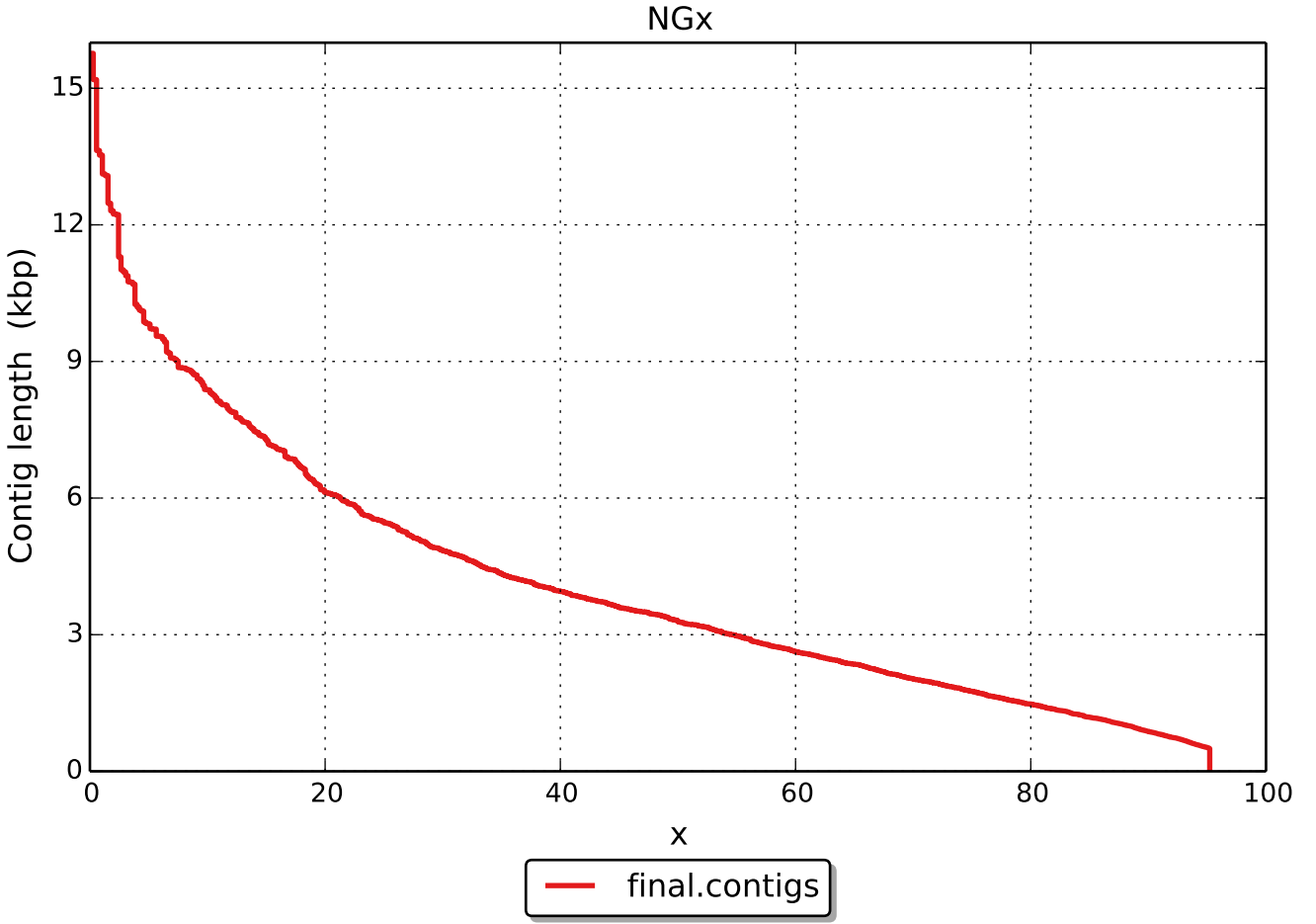
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2369
# N's	0

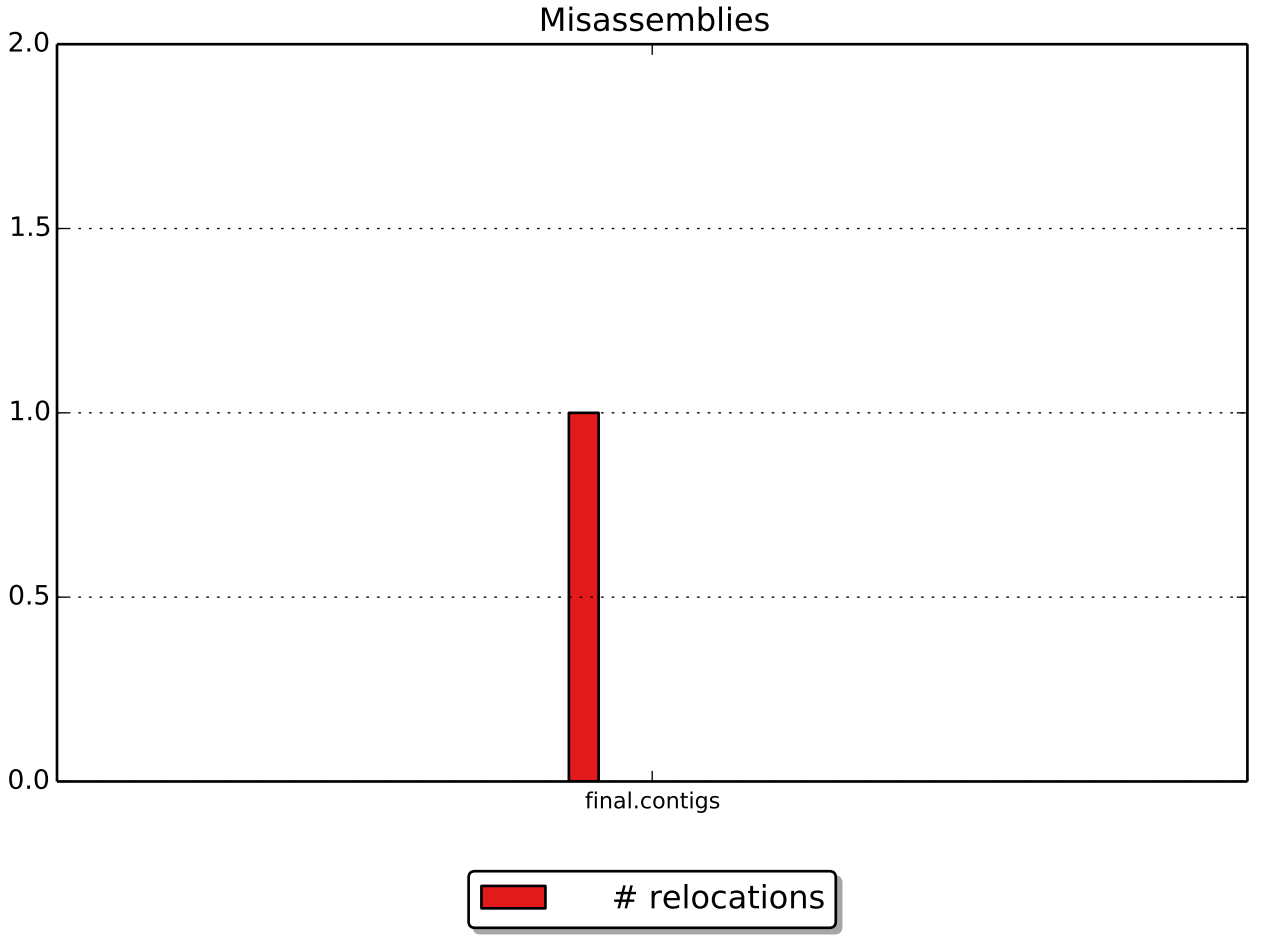
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

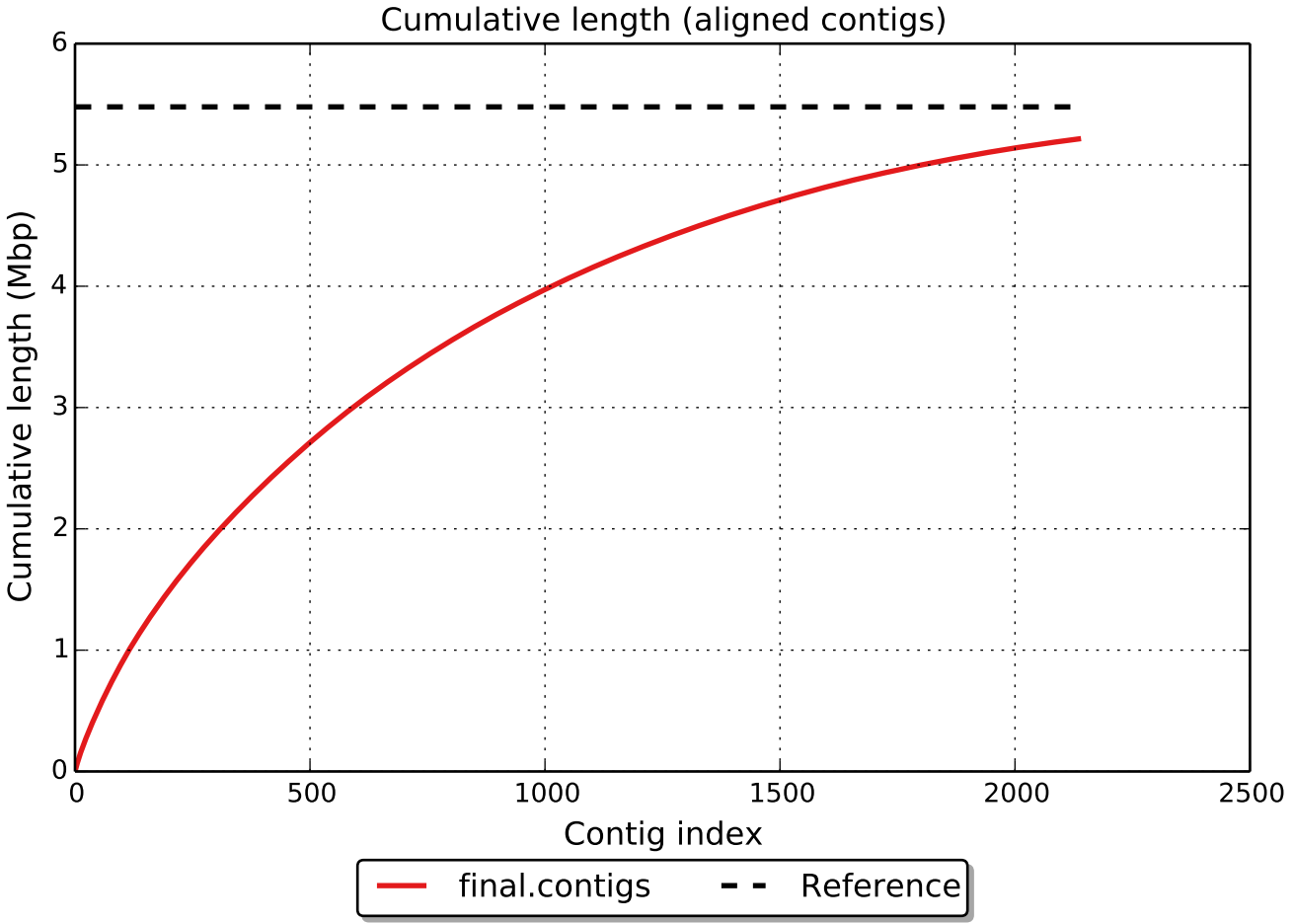

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

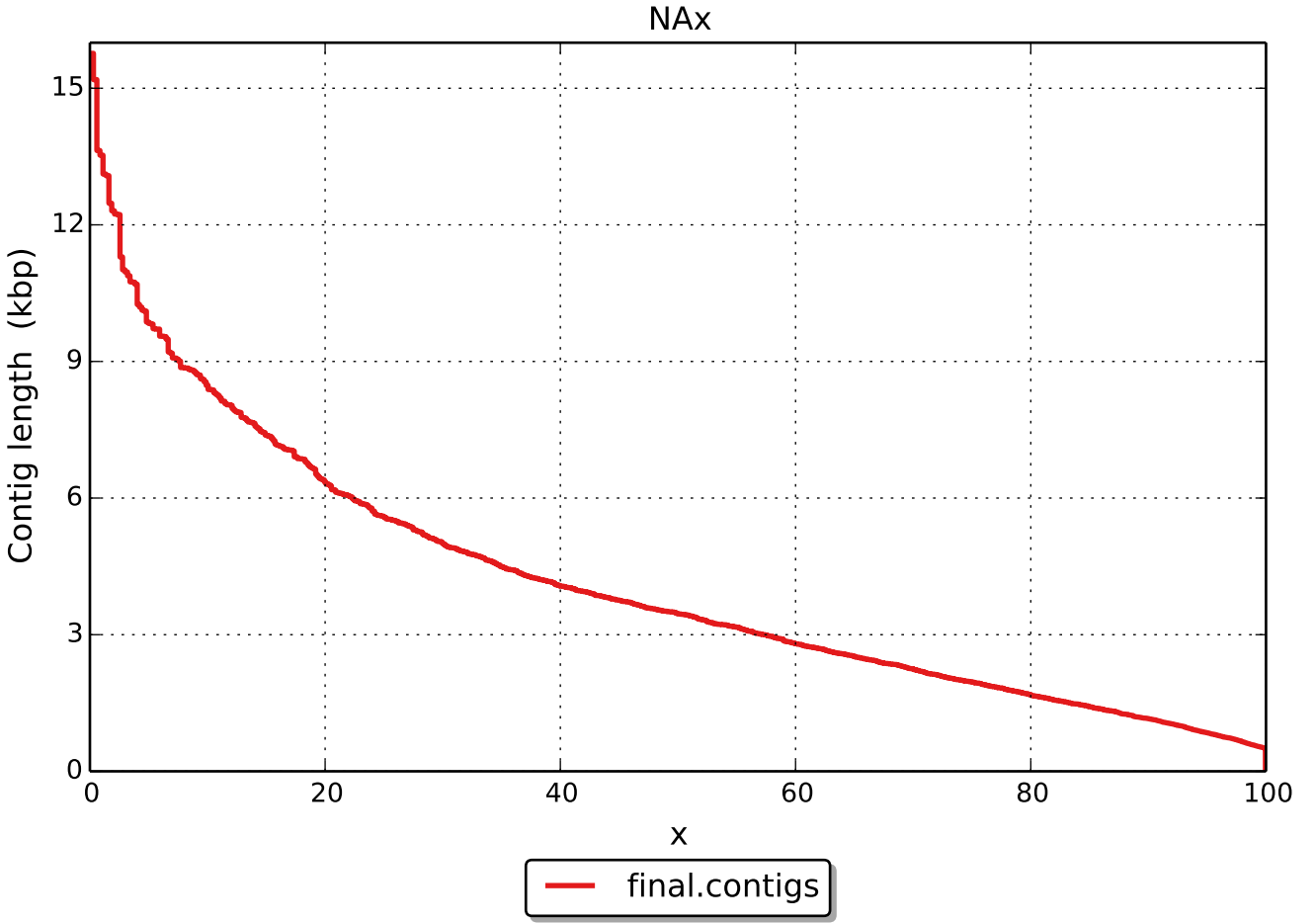

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

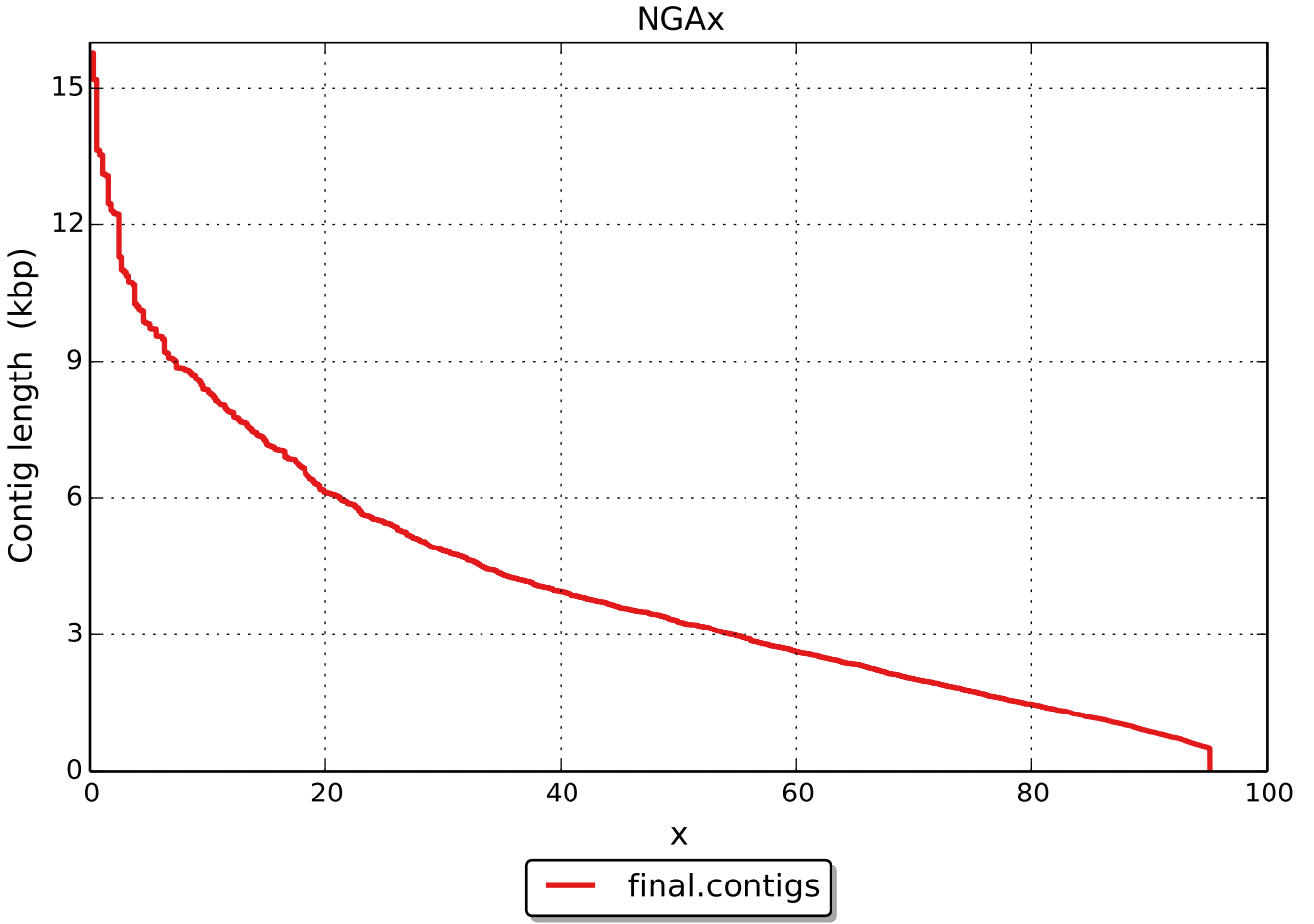

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs