Report

	final.contigs
# contigs (>= 0 bp)	2643
# contigs (>= 1000 bp)	1851
Total length (>= 0 bp)	5179372
Total length (>= 1000 bp)	4603624
# contigs	2643
Largest contig	10567
Total length	5179372
Reference length	5478683
GC (%)	50.27
Reference GC (%)	50.49
N50	2616
NG50	2477
N75	1540
NG75	1374
L50	630
LG50	689
L75	1275
LG75	1429
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.531
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.48
# indels per 100 kbp	0.10
Largest alignment	10567
NA50	2616
NGA50	2471
NA75	1540
NGA75	1374
LA50	631
LGA50	690
LA75	1276
LGA75	1430

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

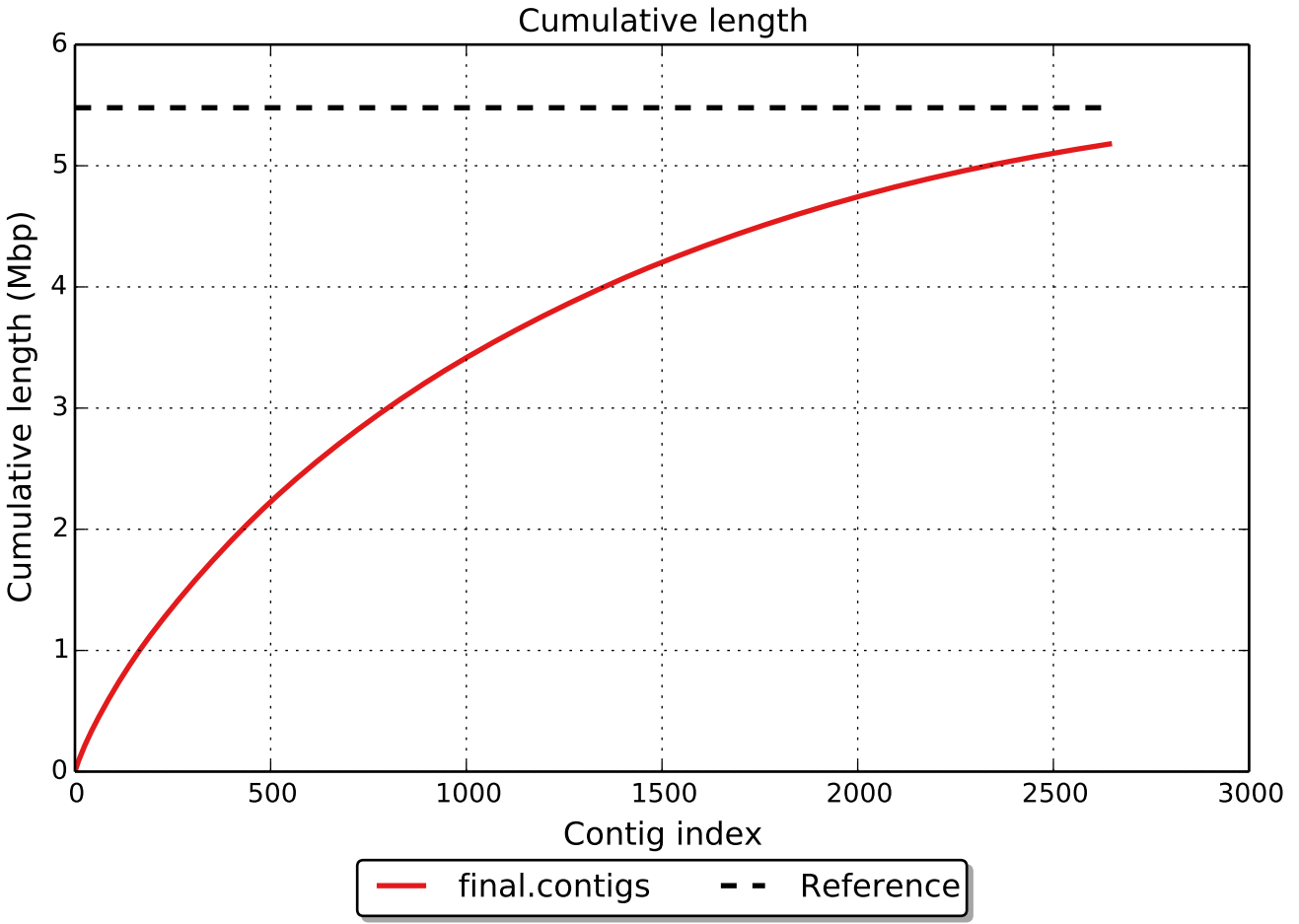
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	1
# mismatches	1428
# indels	5
# short indels	3
# long indels	2
Indels length	33

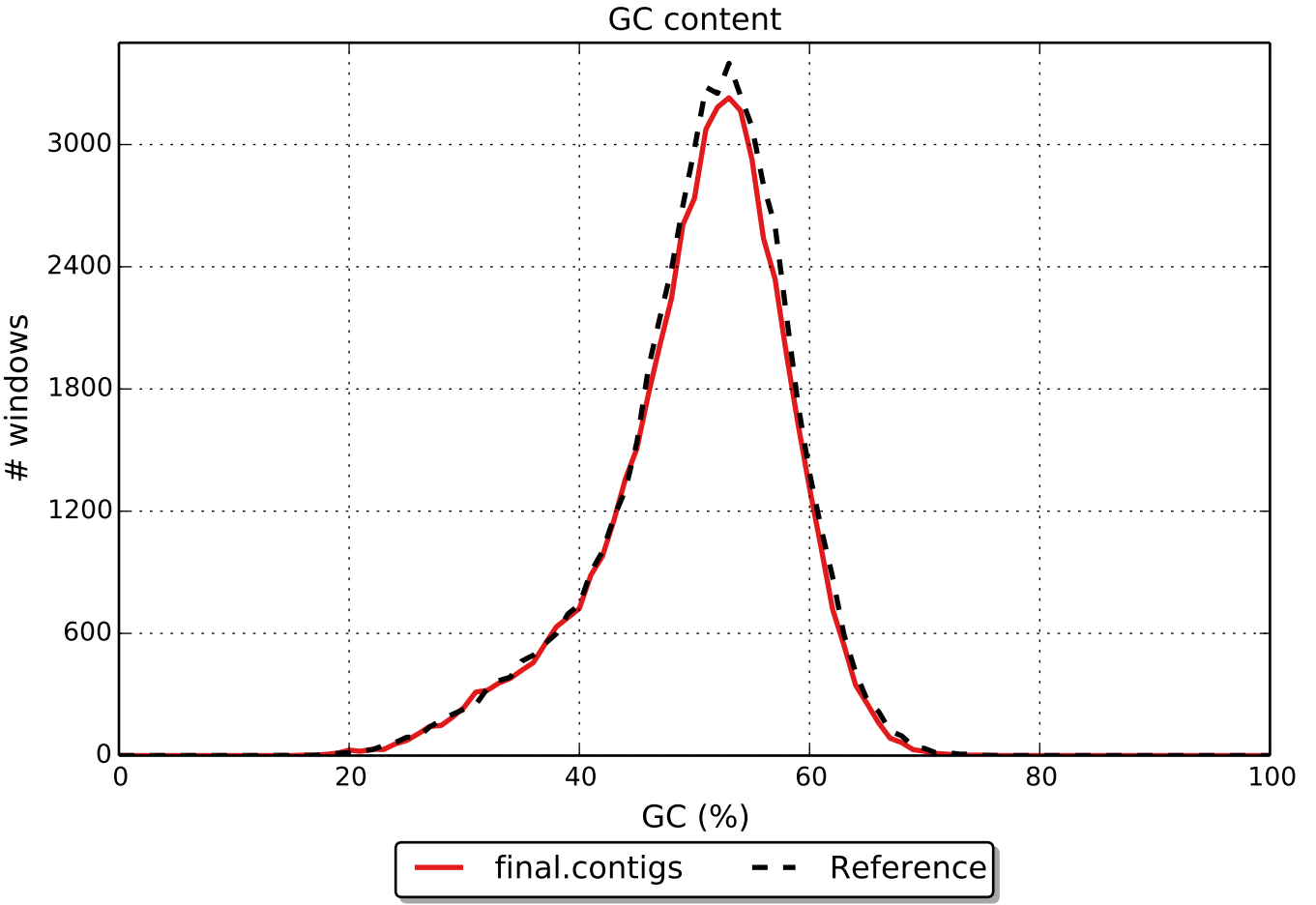
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

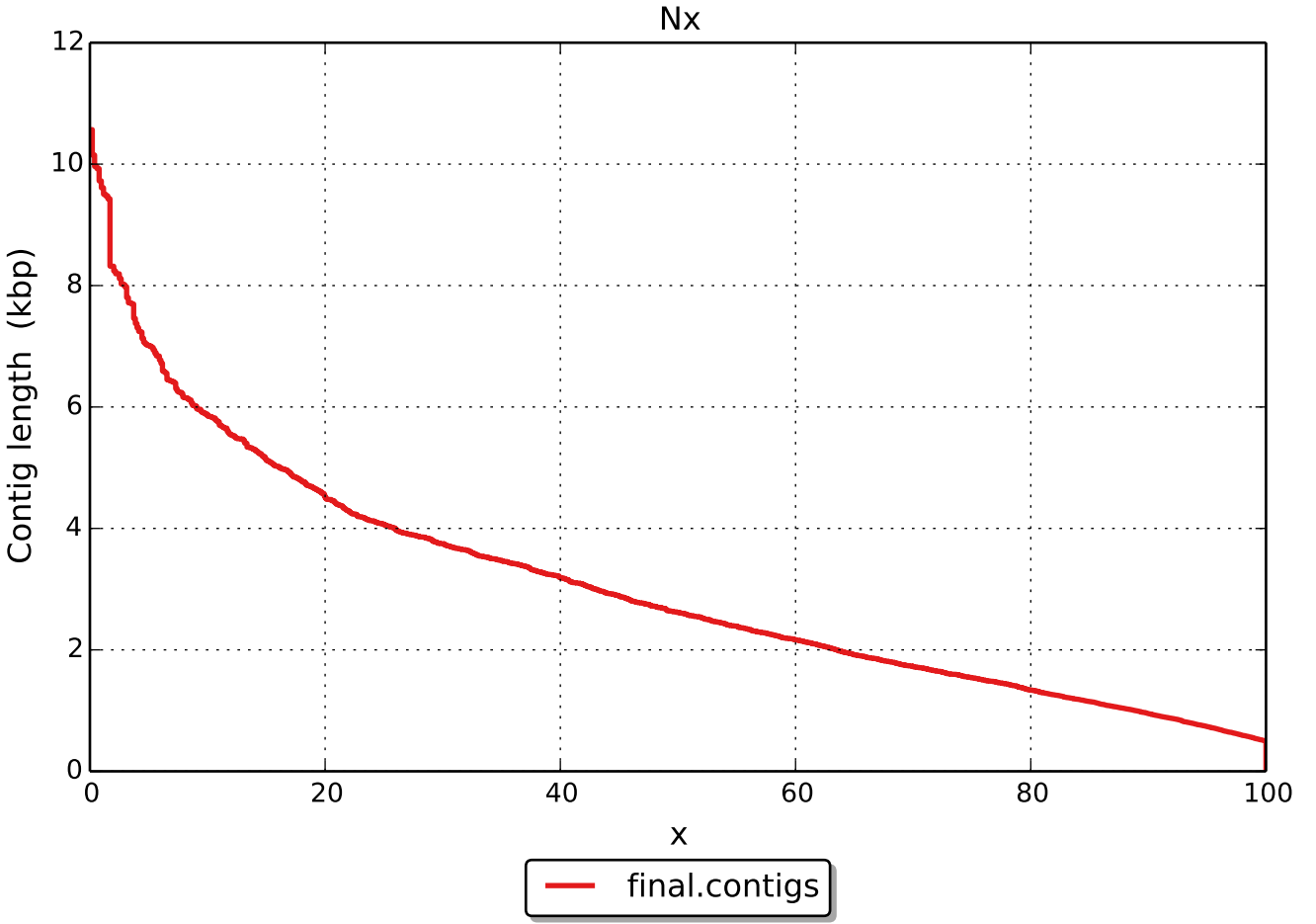
Unaligned report

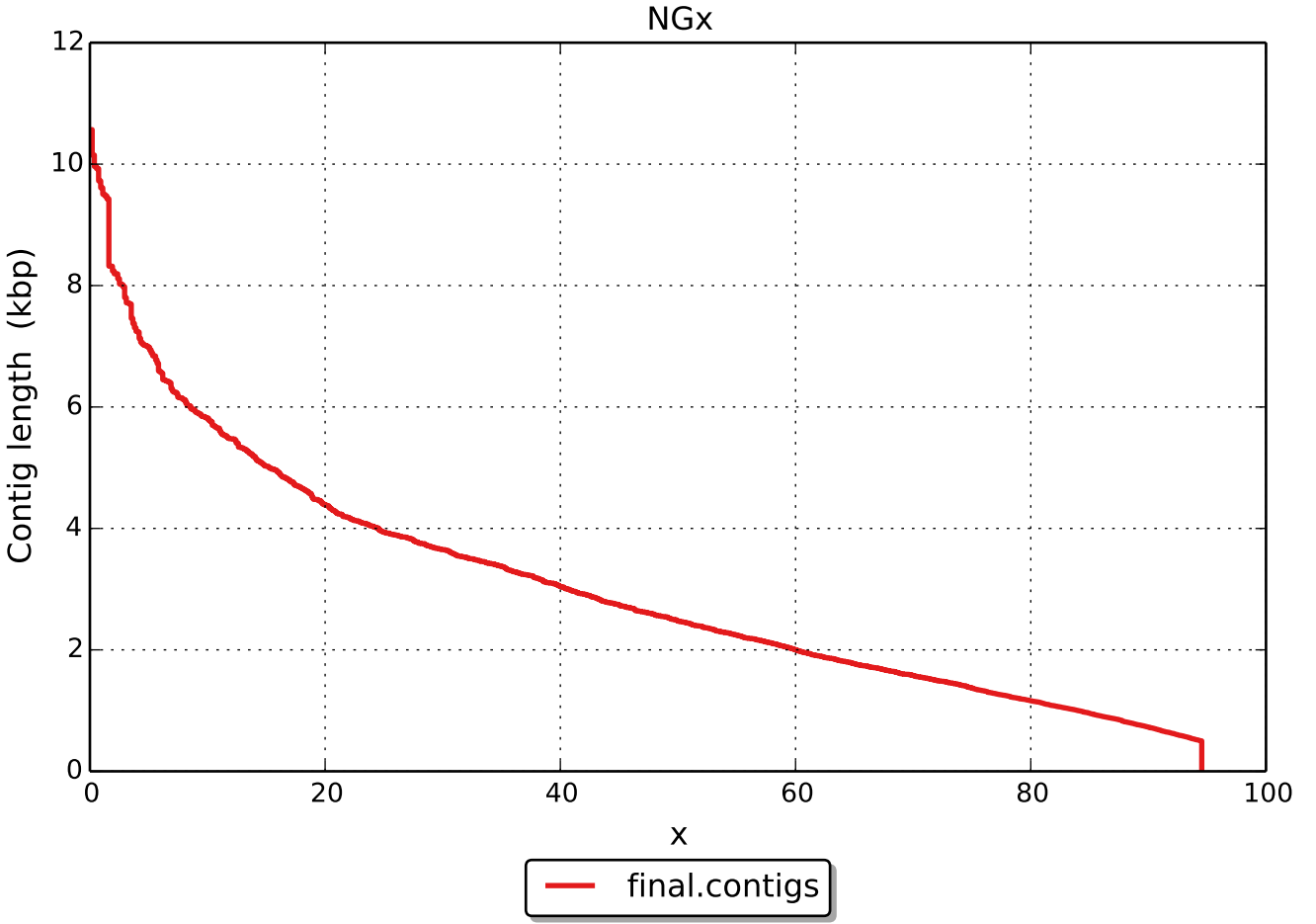
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

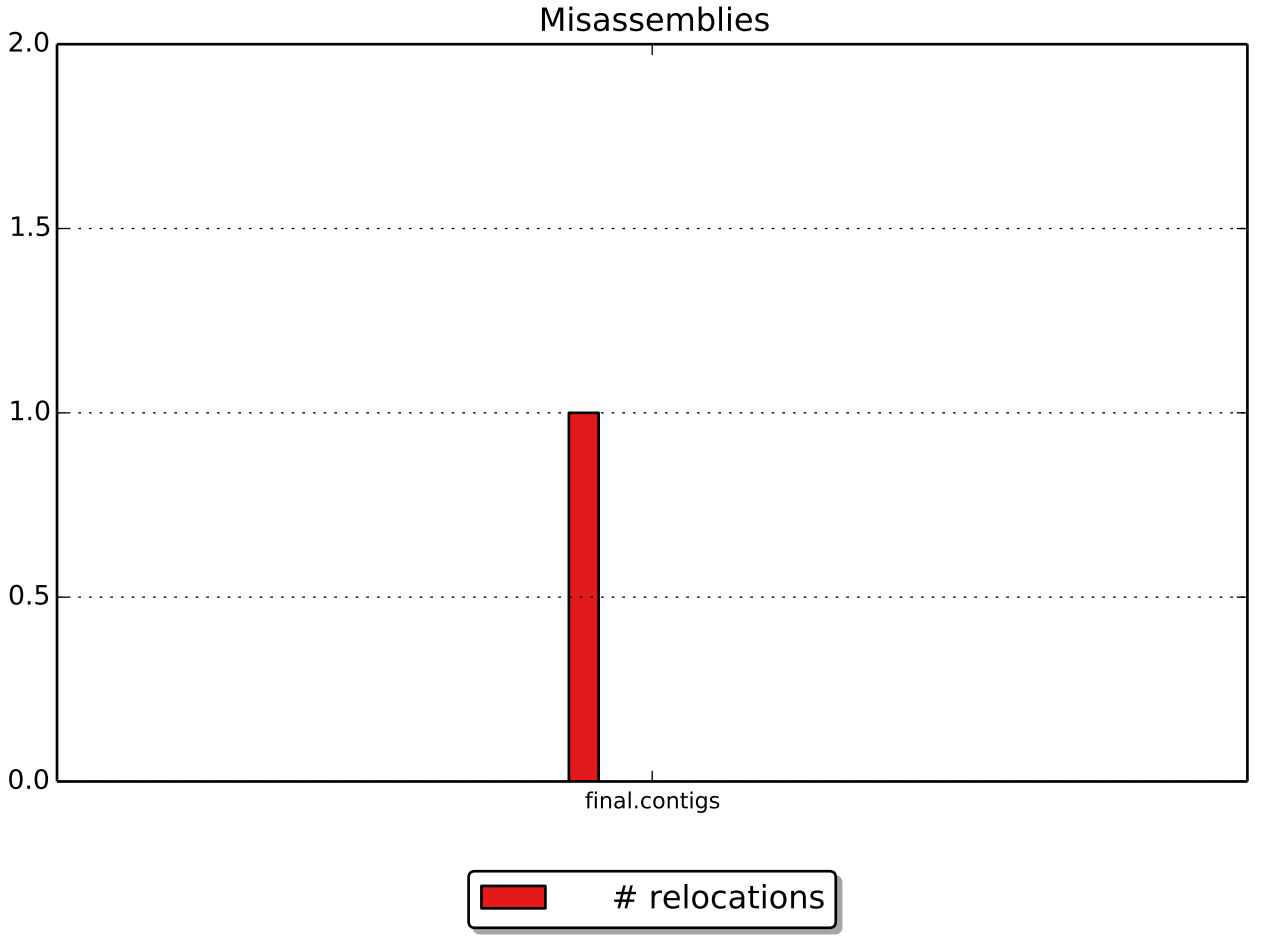
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

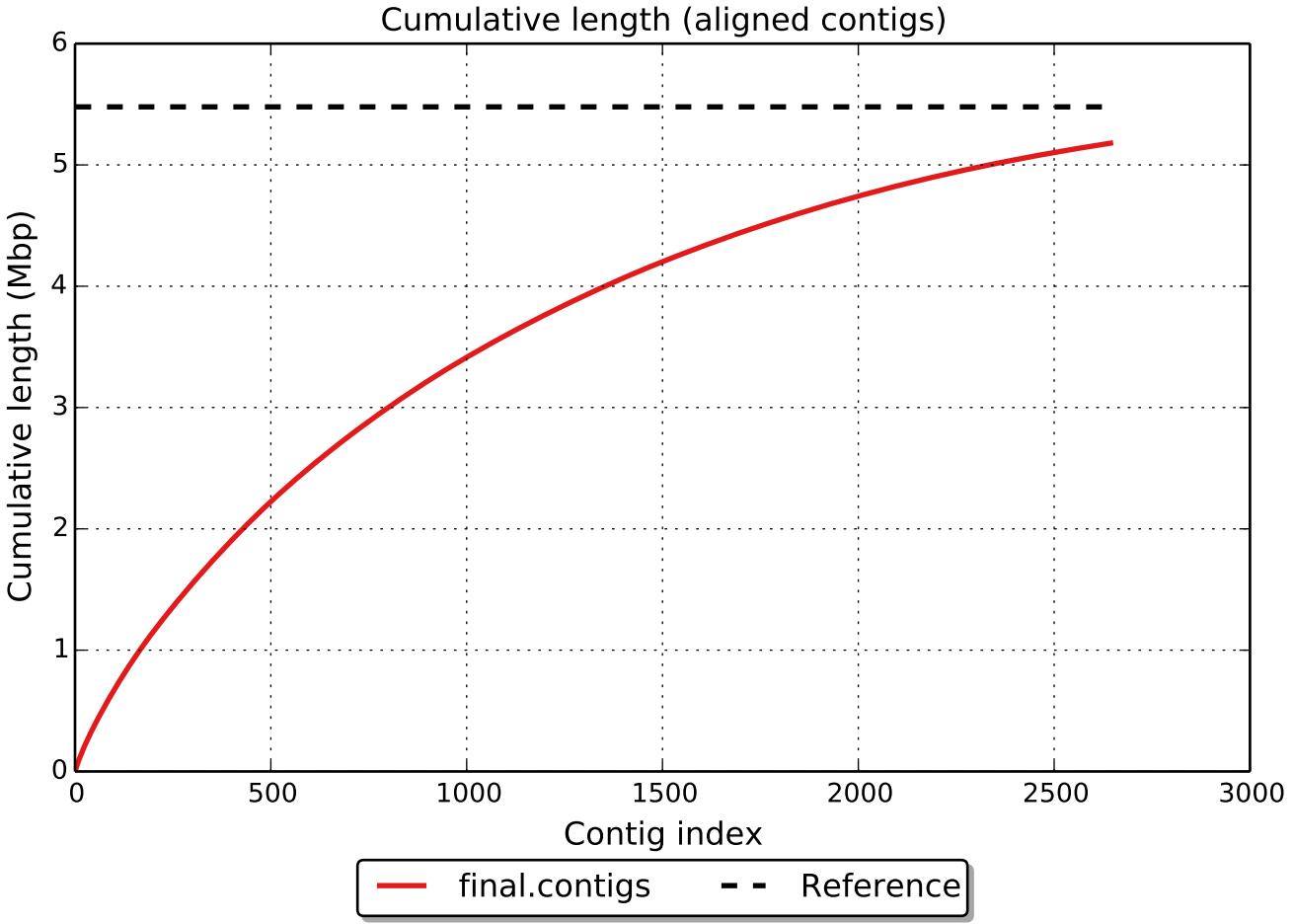

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

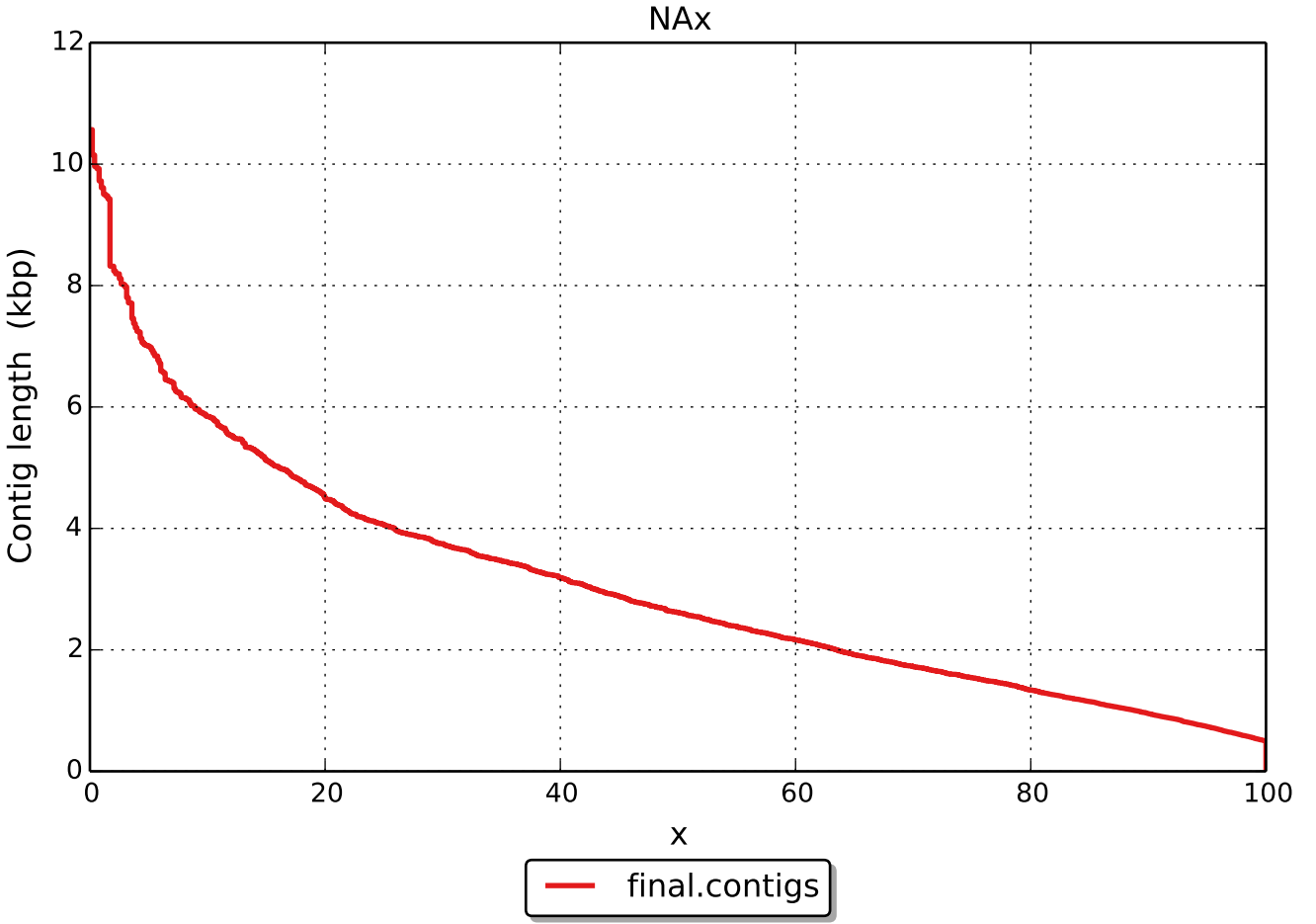

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

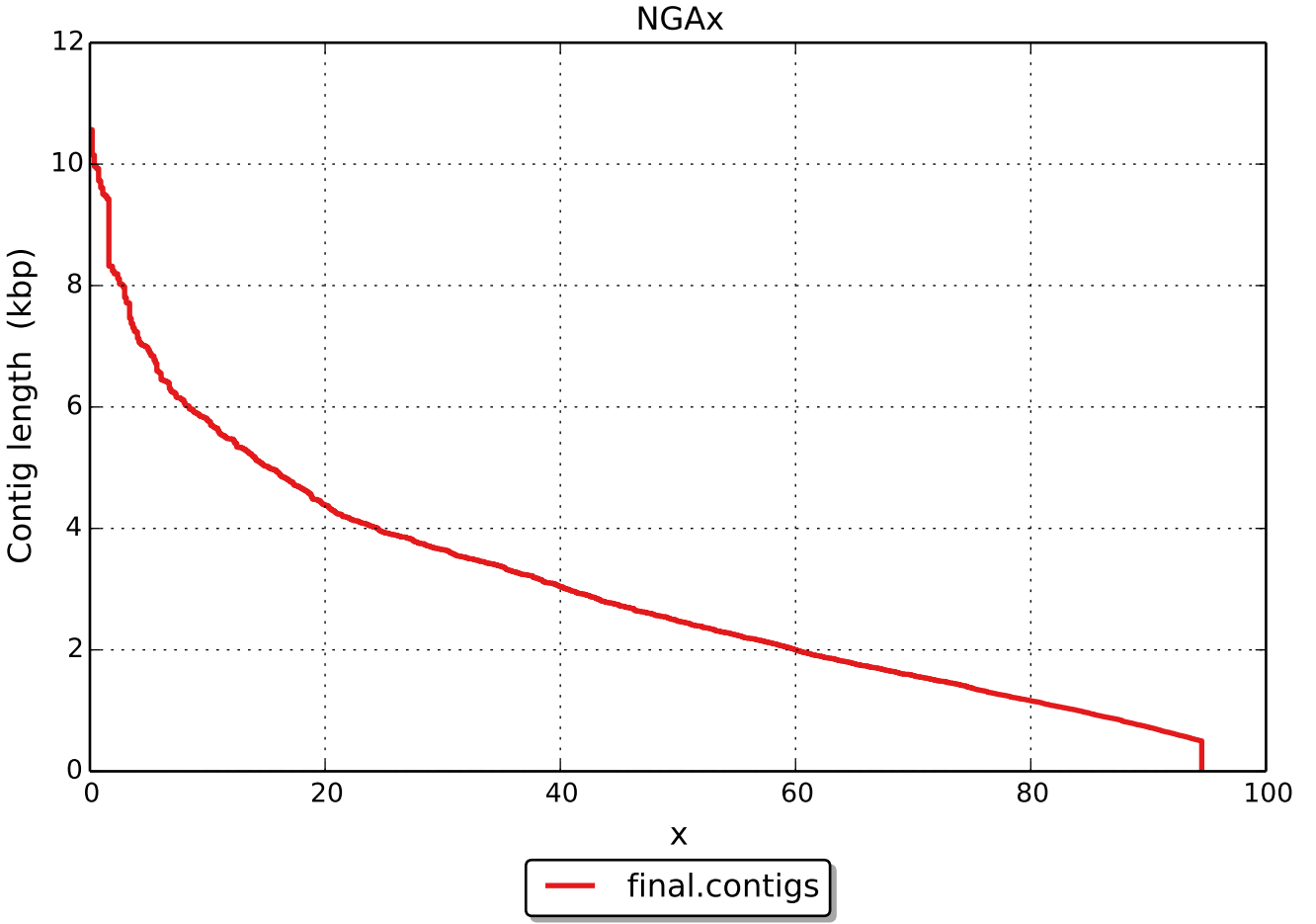

Nx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


NGx
Contig length (kbp)
0
2
4
6
8
10
12
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
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
x
0
2
4
6
8
10
12
0
20
40
60
80
100
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
10
12
0
20
40
60
80
100
x
final.contigs