Report

	final.contigs
# contigs (>= 0 bp)	2694
# contigs (>= 1000 bp)	1951
Total length (>= 0 bp)	5552762
Total length (>= 1000 bp)	5005411
# contigs	2694
Largest contig	12275
Total length	5552762
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.49
N50	2716
NG50	2753
N75	1643
NG75	1677
L50	644
LG50	631
L75	1297
LG75	1264
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.576
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.35
# indels per 100 kbp	0.02
Largest alignment	12275
NA50	2715
NGA50	2750
NA75	1643
NGA75	1677
LA50	645
LGA50	632
LA75	1298
LGA75	1265

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

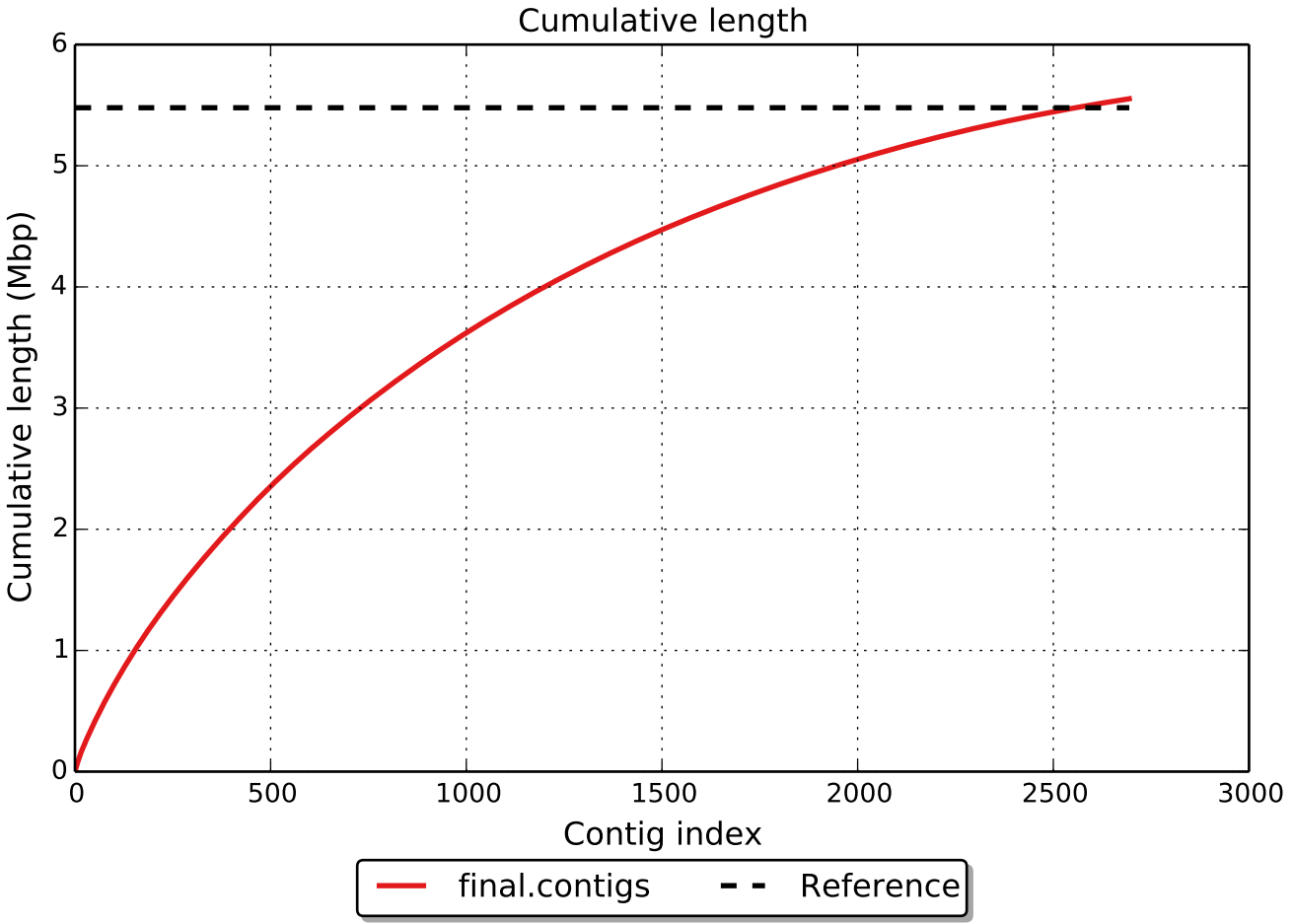
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7696
# local misassemblies	0
# mismatches	1783
# indels	1
# short indels	0
# long indels	1
Indels length	9

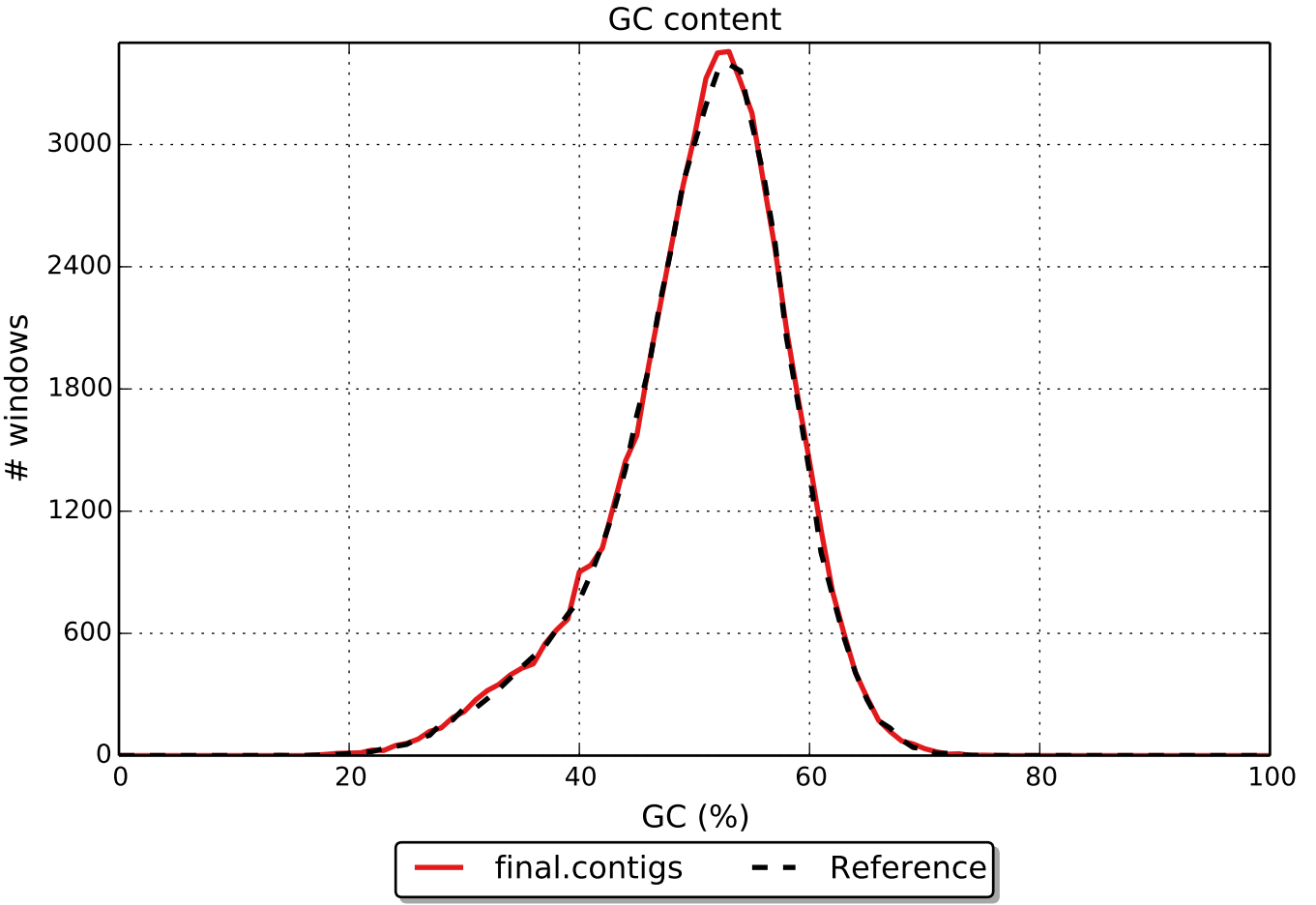
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

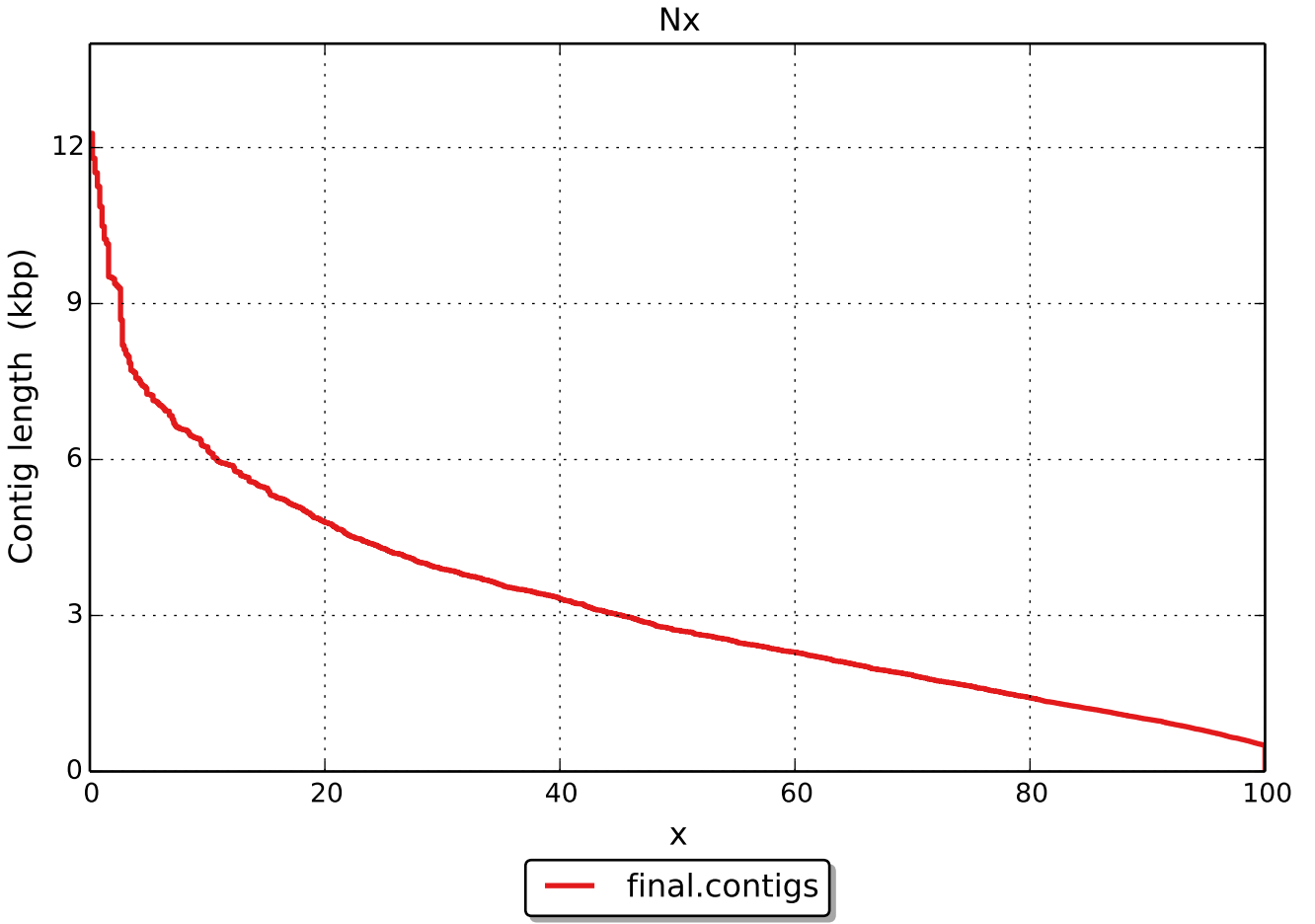
Unaligned report

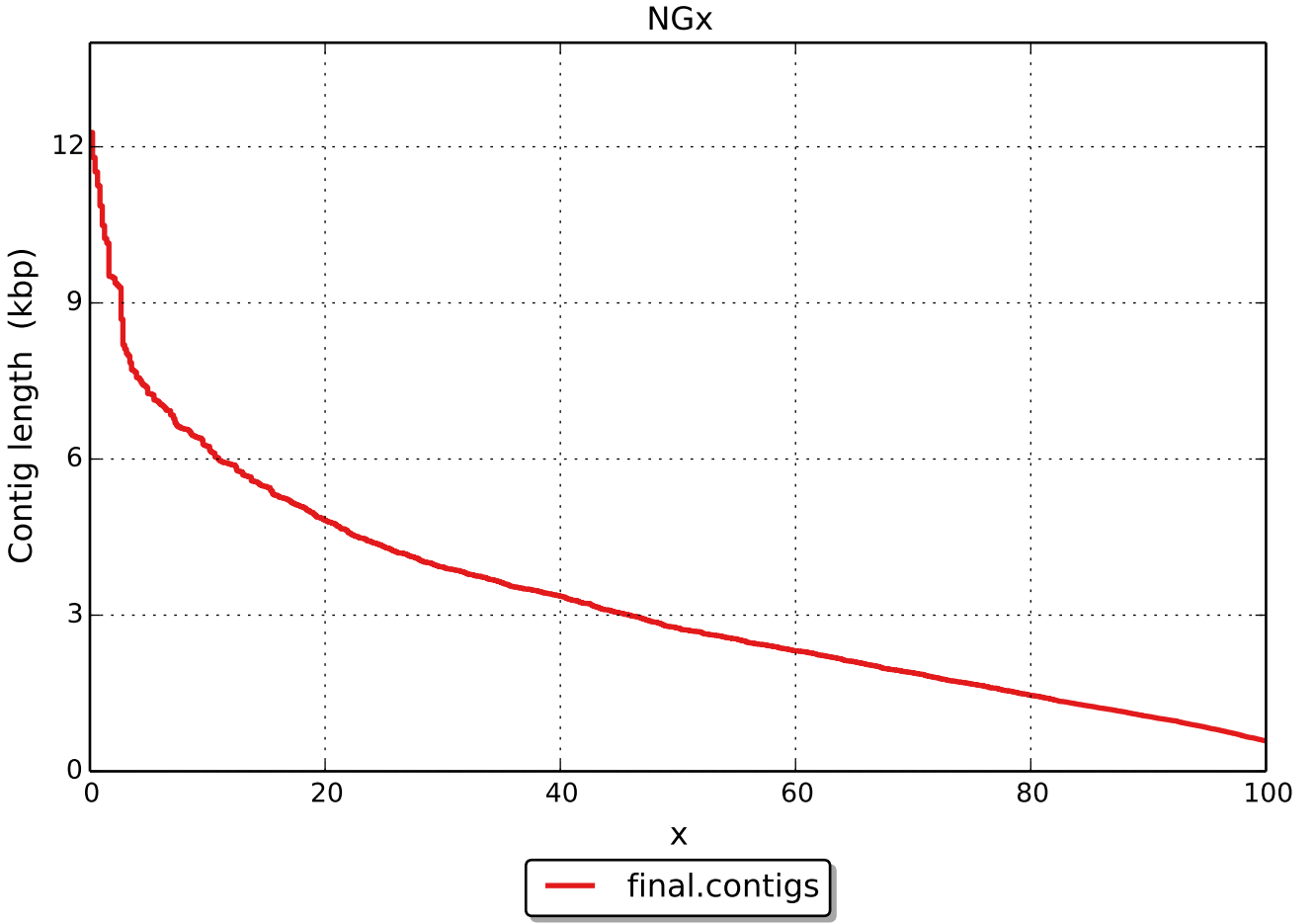
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

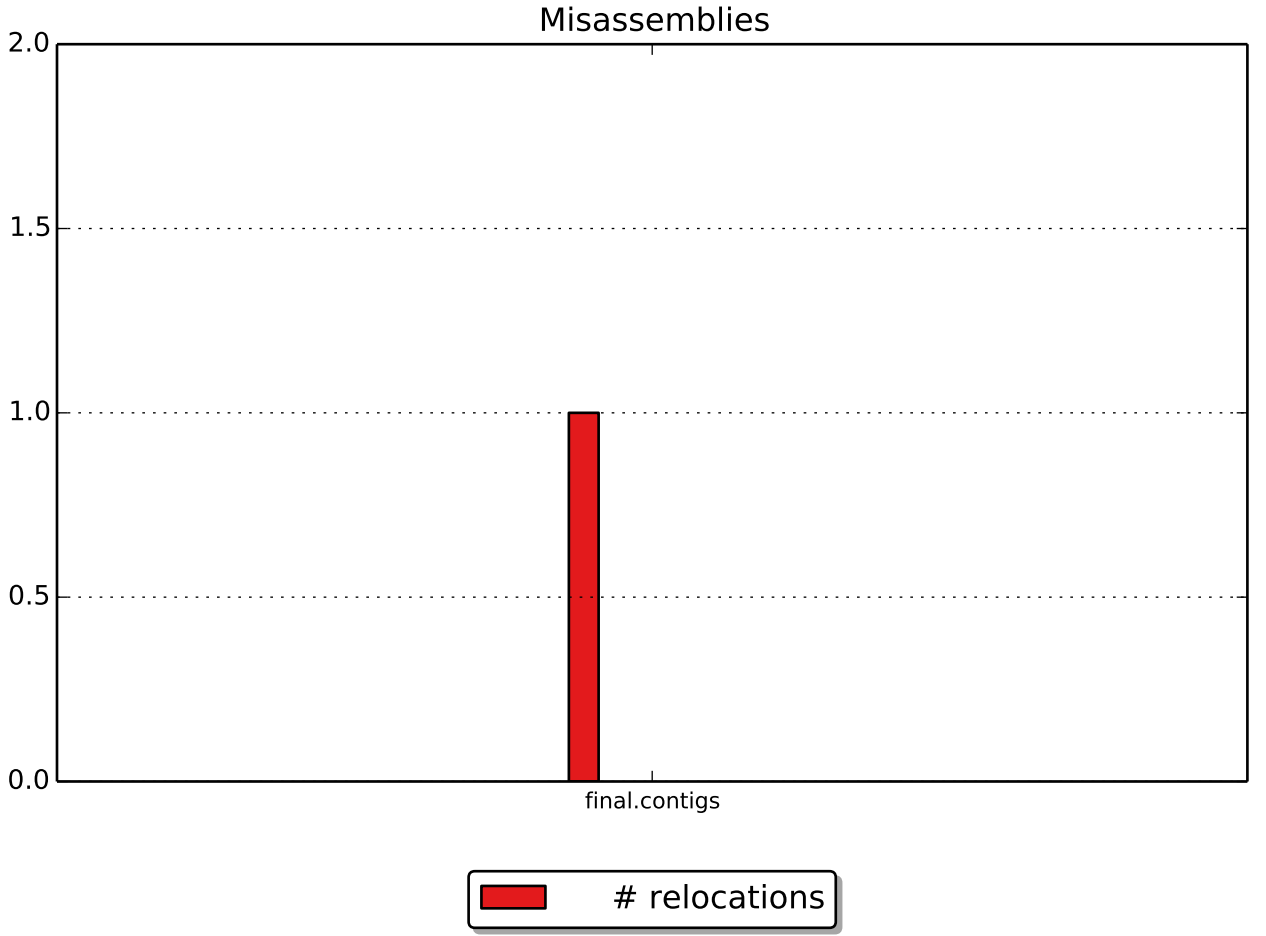
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

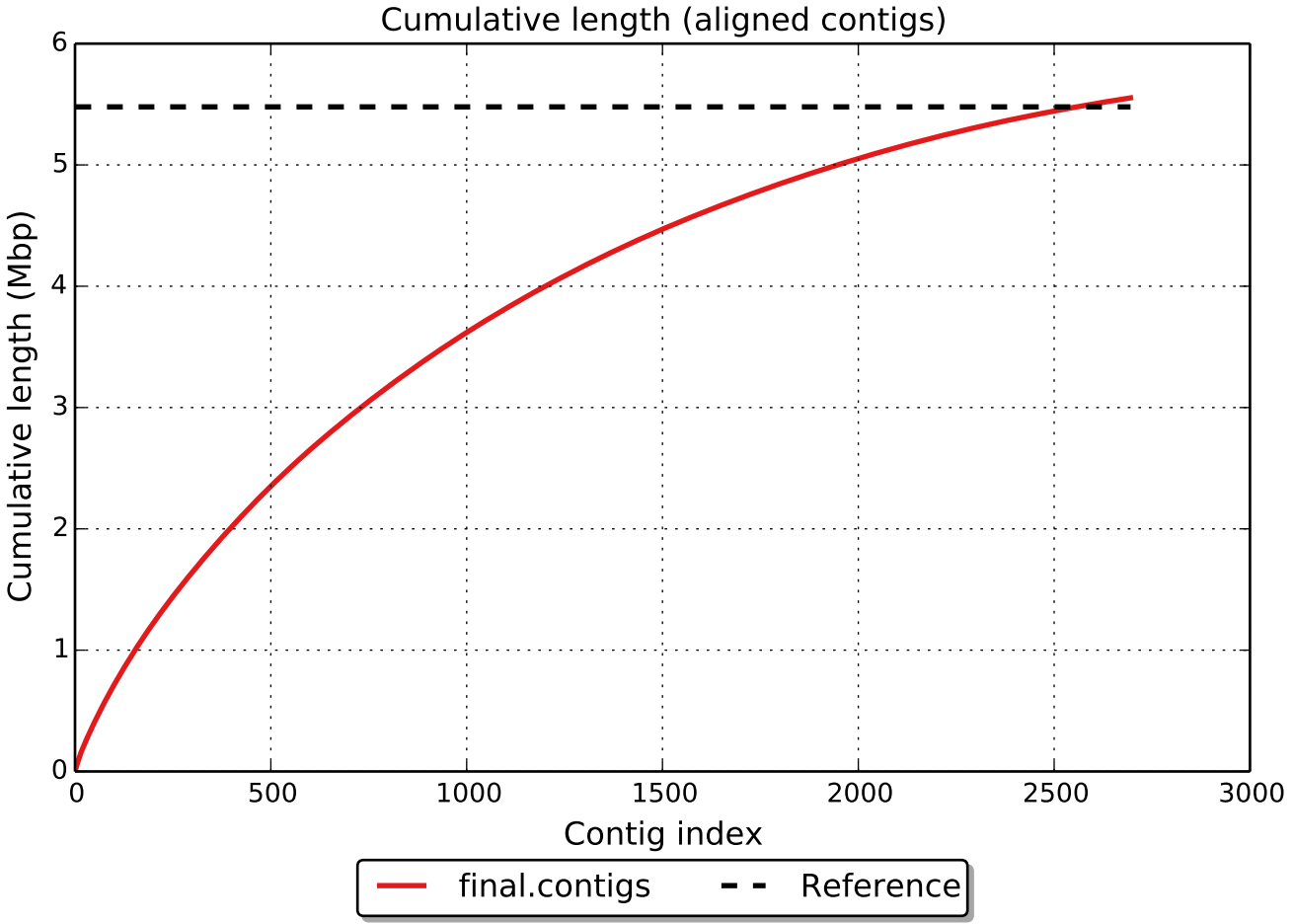

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

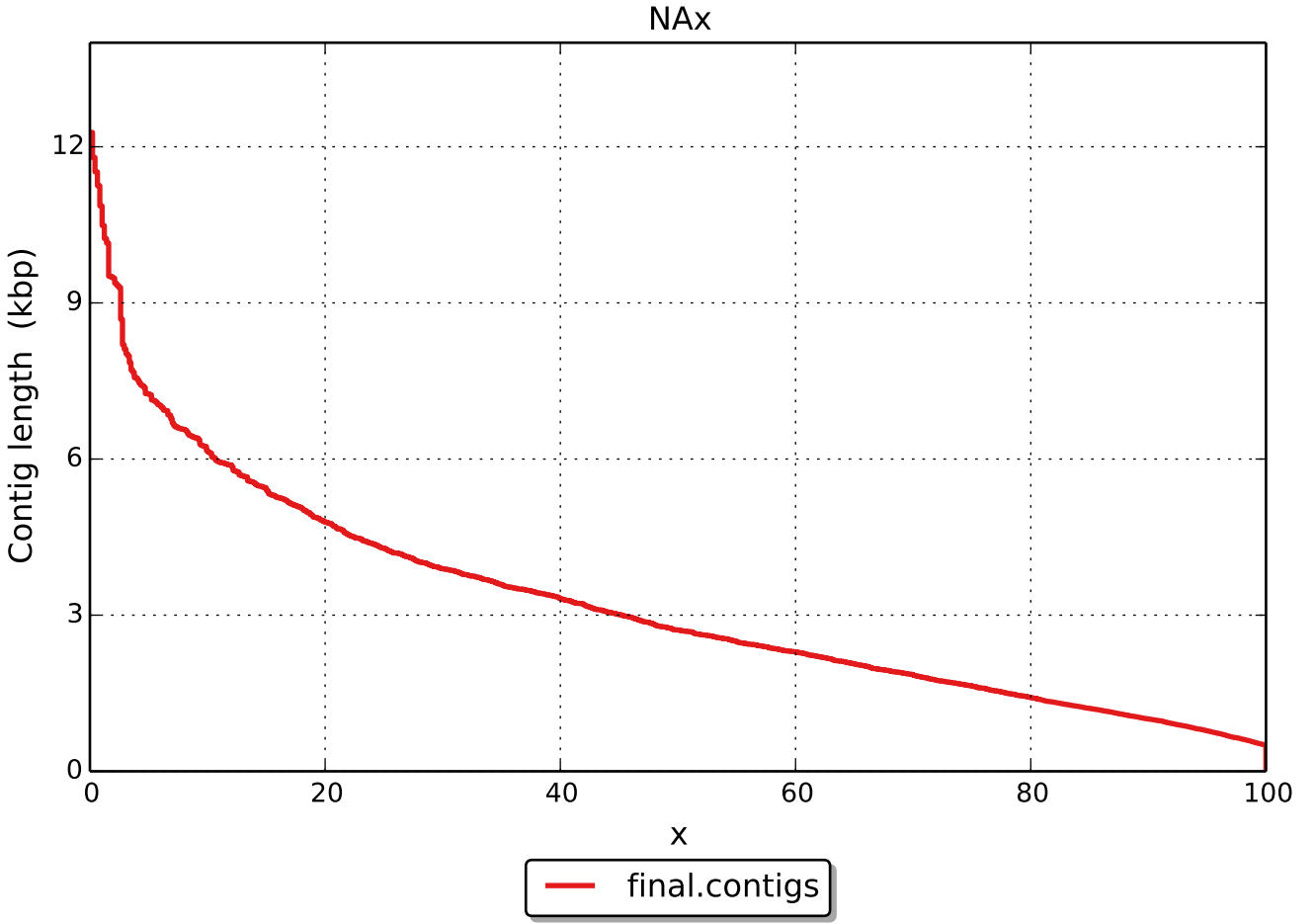

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

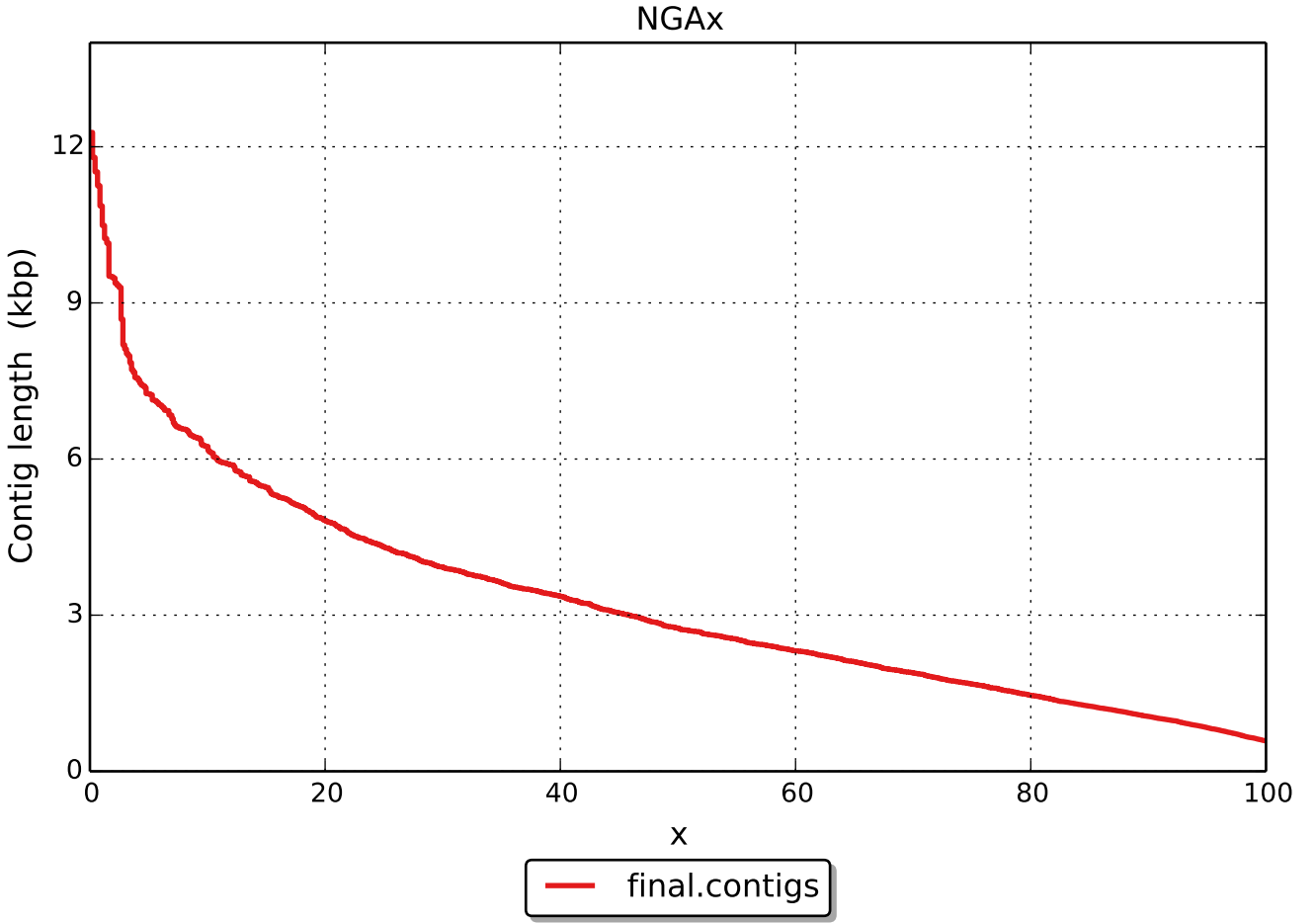

Nx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
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
3000
Contig index
final.contigs
Reference


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


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