Report

	final.contigs
# contigs (>= 0 bp)	5100
# contigs (>= 1000 bp)	795
Total length (>= 0 bp)	3436600
Total length (>= 1000 bp)	1132122
# contigs	3004
Largest contig	3974
Total length	2682035
Reference length	3785550
GC (%)	32.30
Reference GC (%)	32.26
N50	914
NG50	723
N75	682
L50	1014
LG50	1694
L75	1863
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	67.685
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	141.16
# indels per 100 kbp	0.00
Largest alignment	3974
NA50	914
NGA50	723
NA75	682
LA50	1014
LGA50	1694
LA75	1863

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

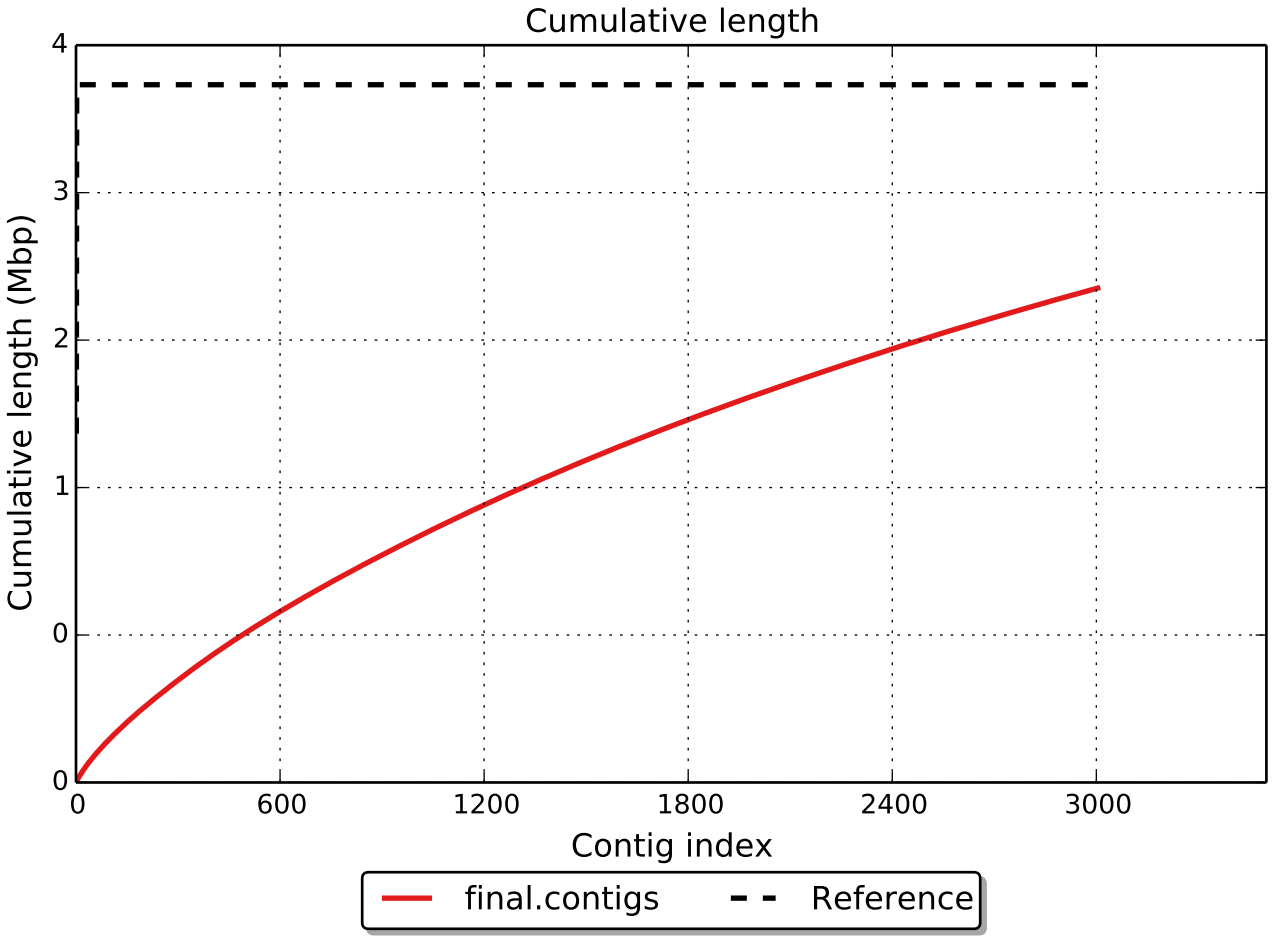
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	3617
# indels	0
# short indels	0
# long indels	0
Indels length	0

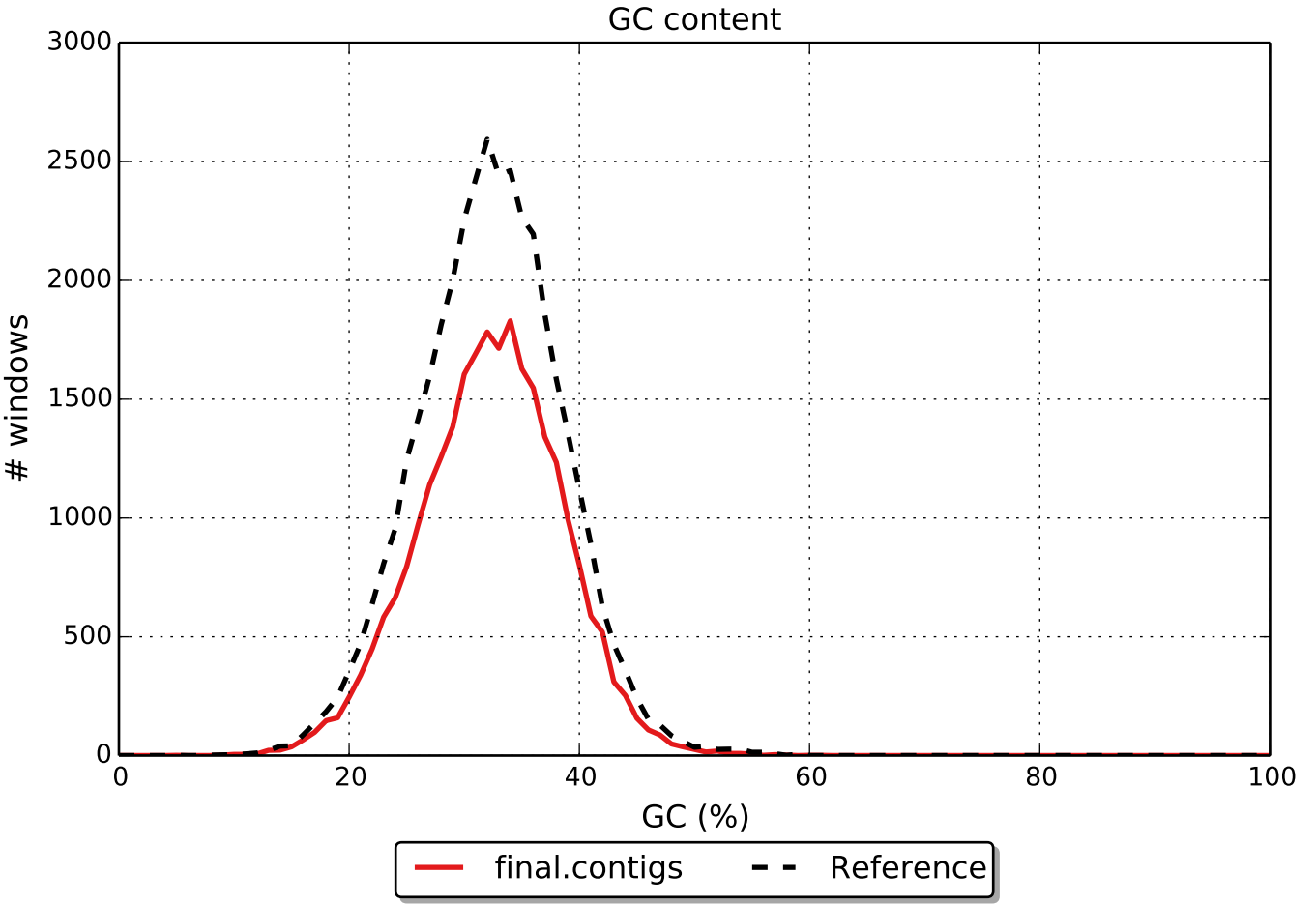
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

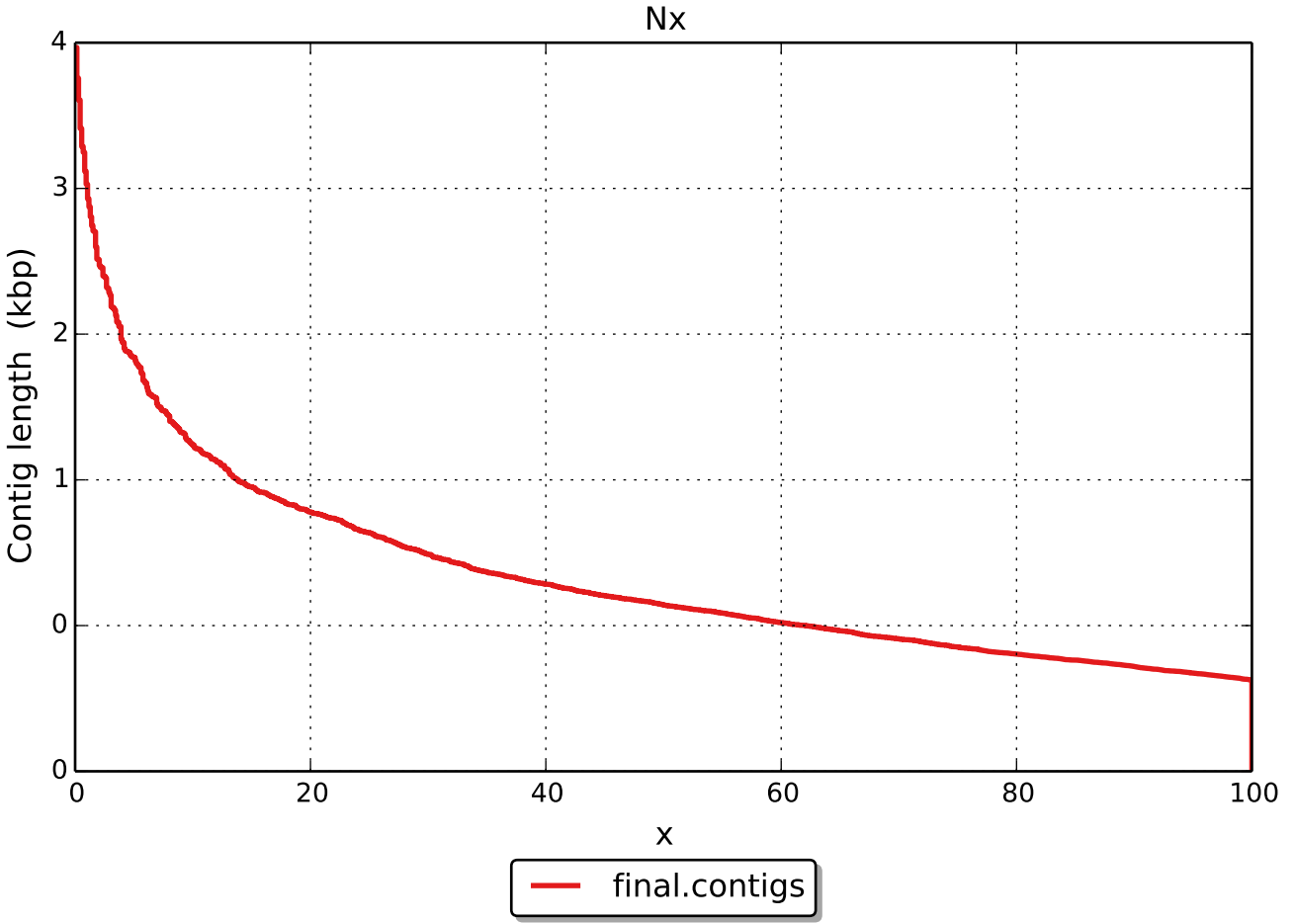
Unaligned report

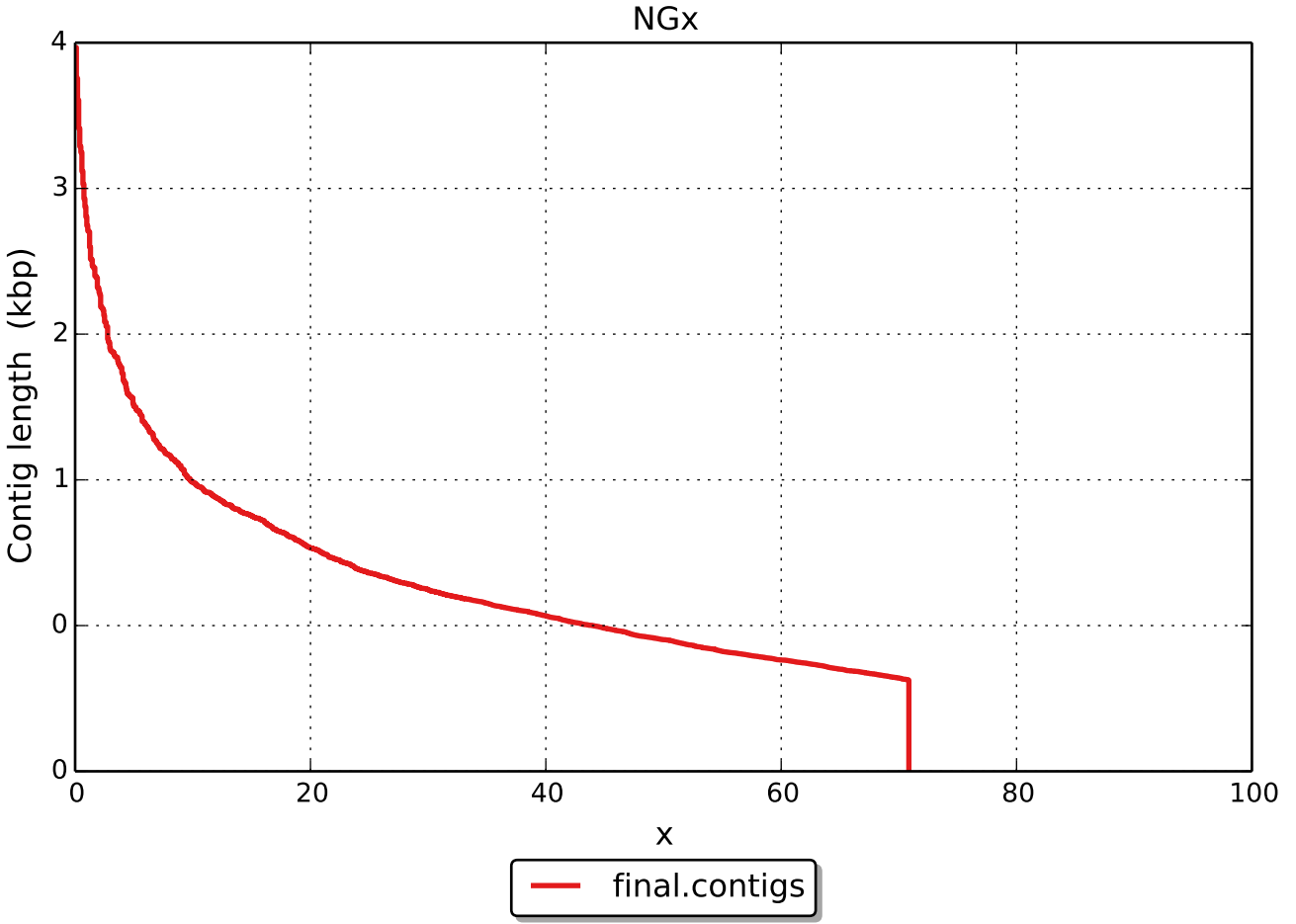
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

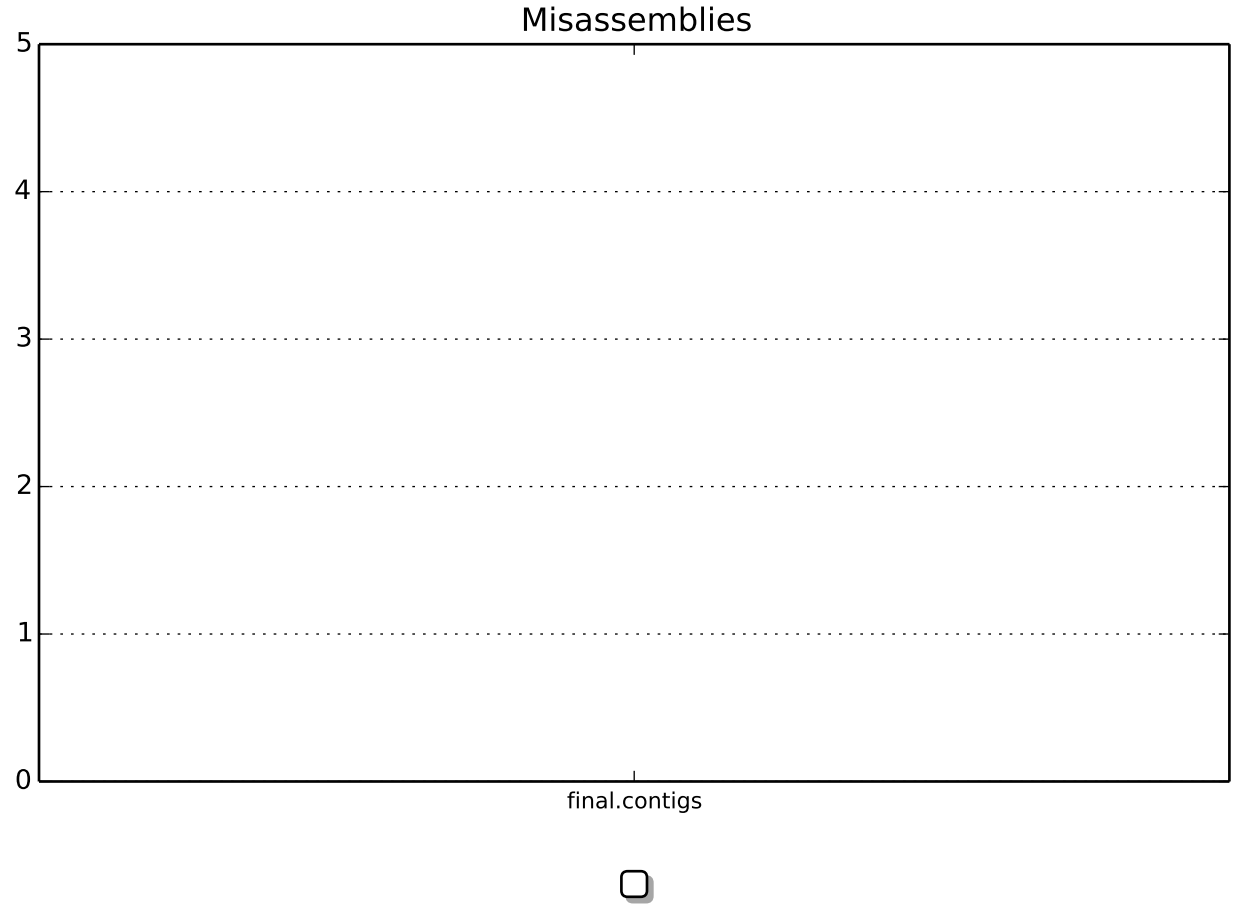
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

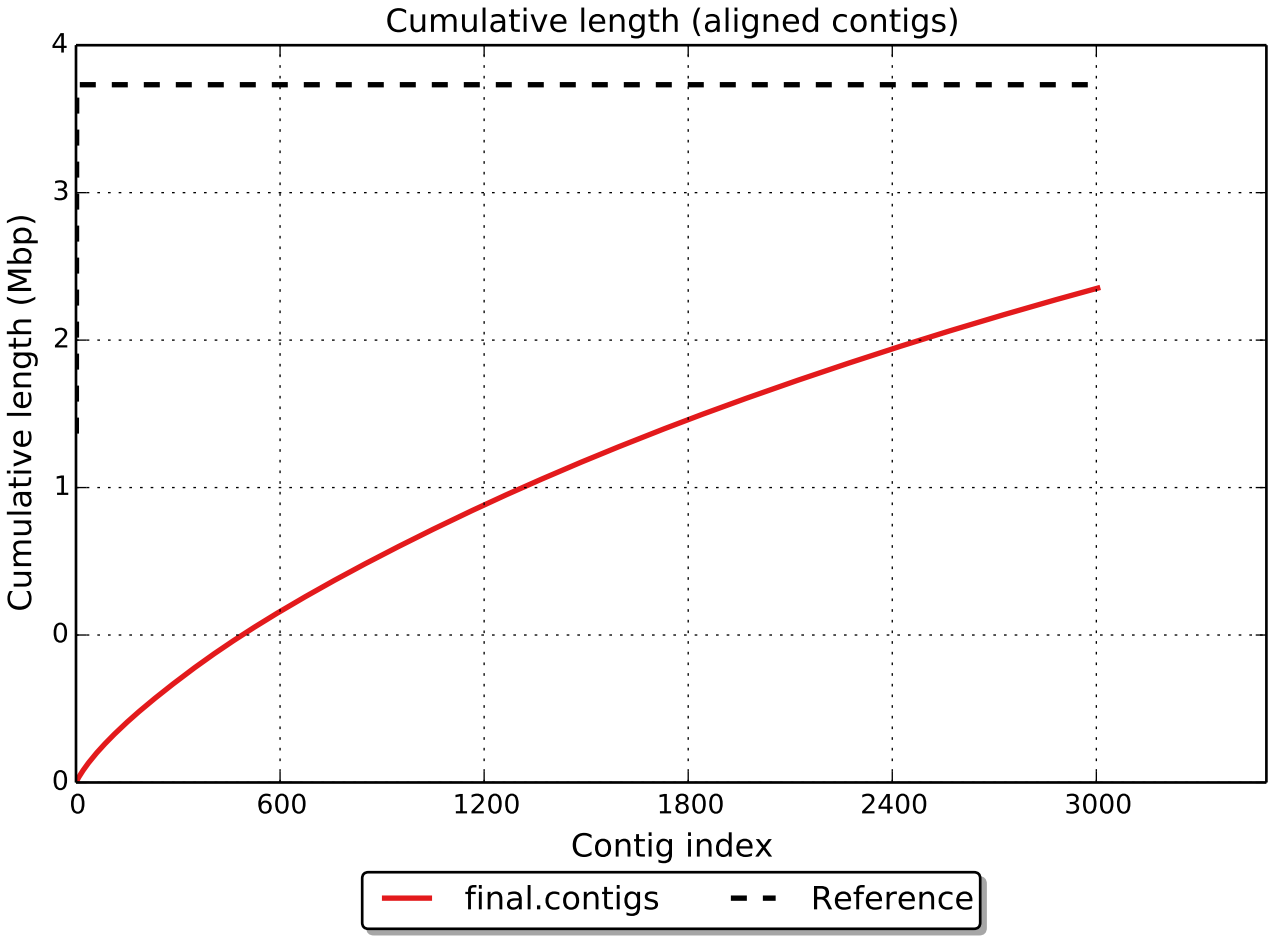

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference

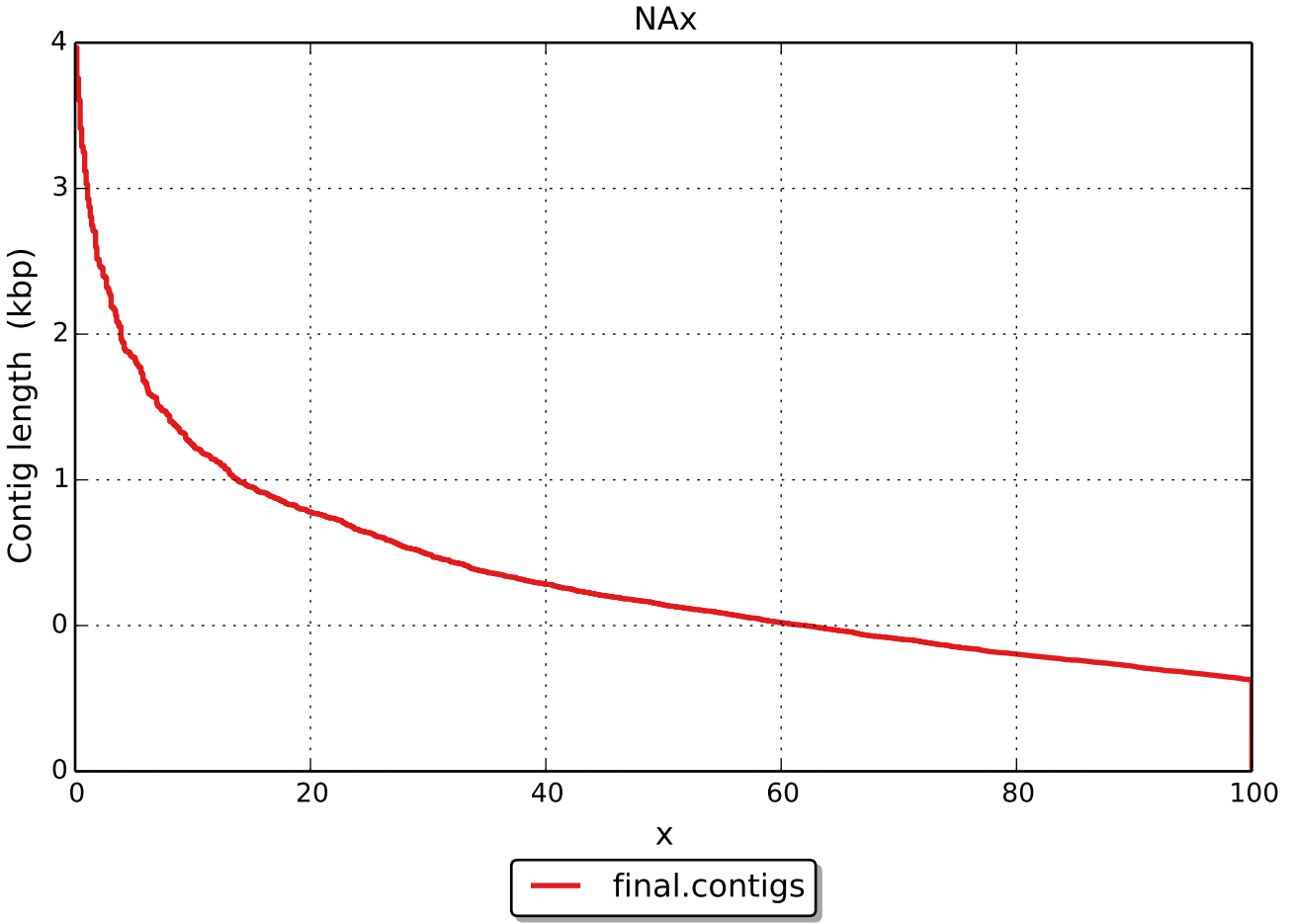

GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
final.contigs
Reference

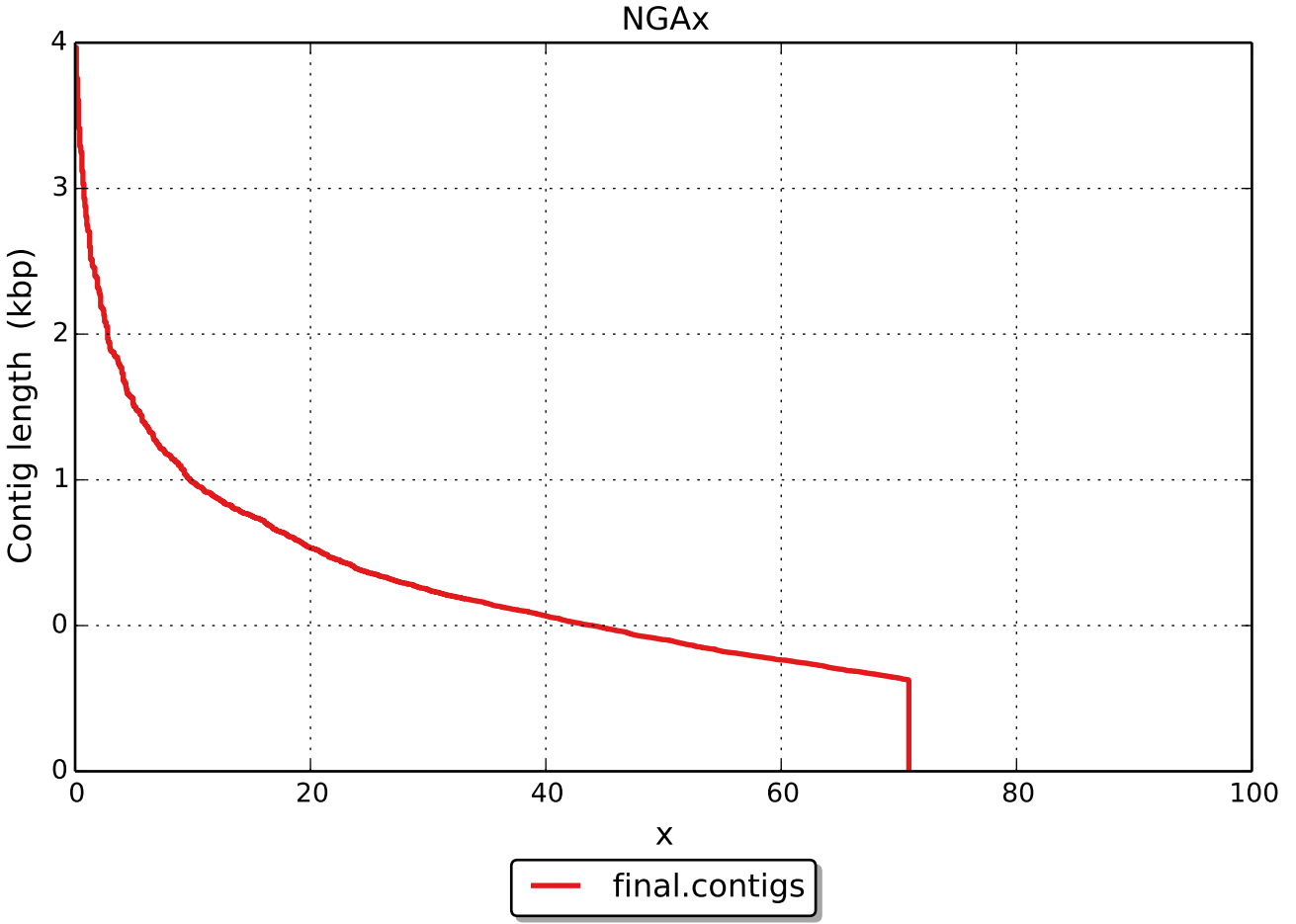

Nx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
4
3
2
1
0
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
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
4
3
2
1
0
0
20
40
60
80
100
x
final.contigs