Report

	final.contigs
# contigs (>= 0 bp)	5106
# contigs (>= 1000 bp)	1545
Total length (>= 0 bp)	4698745
Total length (>= 1000 bp)	2177704
# contigs	5106
Largest contig	4380
Total length	4698745
Reference length	5478683
GC (%)	50.43
Reference GC (%)	50.50
N50	959
NG50	873
N75	712
NG75	605
L50	1721
LG50	2148
L75	3144
LG75	4036
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.533
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	234.19
# indels per 100 kbp	0.07
Largest alignment	4380
NA50	959
NGA50	873
NA75	712
NGA75	605
LA50	1721
LGA50	2148
LA75	3144
LGA75	4036

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

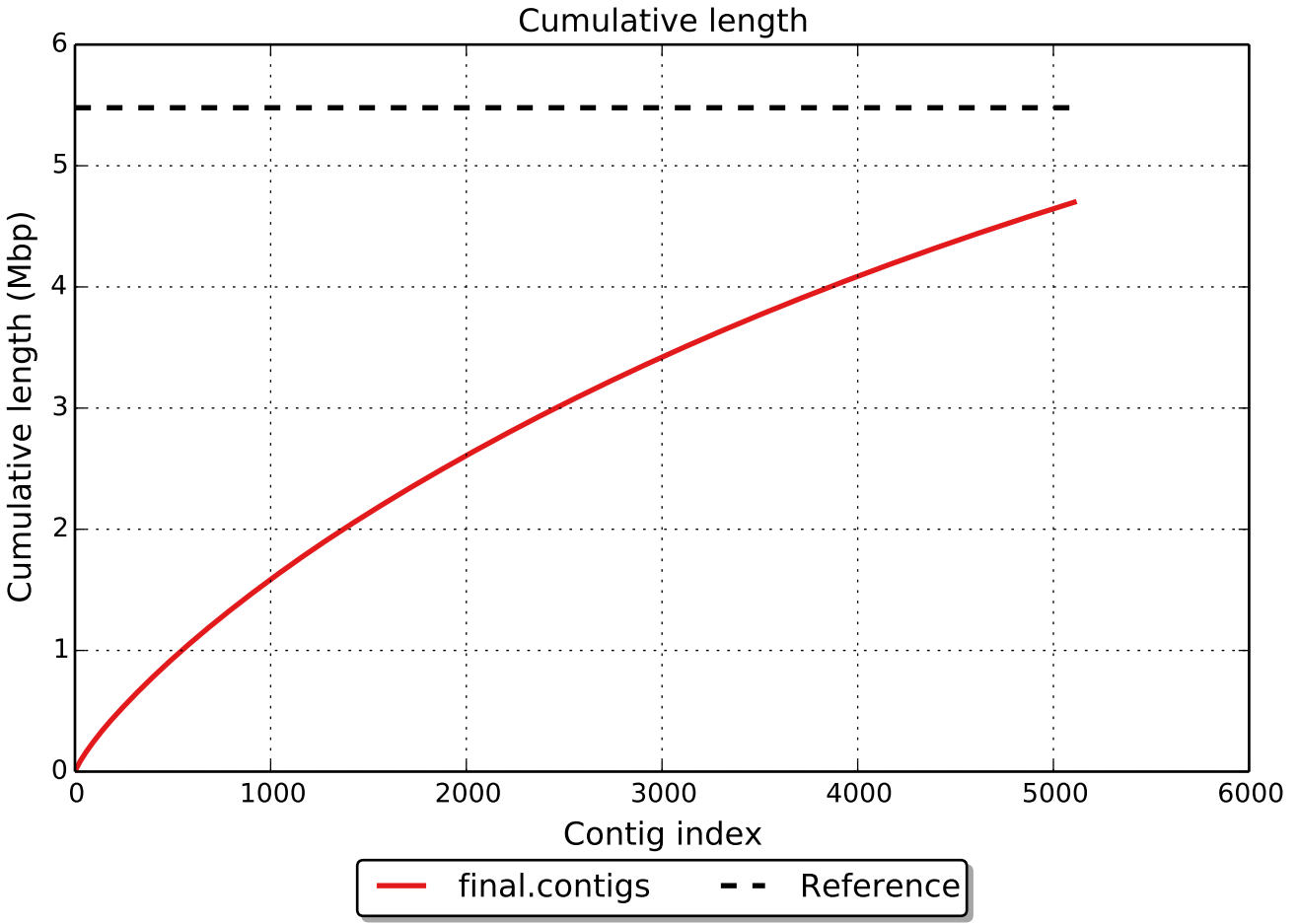
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	10333
# indels	3
# short indels	2
# long indels	1
Indels length	8

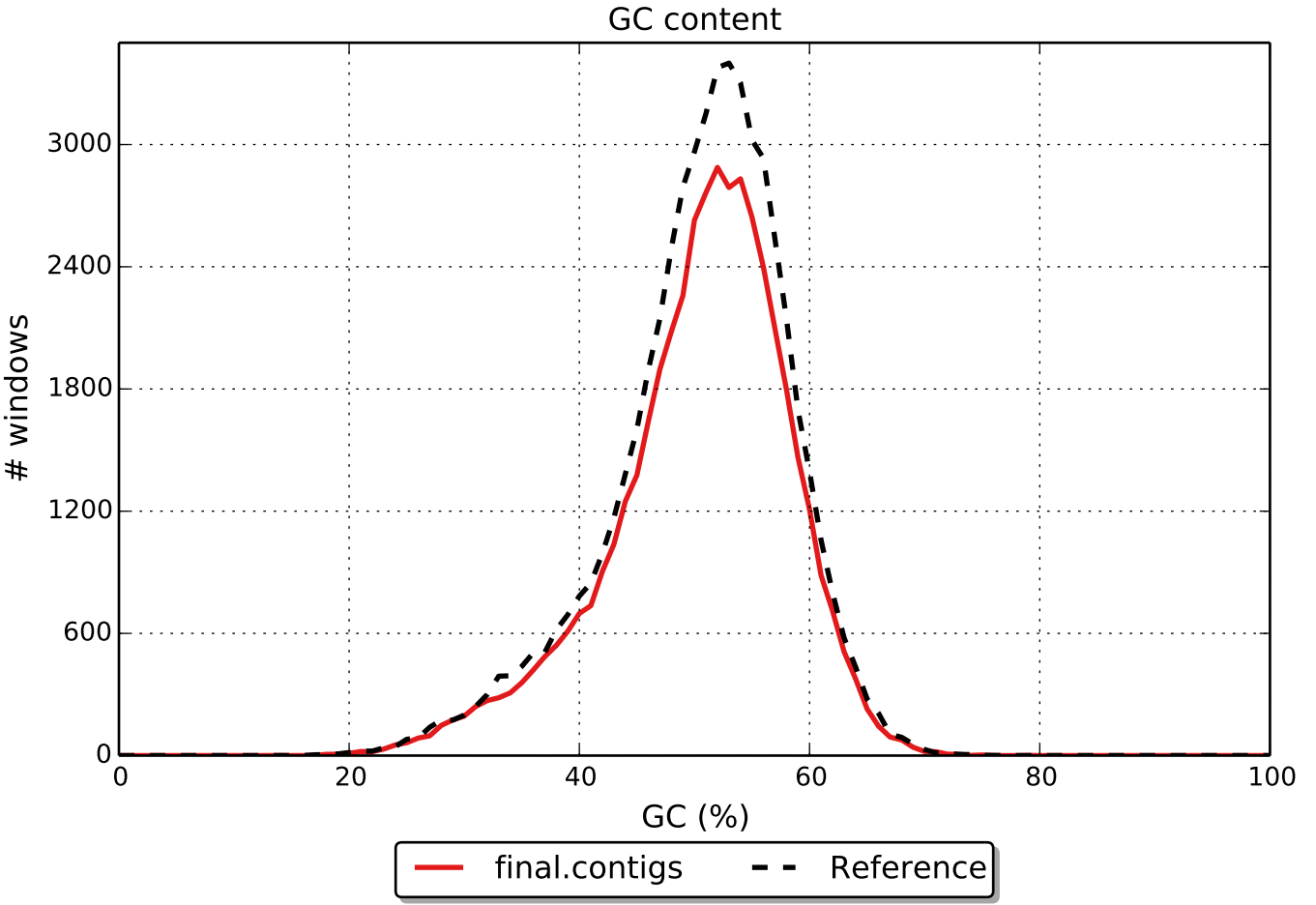
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

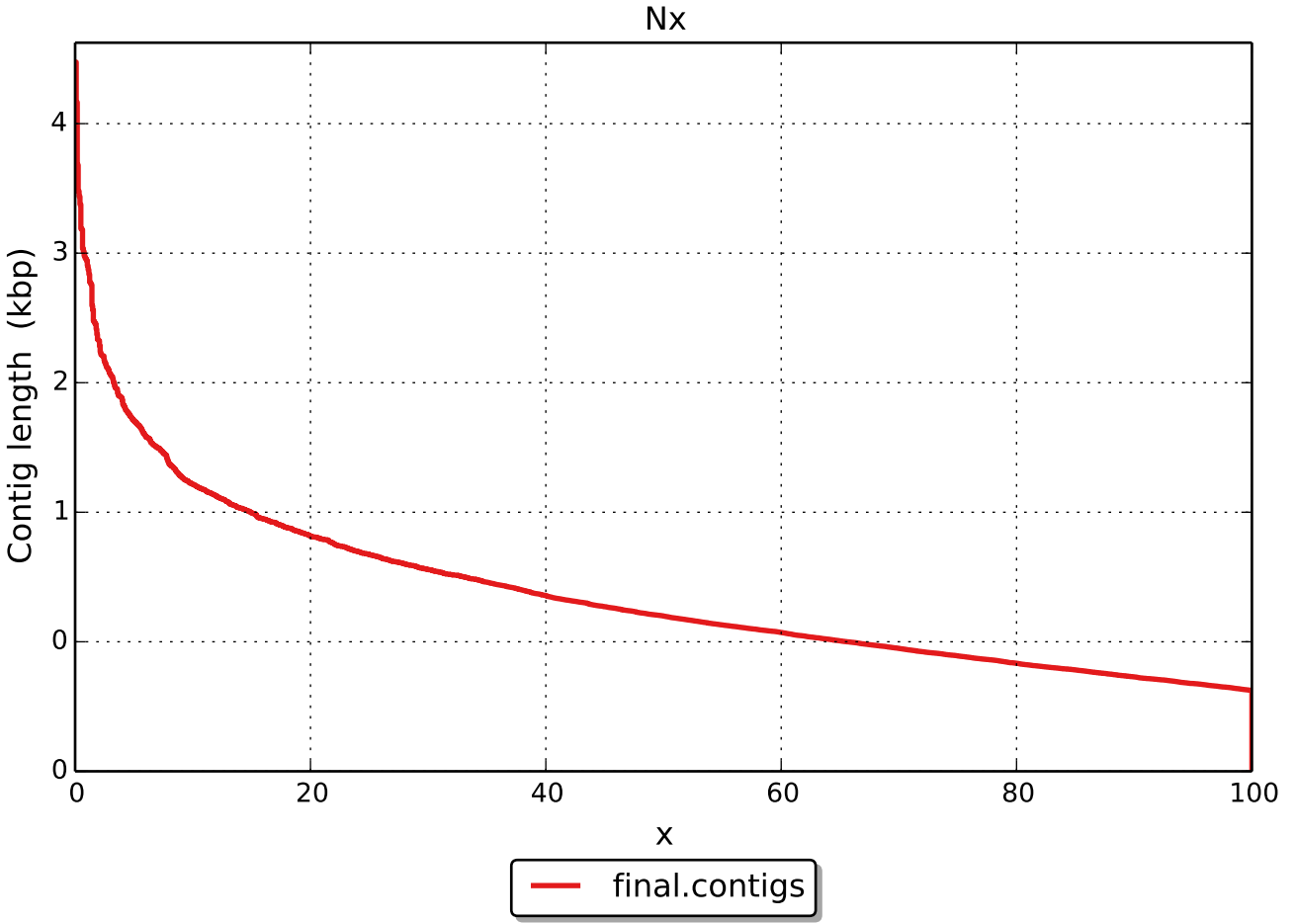
Unaligned report

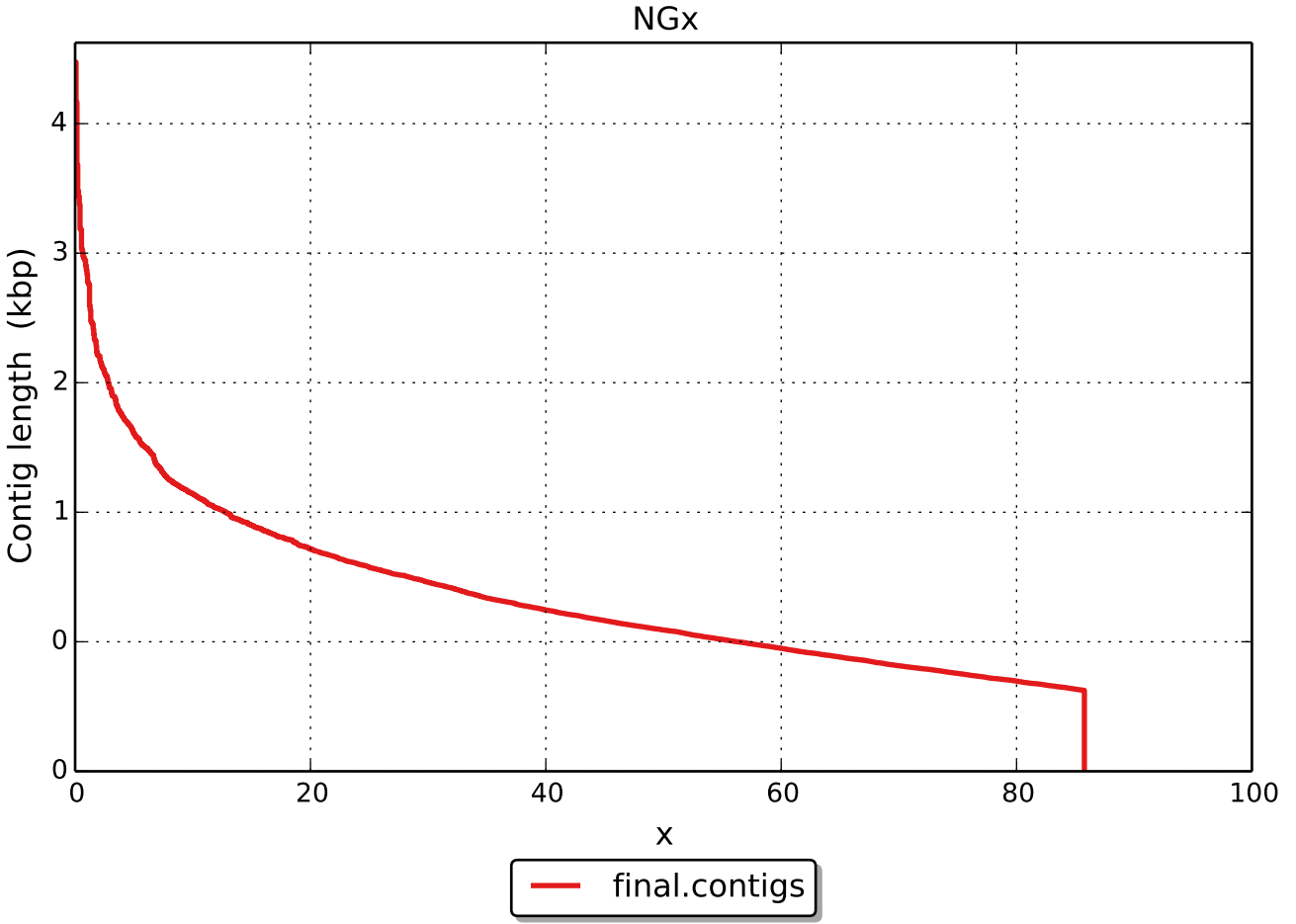
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

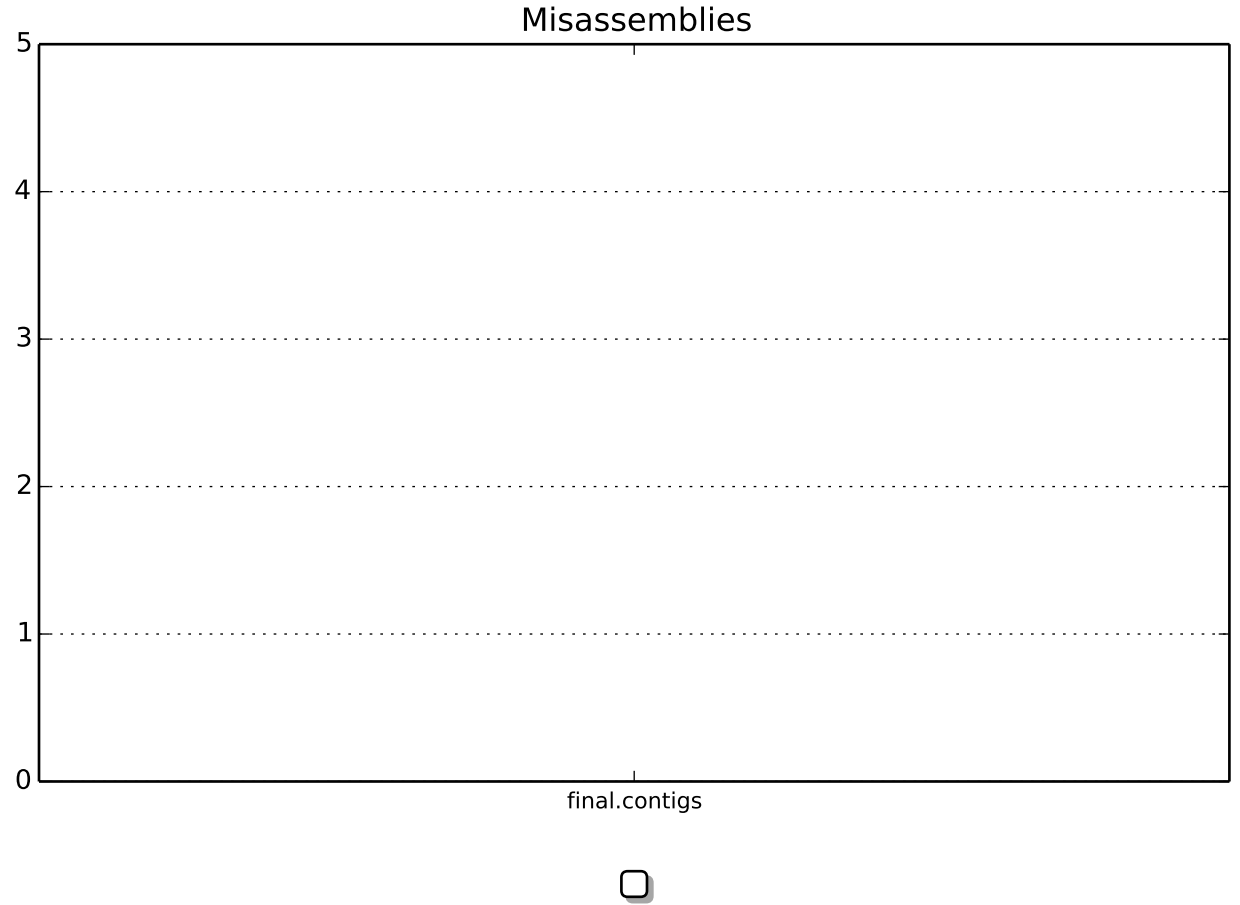
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

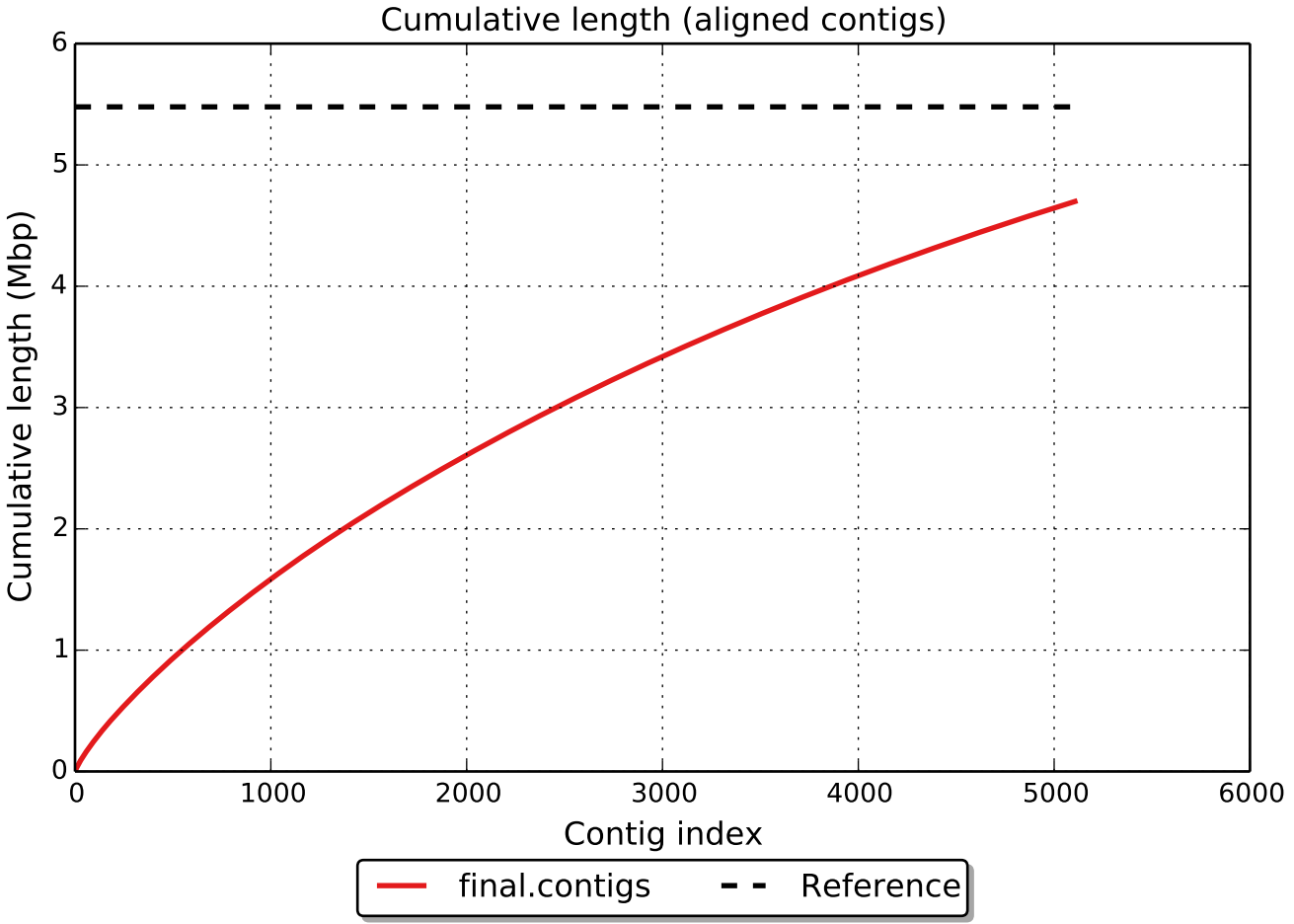

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference

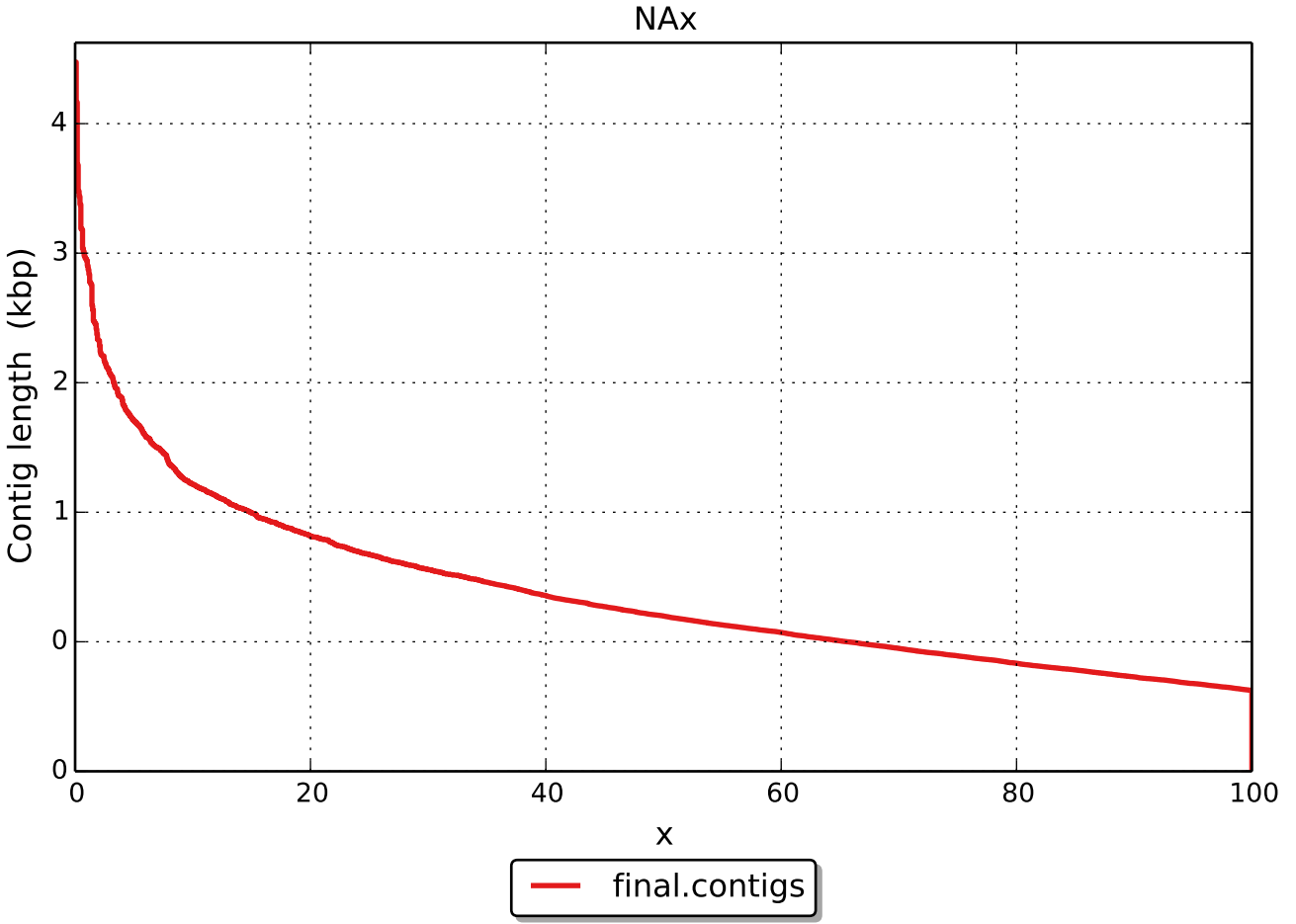

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

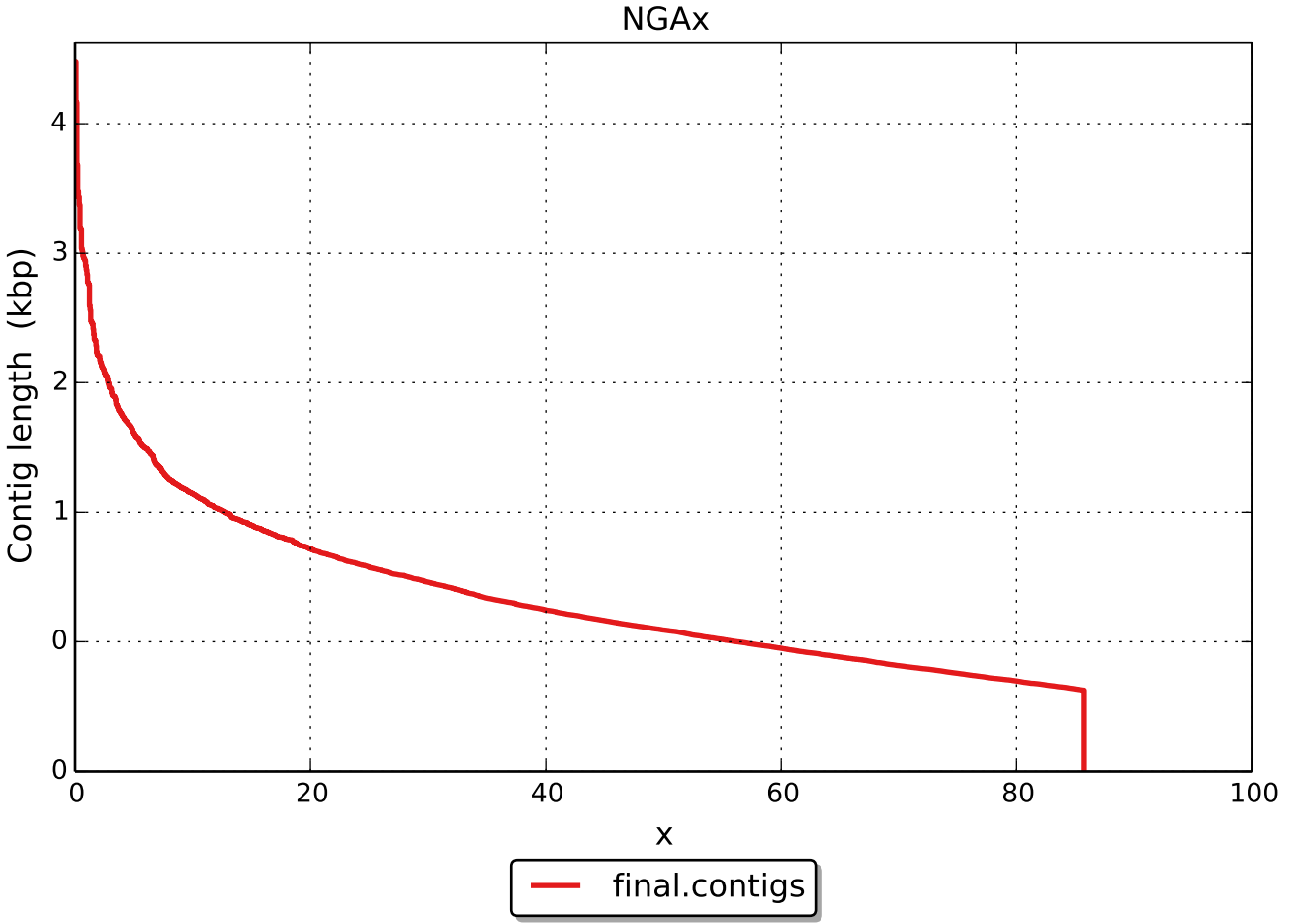

Nx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


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
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
1
2
3
4
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