Report

	final.contigs
# contigs (>= 0 bp)	37328
# contigs (>= 1000 bp)	1913
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16928197
Total length (>= 1000 bp)	2916630
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6182
Largest contig	4310
Total length	5772054
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	1007
NG50	1175
N75	675
NG75	863
L50	1883
LG50	1363
L75	3632
LG75	2522
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4278 + 36 part
Unaligned length	3303242
Genome fraction (%)	51.484
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	516.01
# indels per 100 kbp	0.46
Largest alignment	4310
NGA50	663
LGA50	1642

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

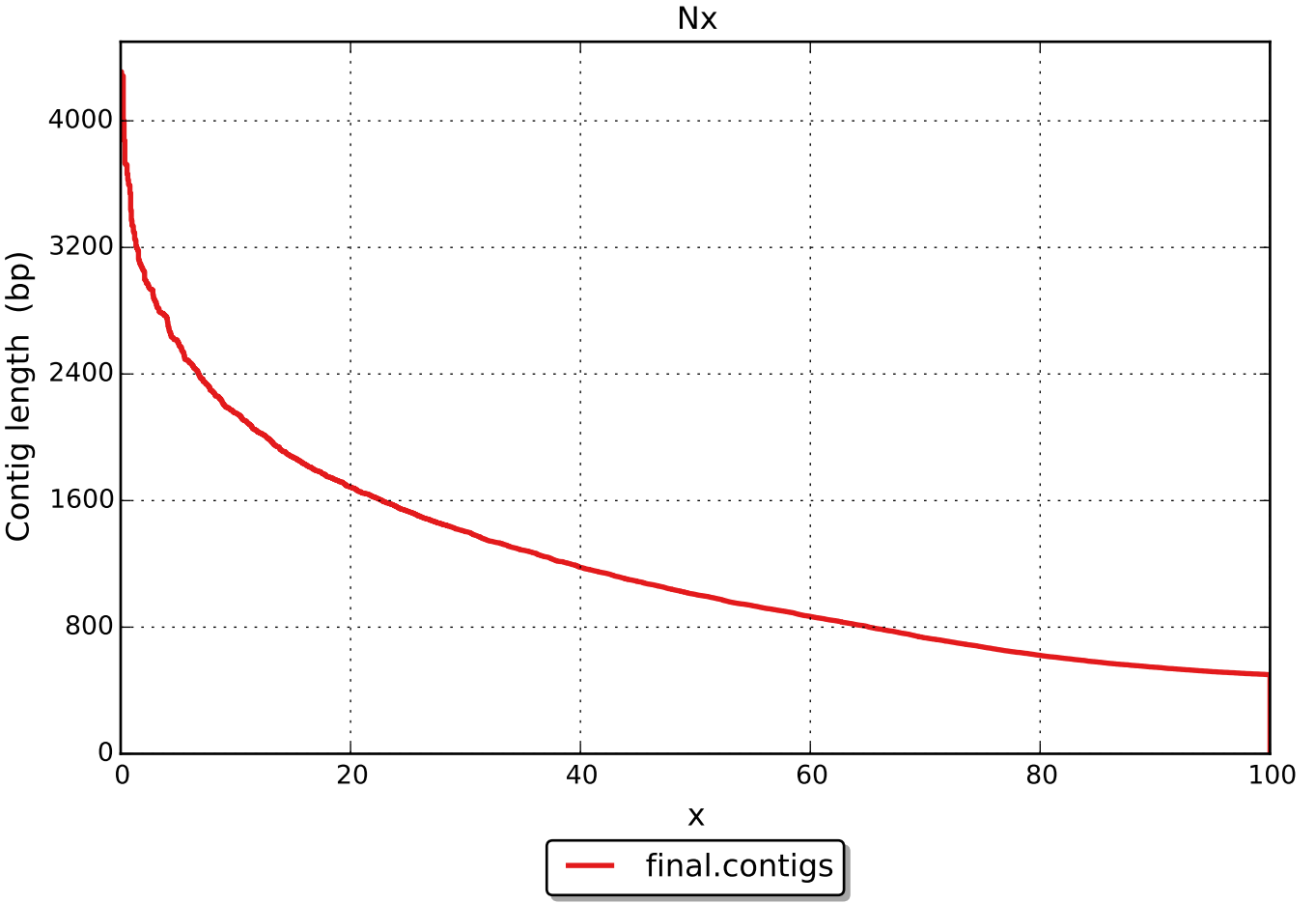
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	12331
# indels	11
# short indels	11
# long indels	0
Indels length	11

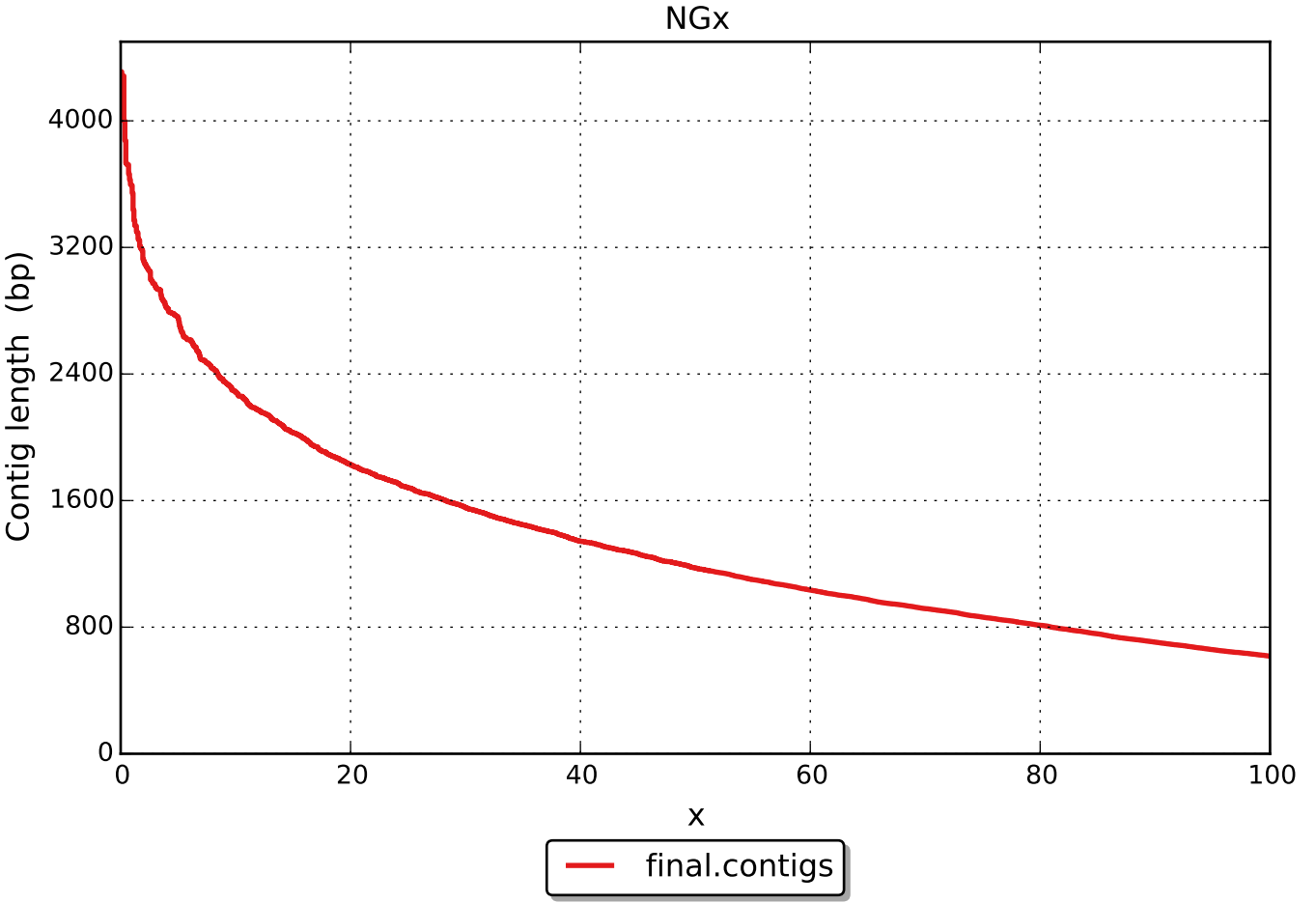
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

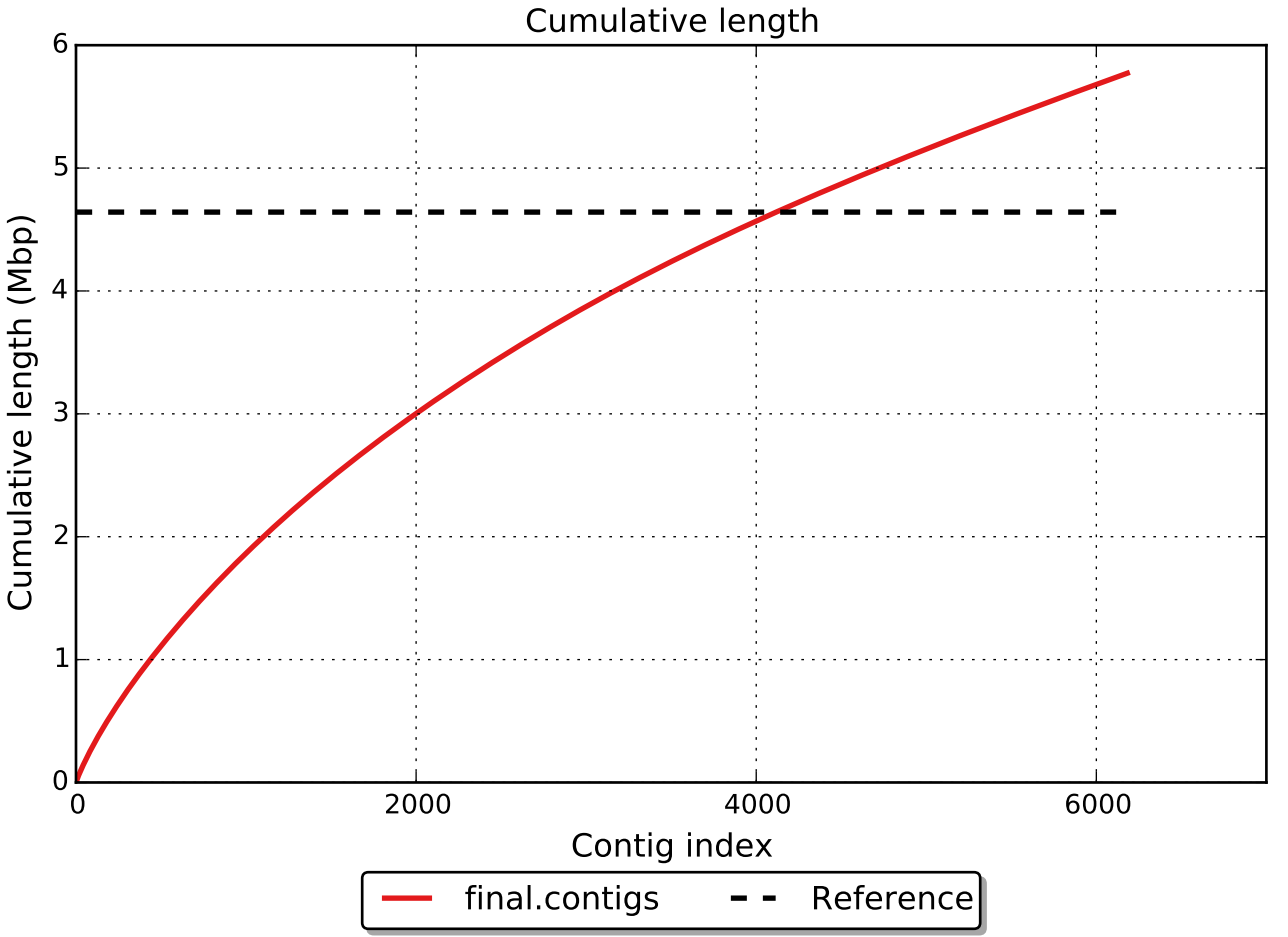
Unaligned report

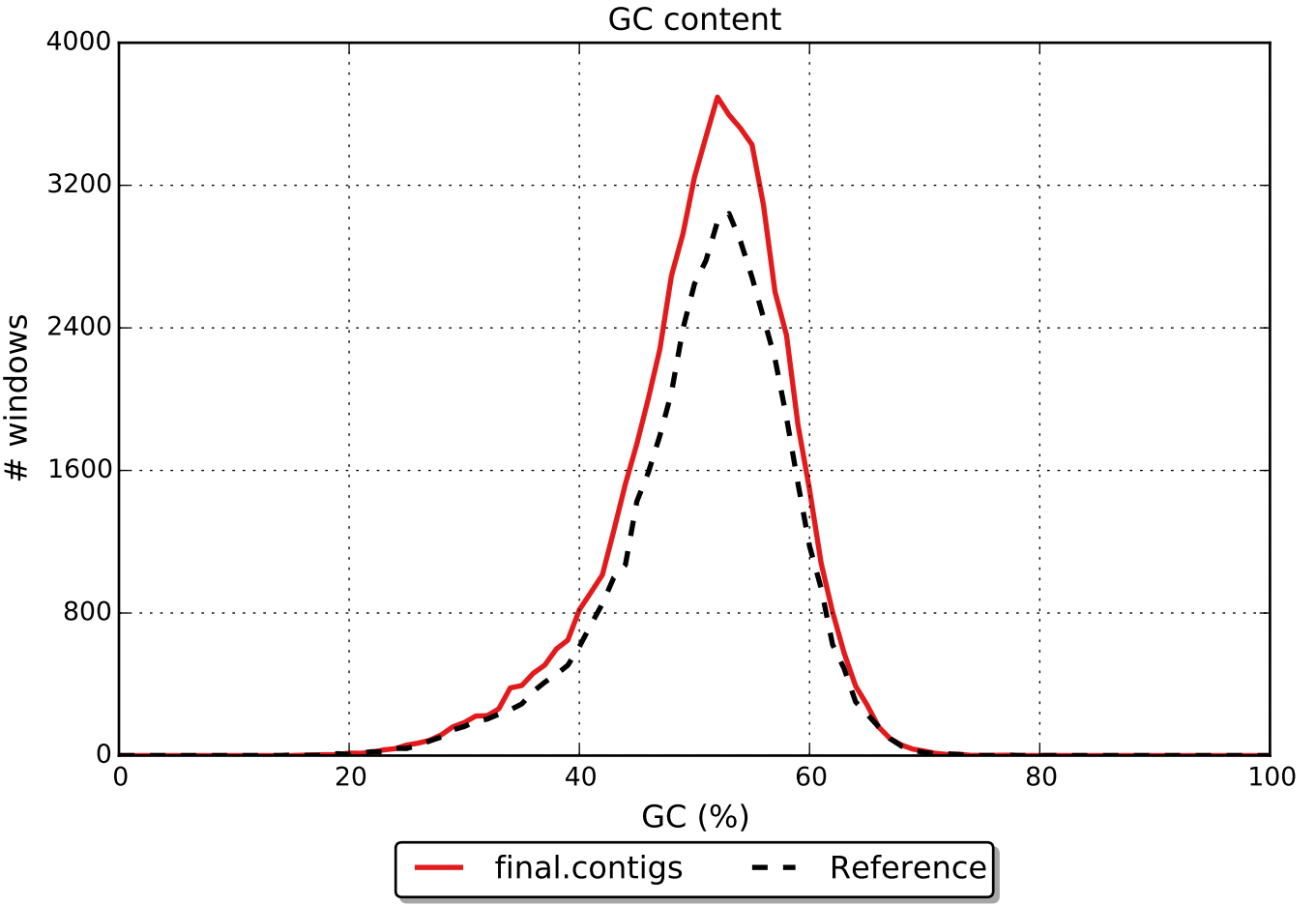
	final.contigs
# fully unaligned contigs	4278
Fully unaligned length	3291939
# partially unaligned contigs	36
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11303
# N's	0

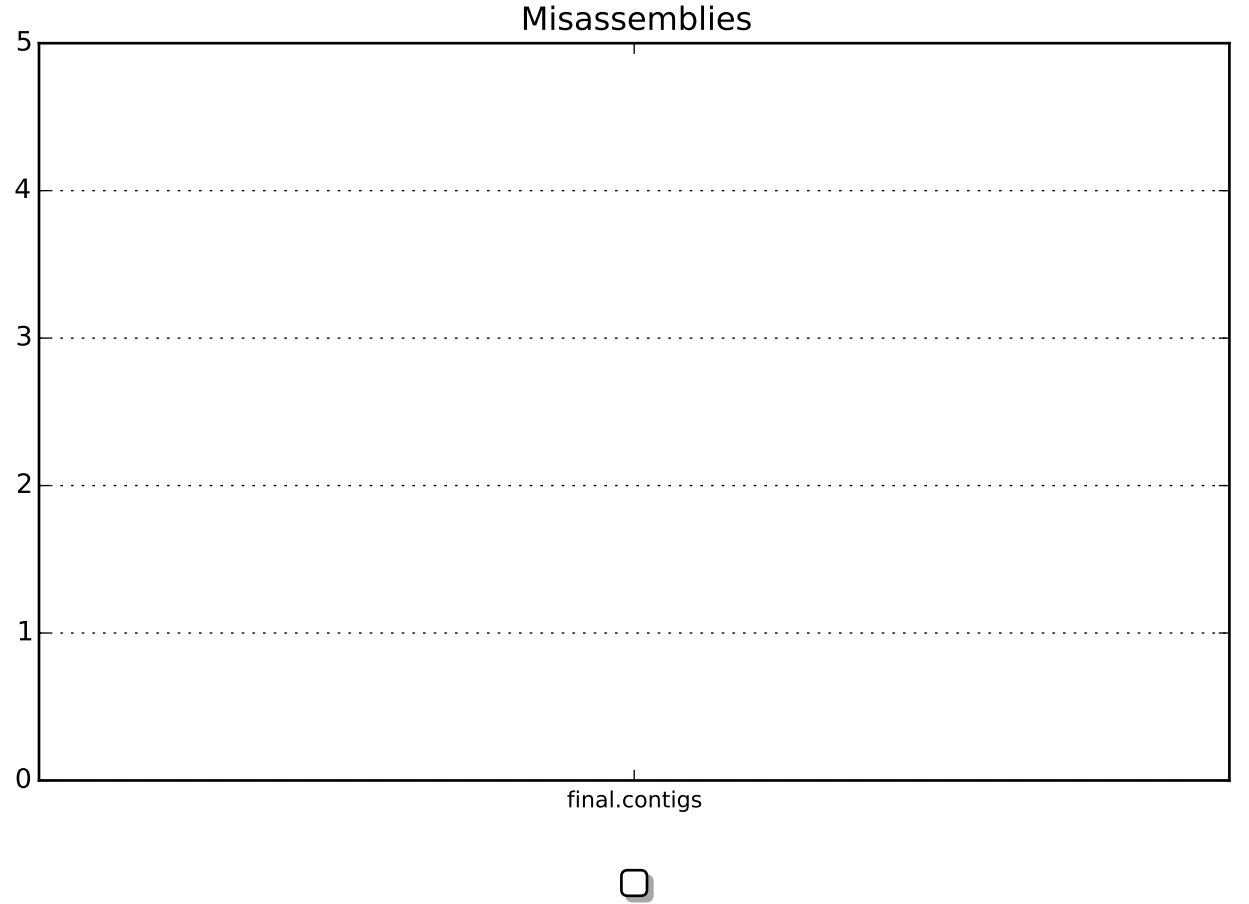
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

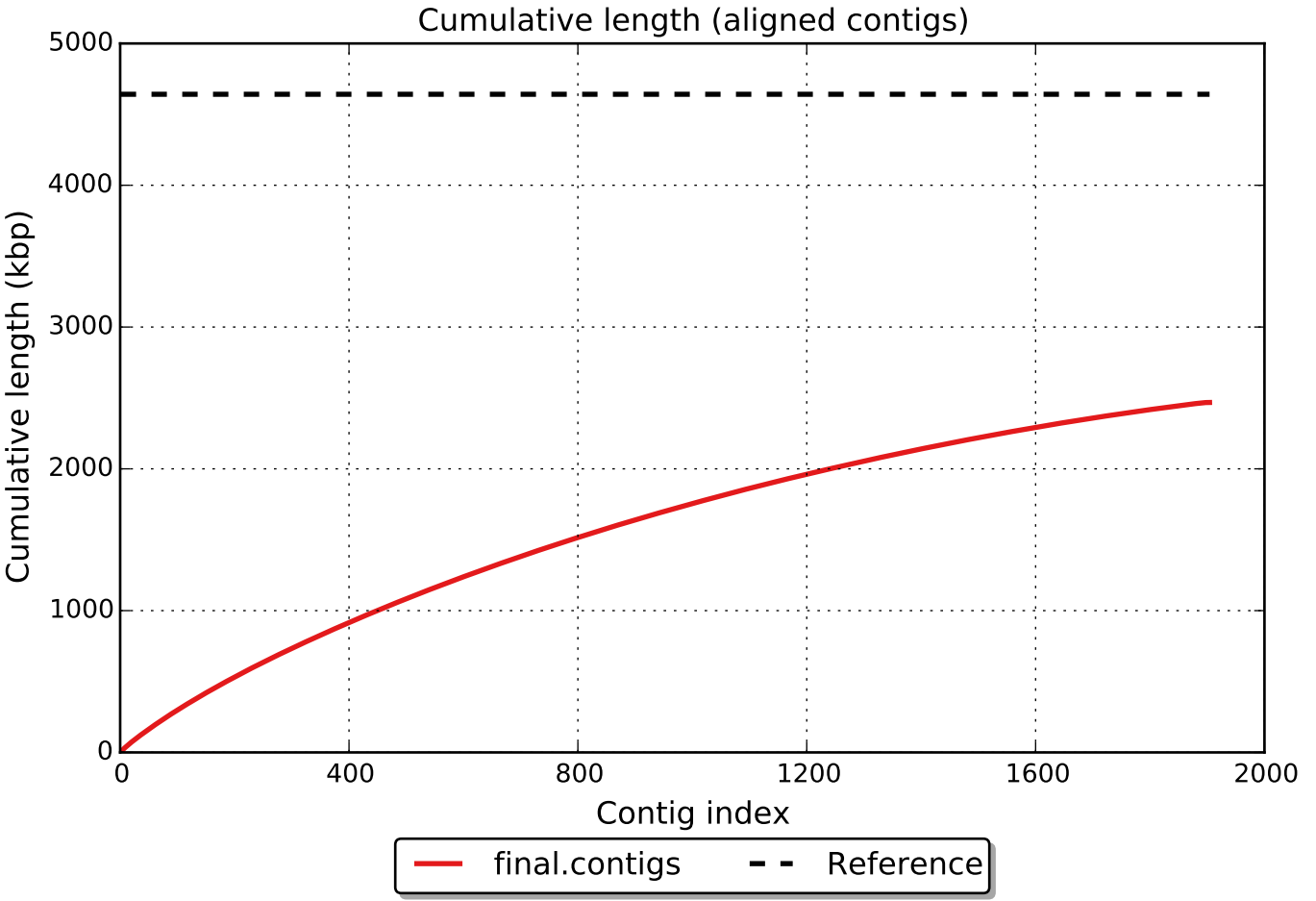

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

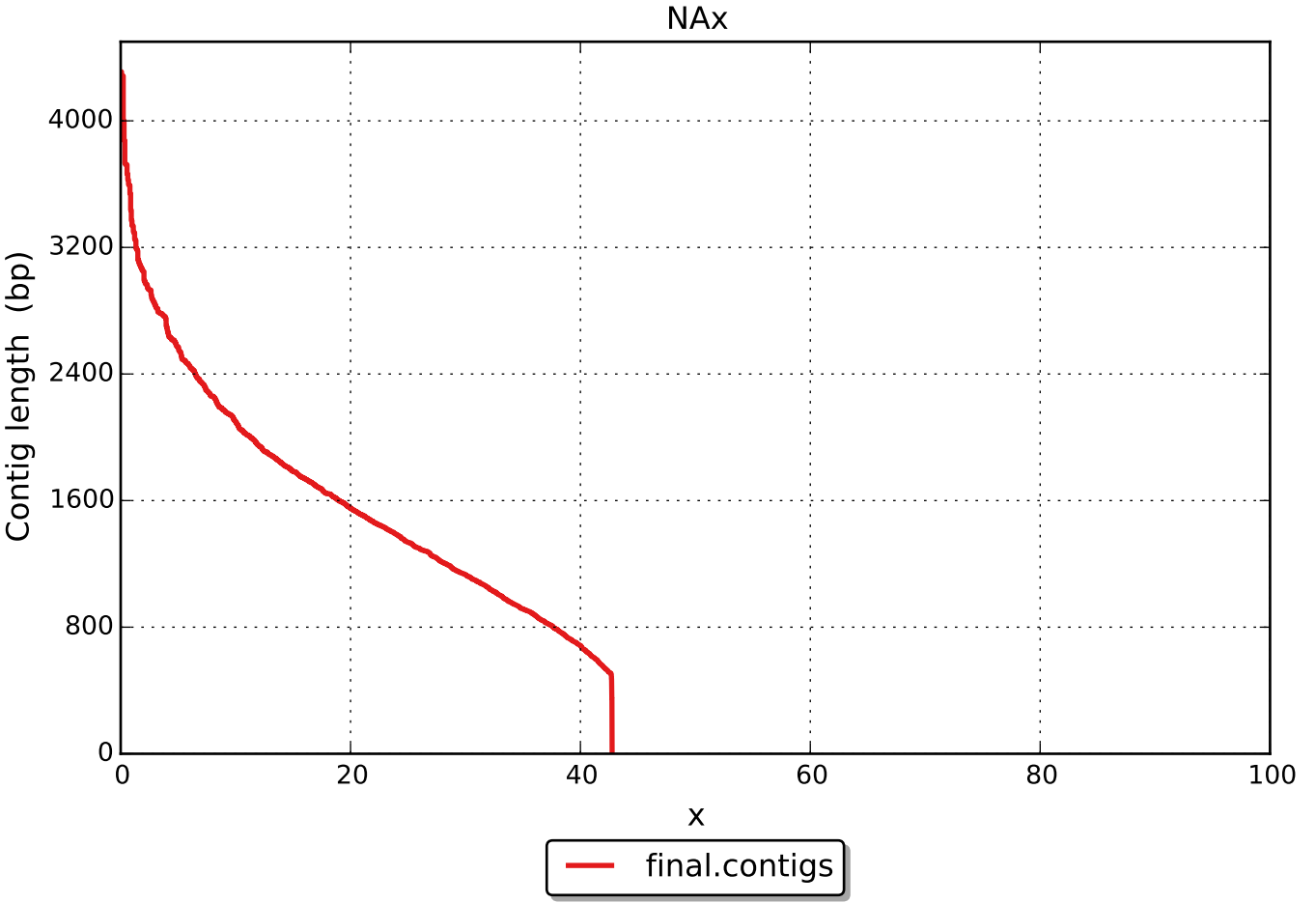

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

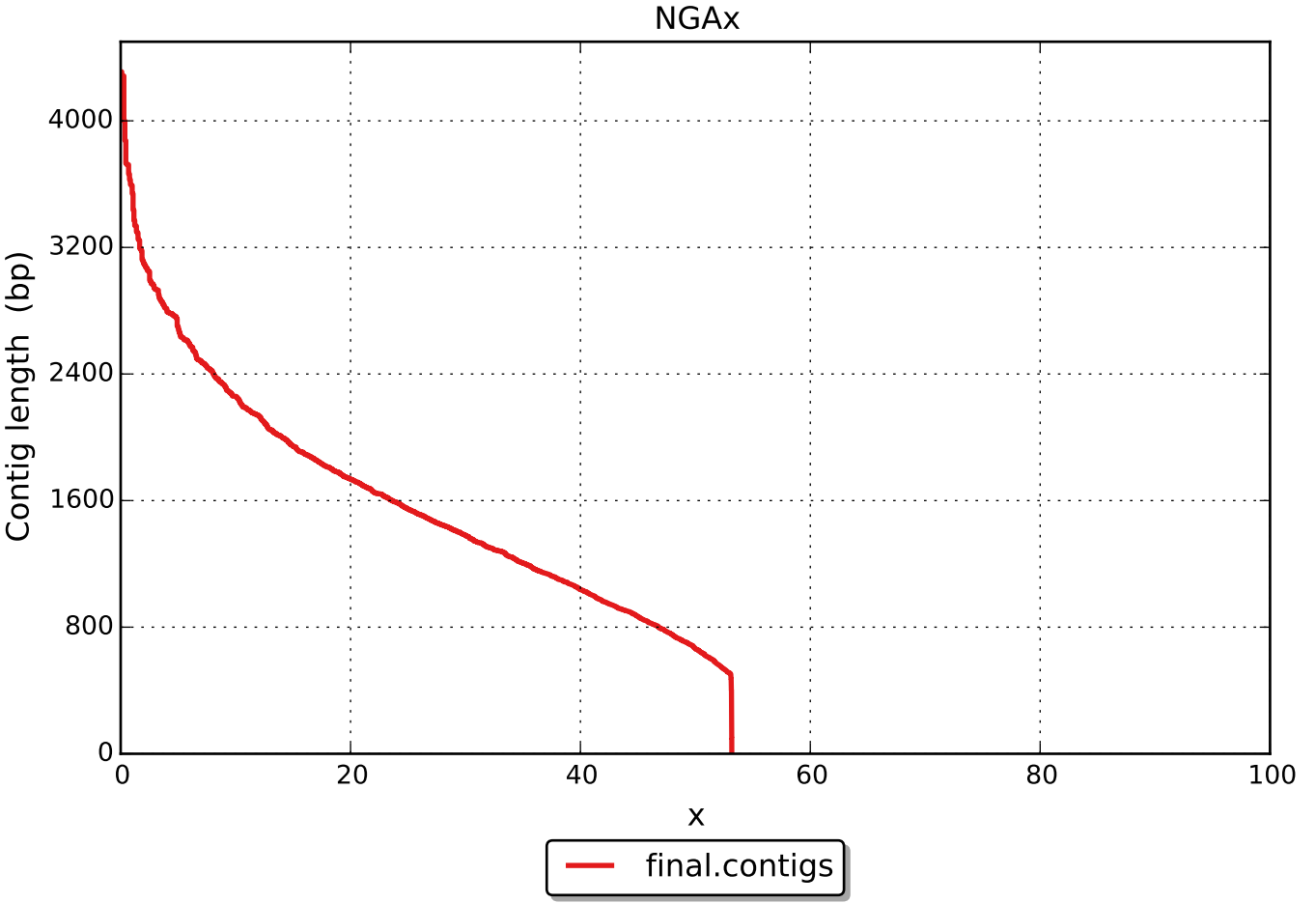

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
2000
4000
6000
Contig index
final.contigs
Reference


GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
Contig index
final.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs