Report

	final.contigs
# contigs (>= 0 bp)	5271
# contigs (>= 1000 bp)	3235
Total length (>= 0 bp)	11145940
Total length (>= 1000 bp)	10060407
# contigs	4235
Largest contig	16890
Total length	10803074
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.48
N50	3589
NG50	3507
N75	2089
NG75	1970
L50	943
LG50	985
L75	1918
LG75	2026
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	94.288
Duplication ratio	1.033
# N's per 100 kbp	0.00
# mismatches per 100 kbp	34.02
# indels per 100 kbp	0.16
Largest alignment	16890
NA50	3589
NGA50	3507
NA75	2088
NGA75	1970
LA50	943
LGA50	985
LA75	1919
LGA75	2026

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

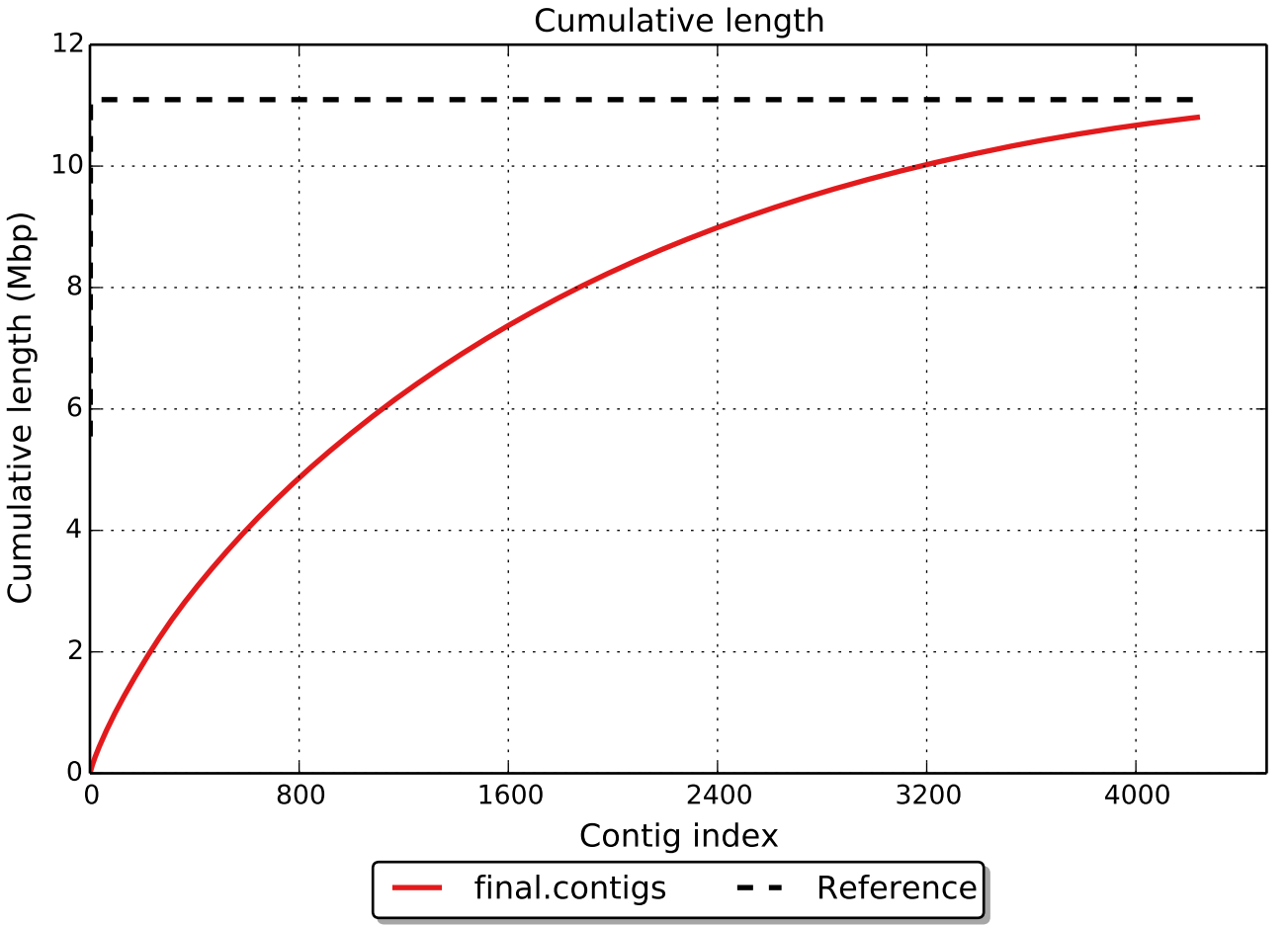
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	6200
# local misassemblies	4
# mismatches	3559
# indels	17
# short indels	13
# long indels	4
Indels length	81

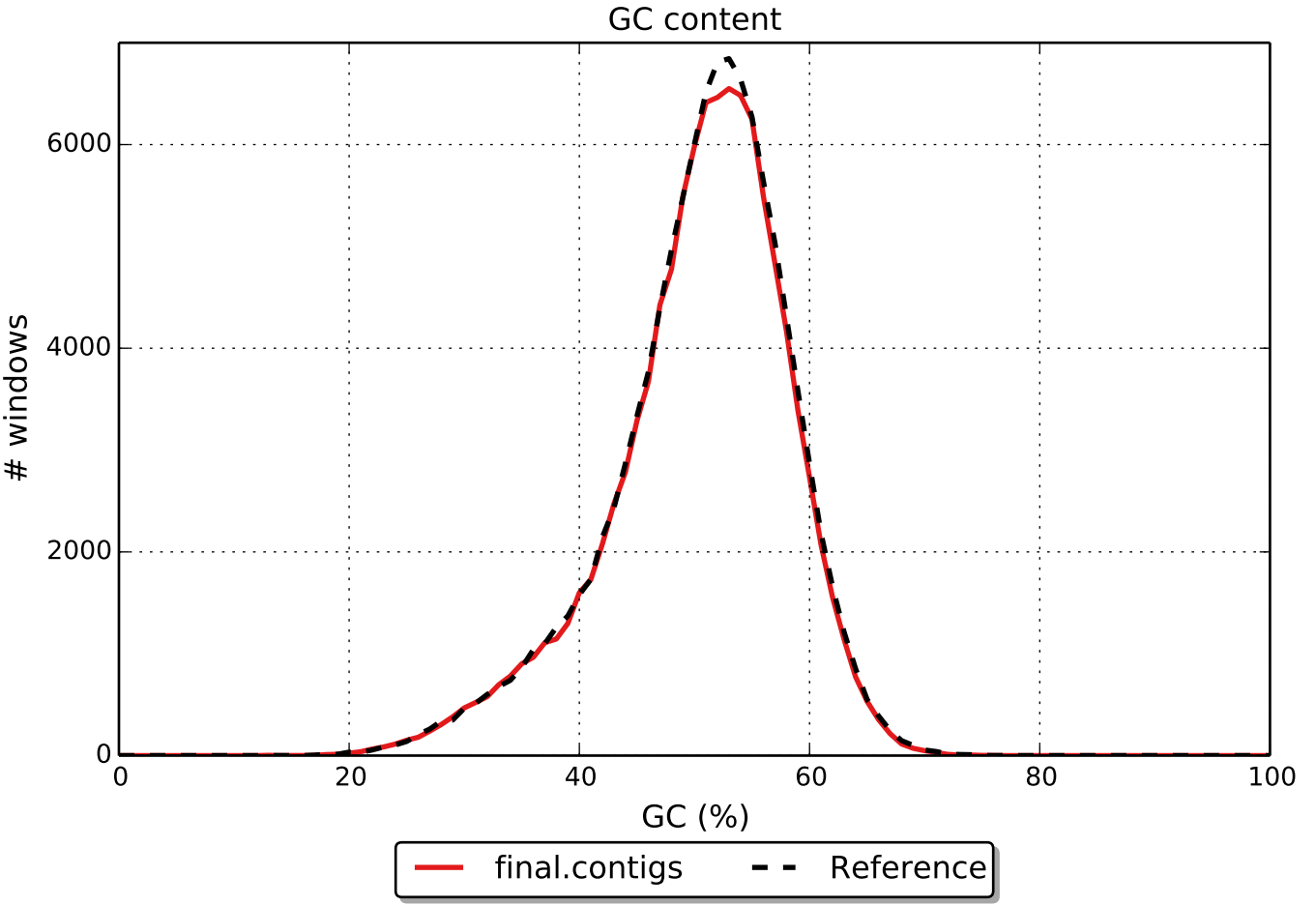
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

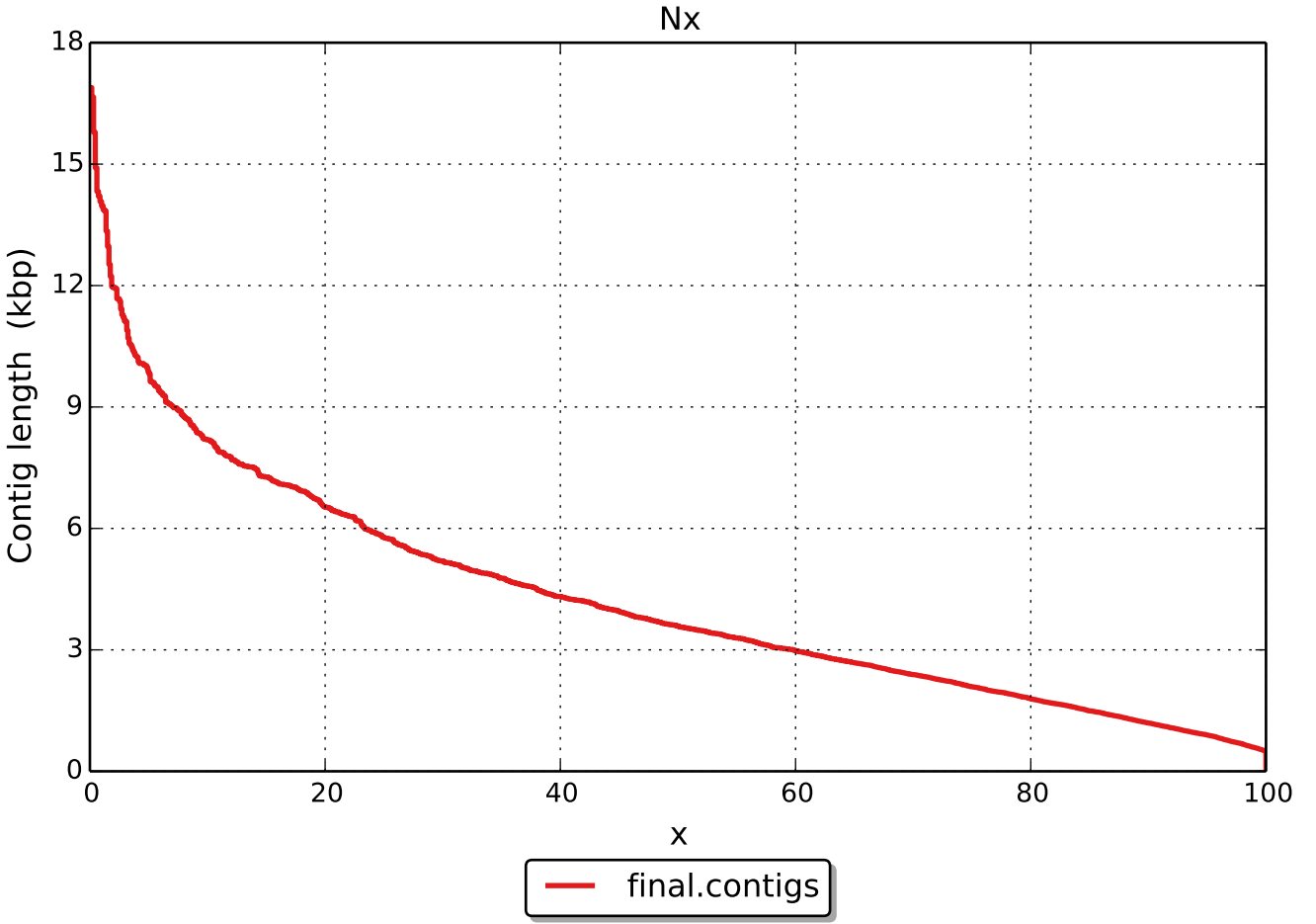
Unaligned report

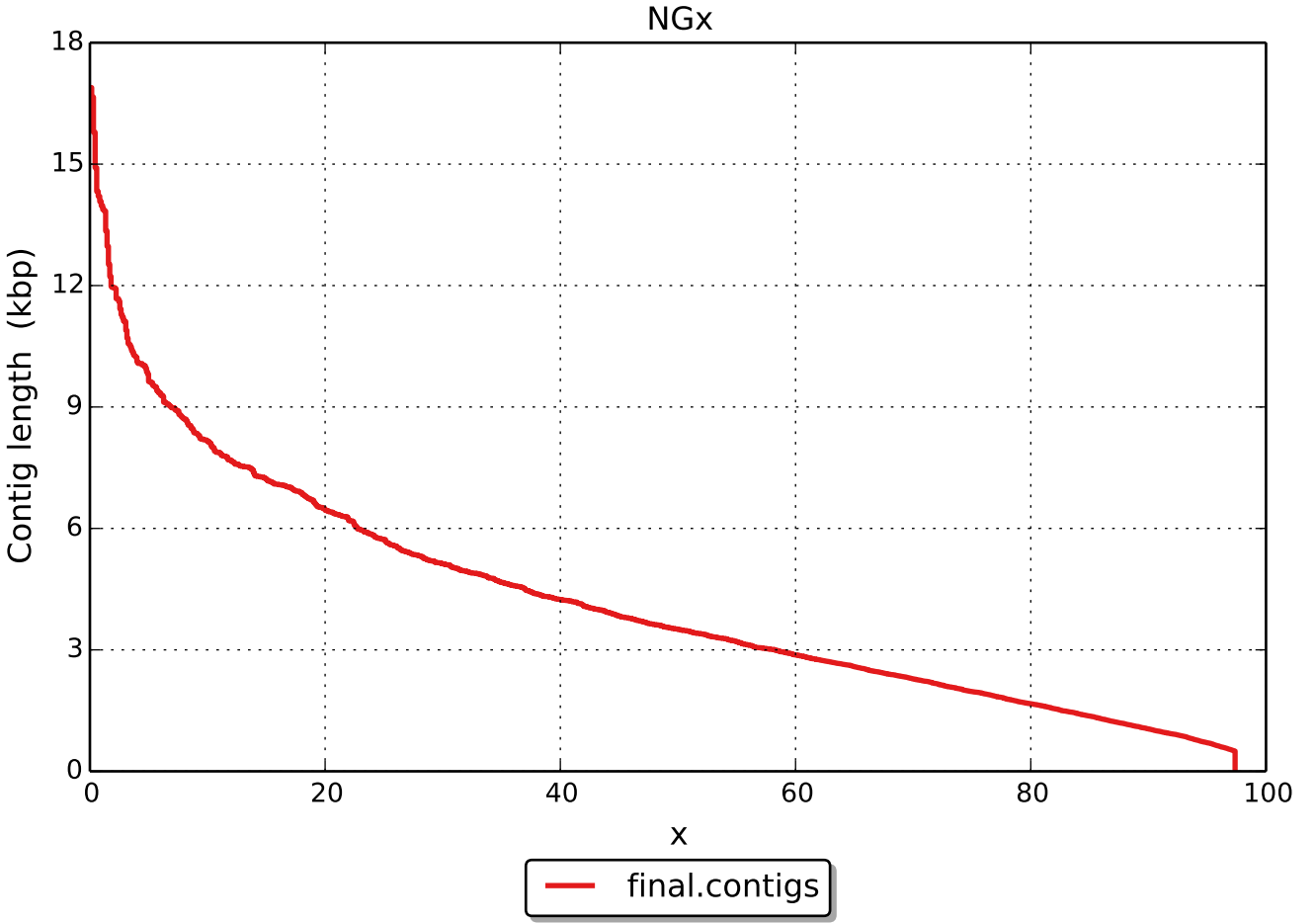
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

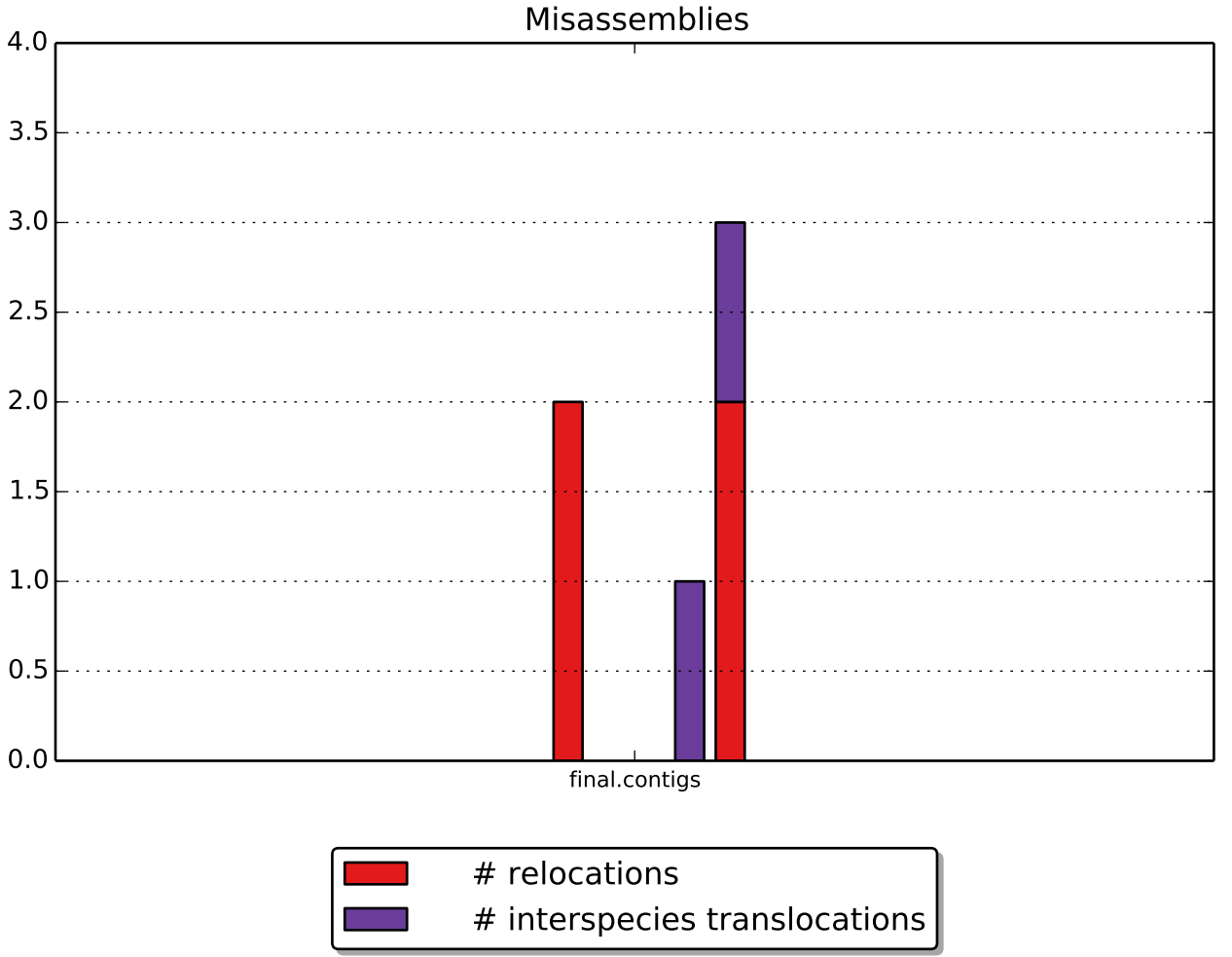
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

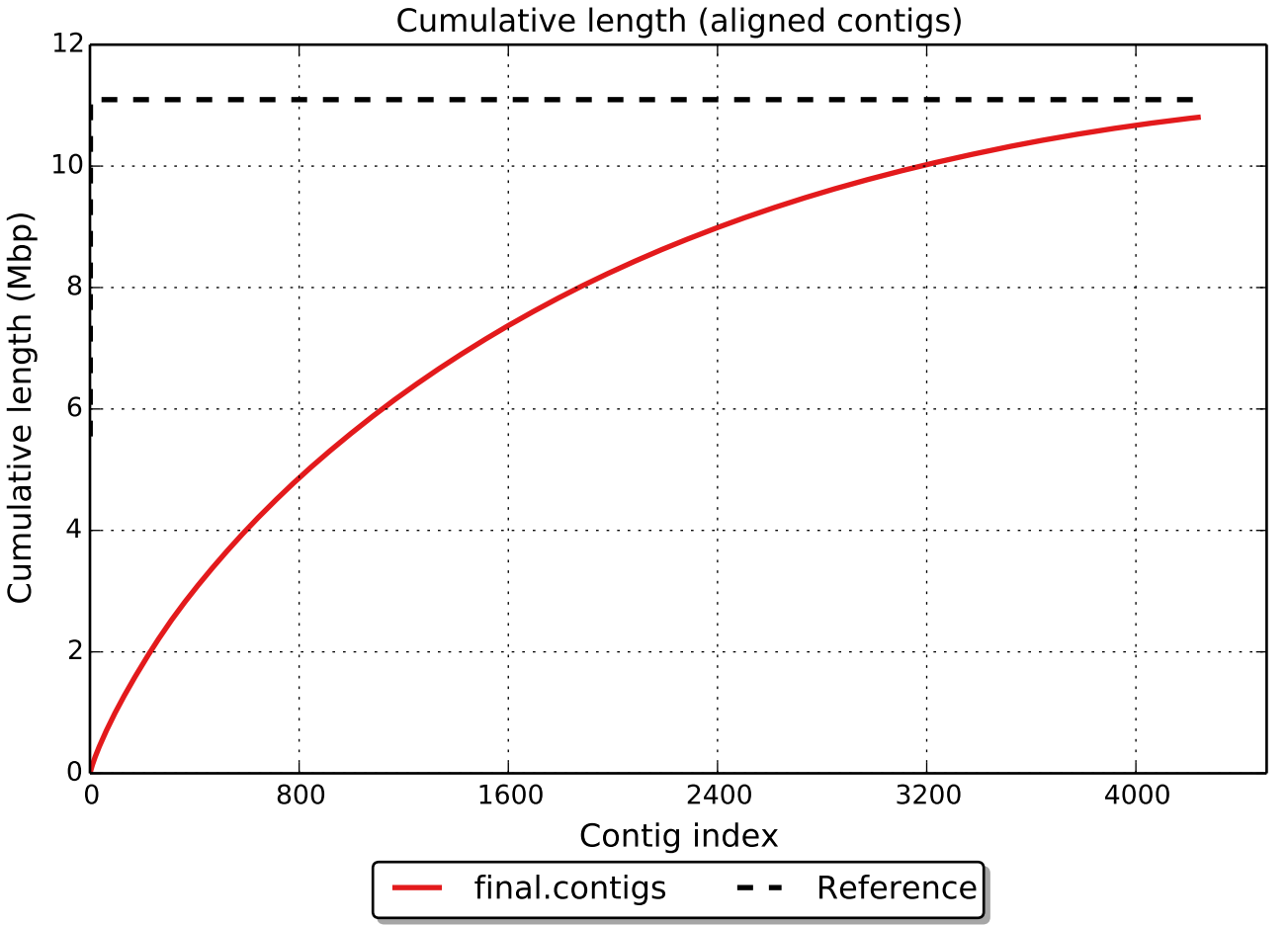

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference

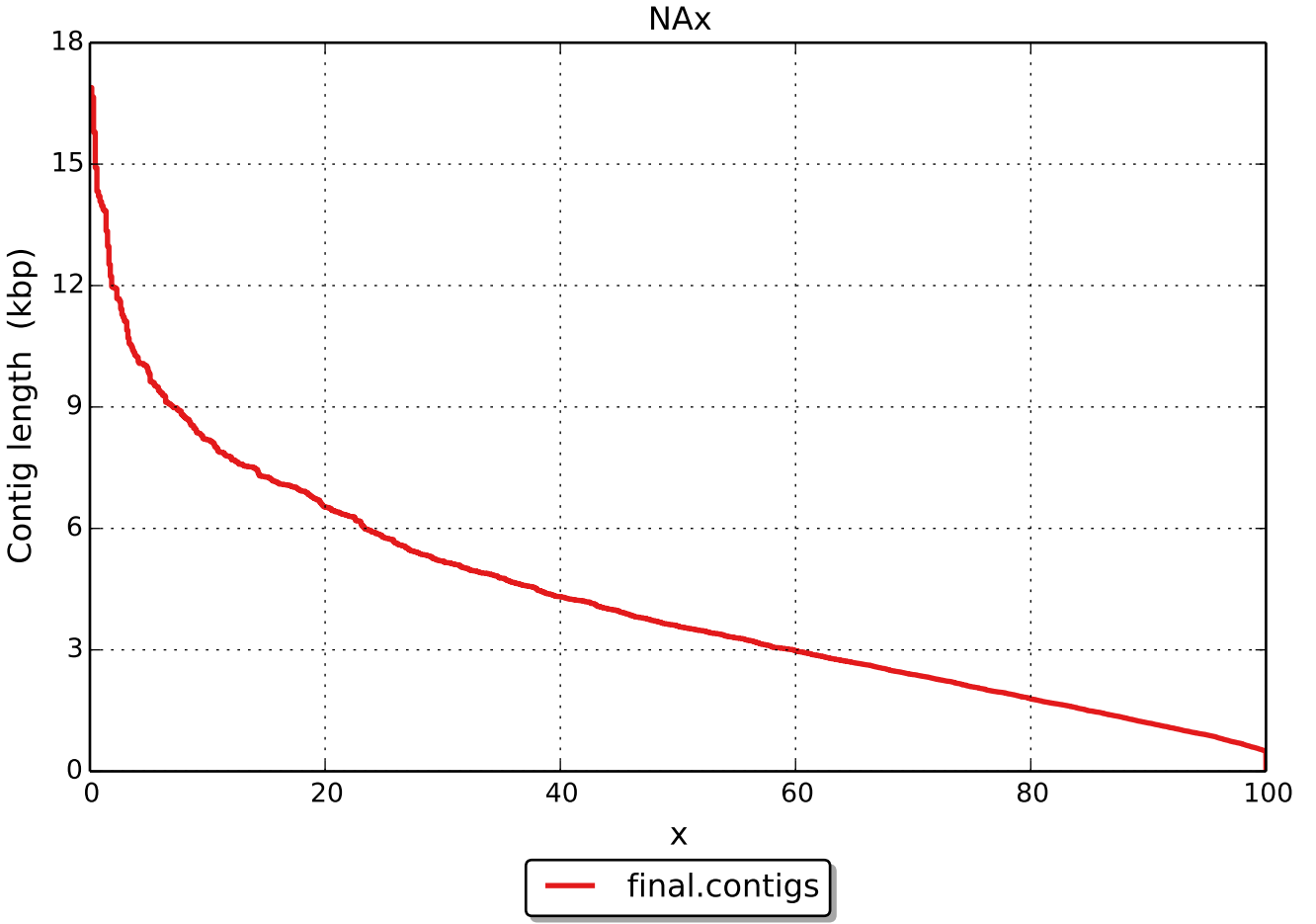

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

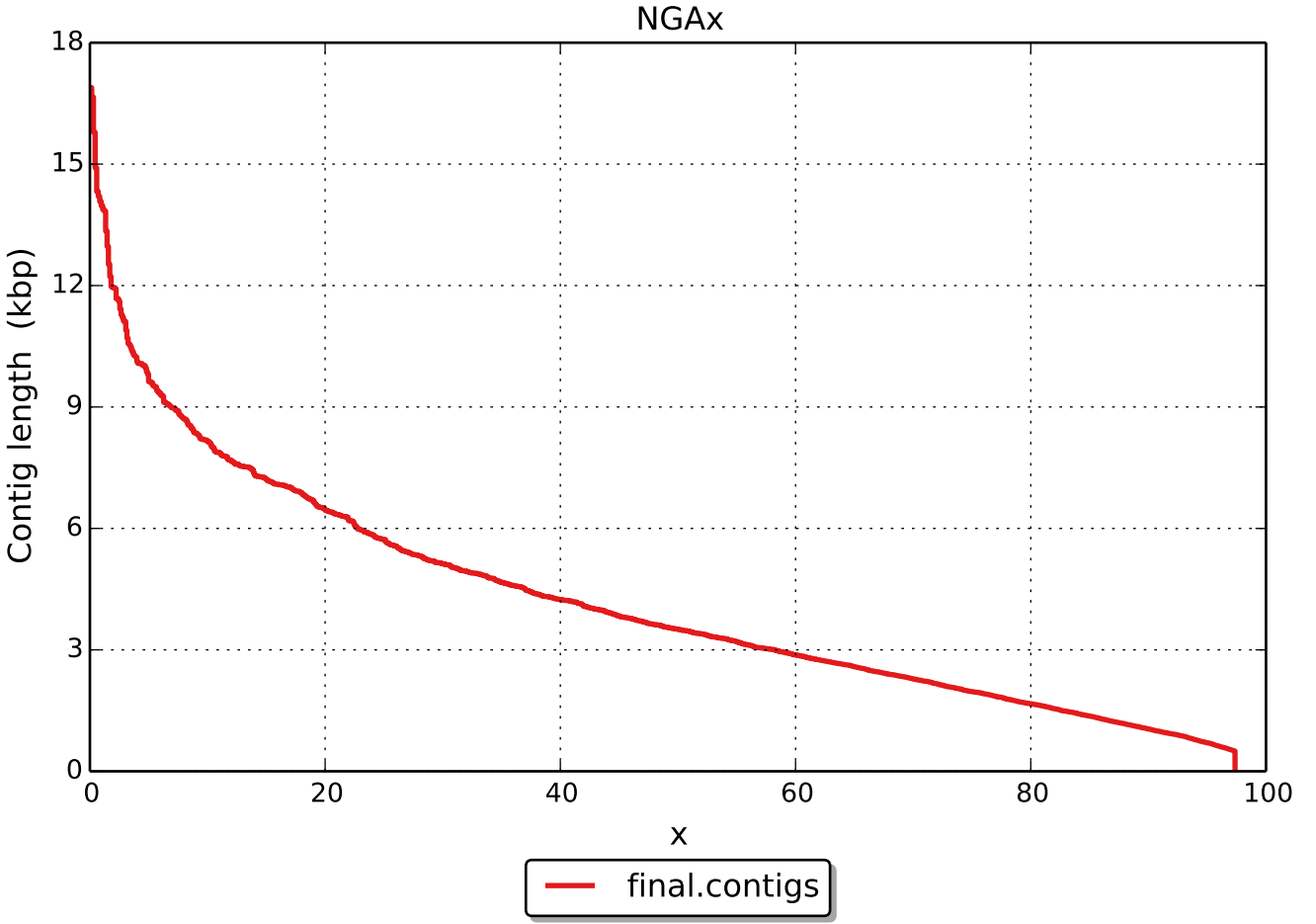

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations
interspecies translocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs