Report

	final.contigs
# contigs (>= 0 bp)	1180
# contigs (>= 1000 bp)	649
Total length (>= 0 bp)	10854981
Total length (>= 1000 bp)	10647989
# contigs	771
Largest contig	129092
Total length	10731026
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.50
N50	31504
NG50	31287
N75	17402
NG75	16524
L50	109
LG50	112
L75	222
LG75	232
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	89775
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.963
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.45
# indels per 100 kbp	0.09
Largest alignment	129092
NA50	31378
NGA50	30865
NA75	17128
NGA75	16080
LA50	109
LGA50	113
LA75	224
LGA75	234

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

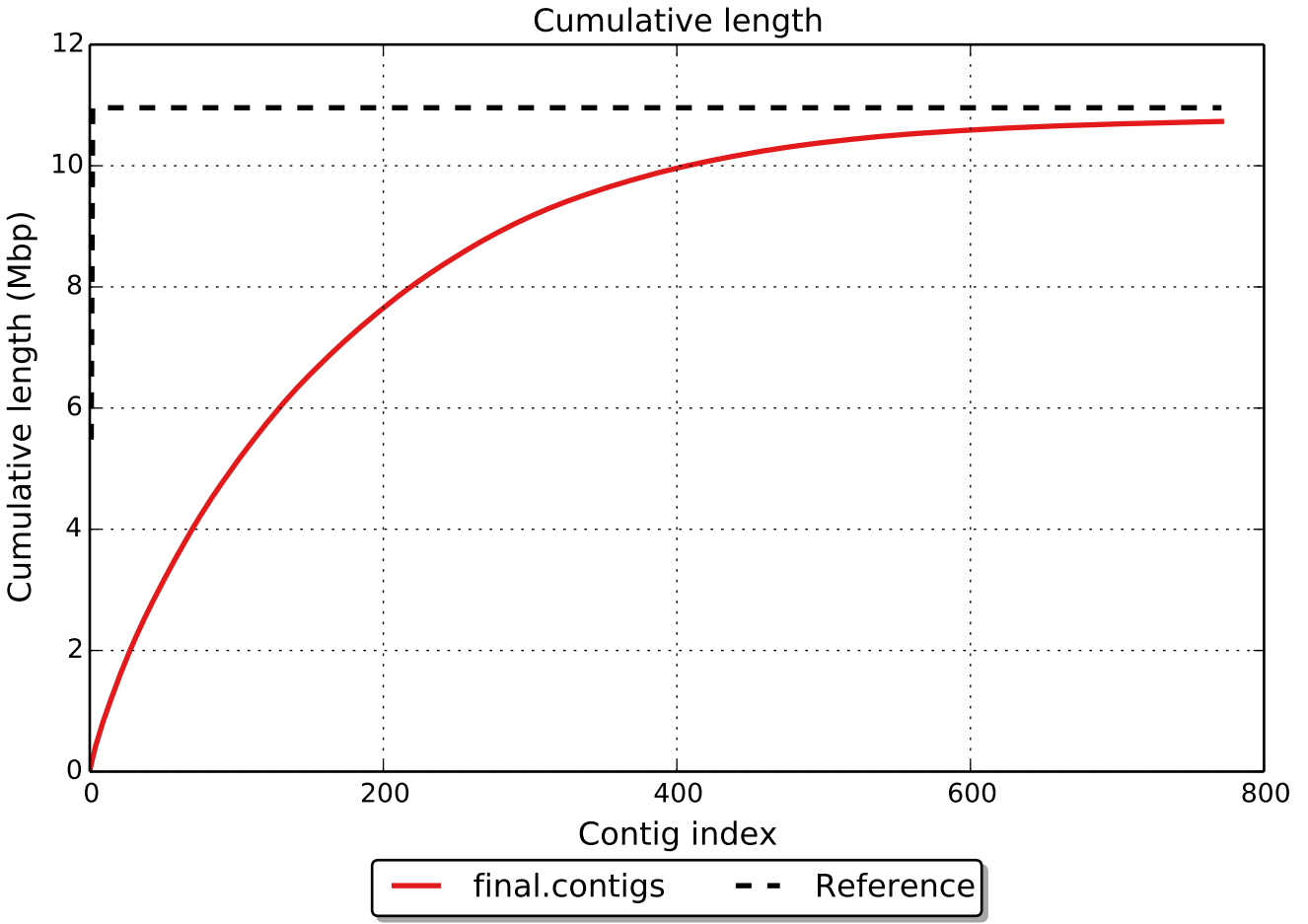
	final.contigs
# misassemblies	3
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	89775
# local misassemblies	0
# mismatches	2302
# indels	10
# short indels	7
# long indels	3
Indels length	70

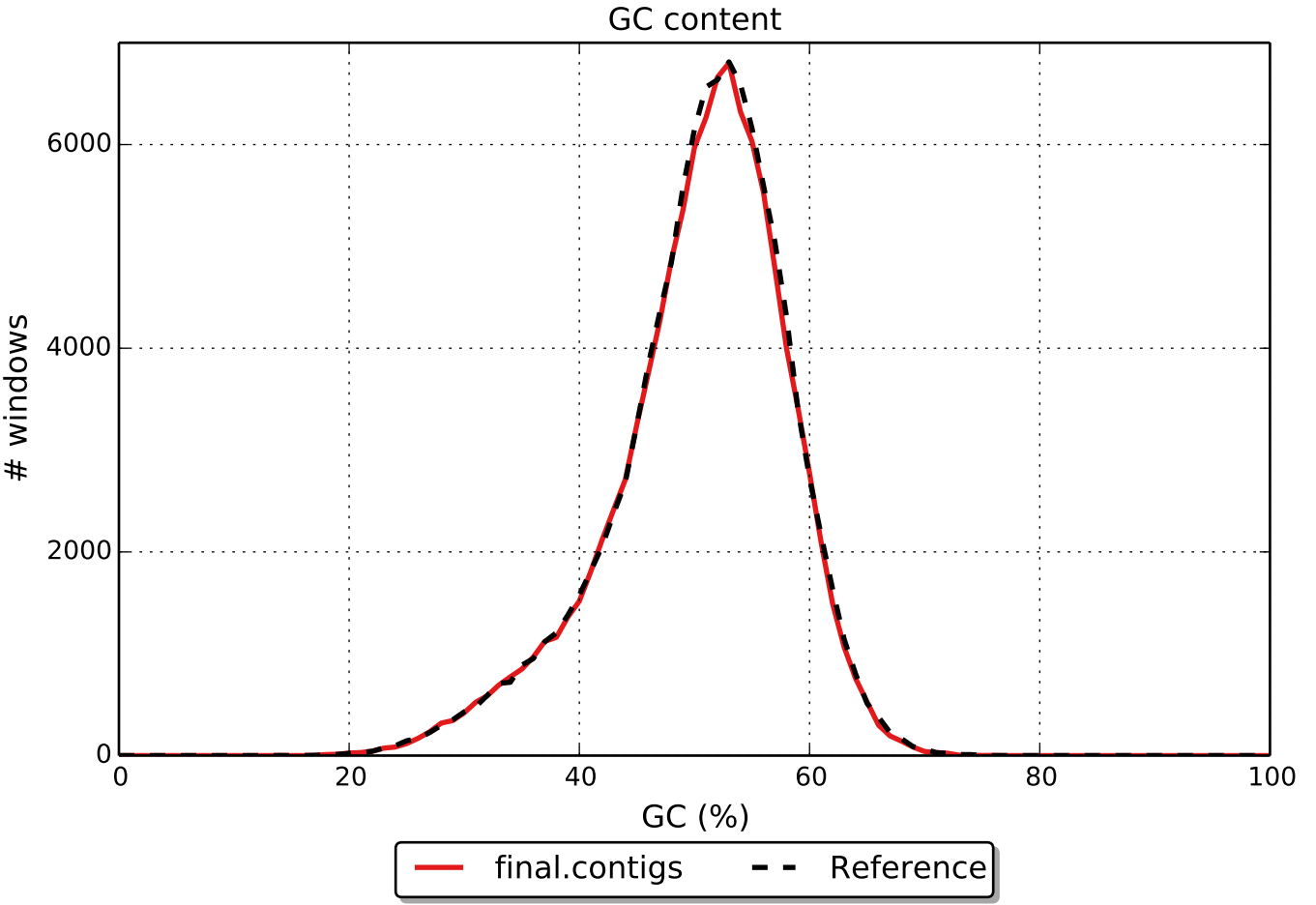
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

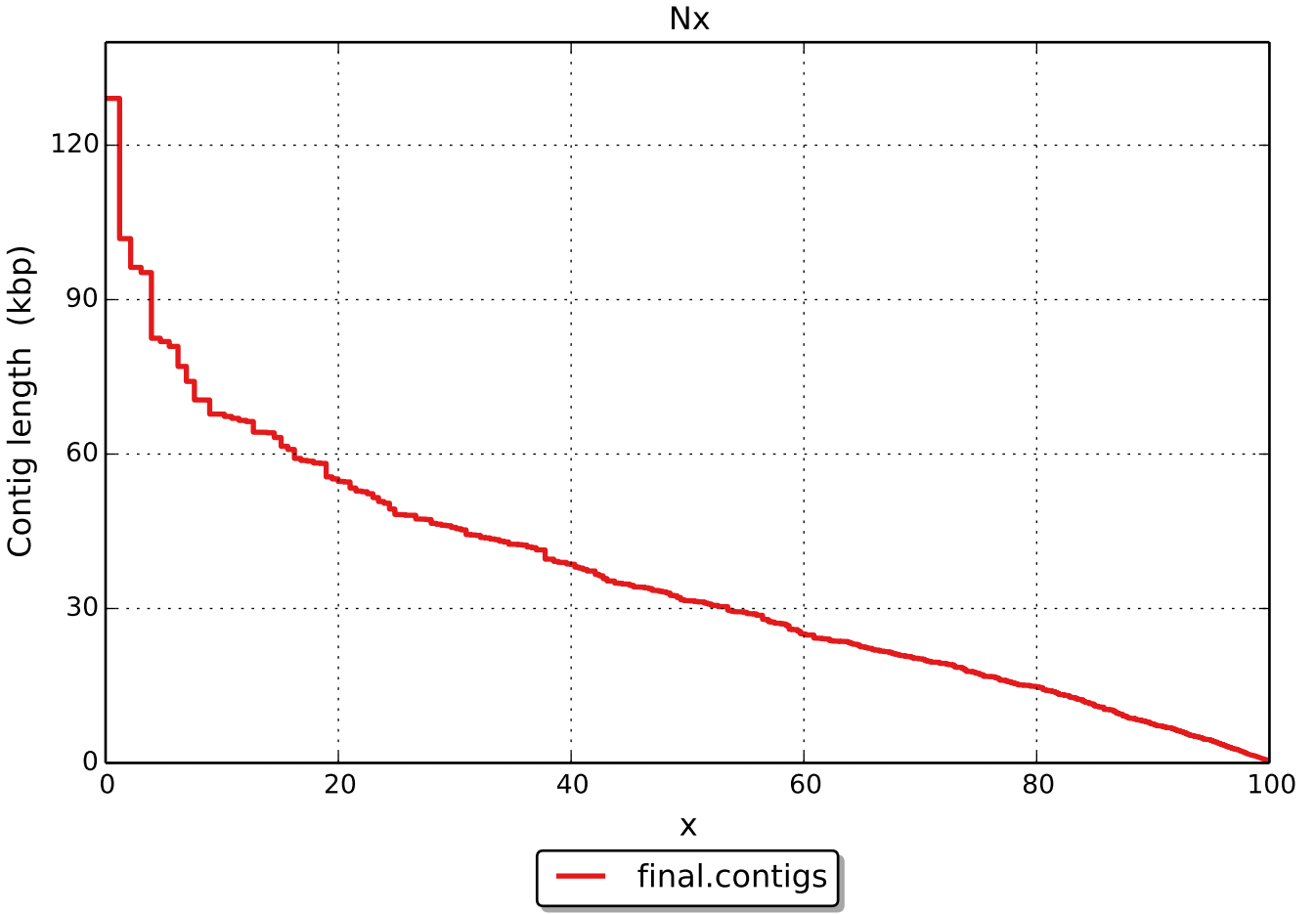
Unaligned report

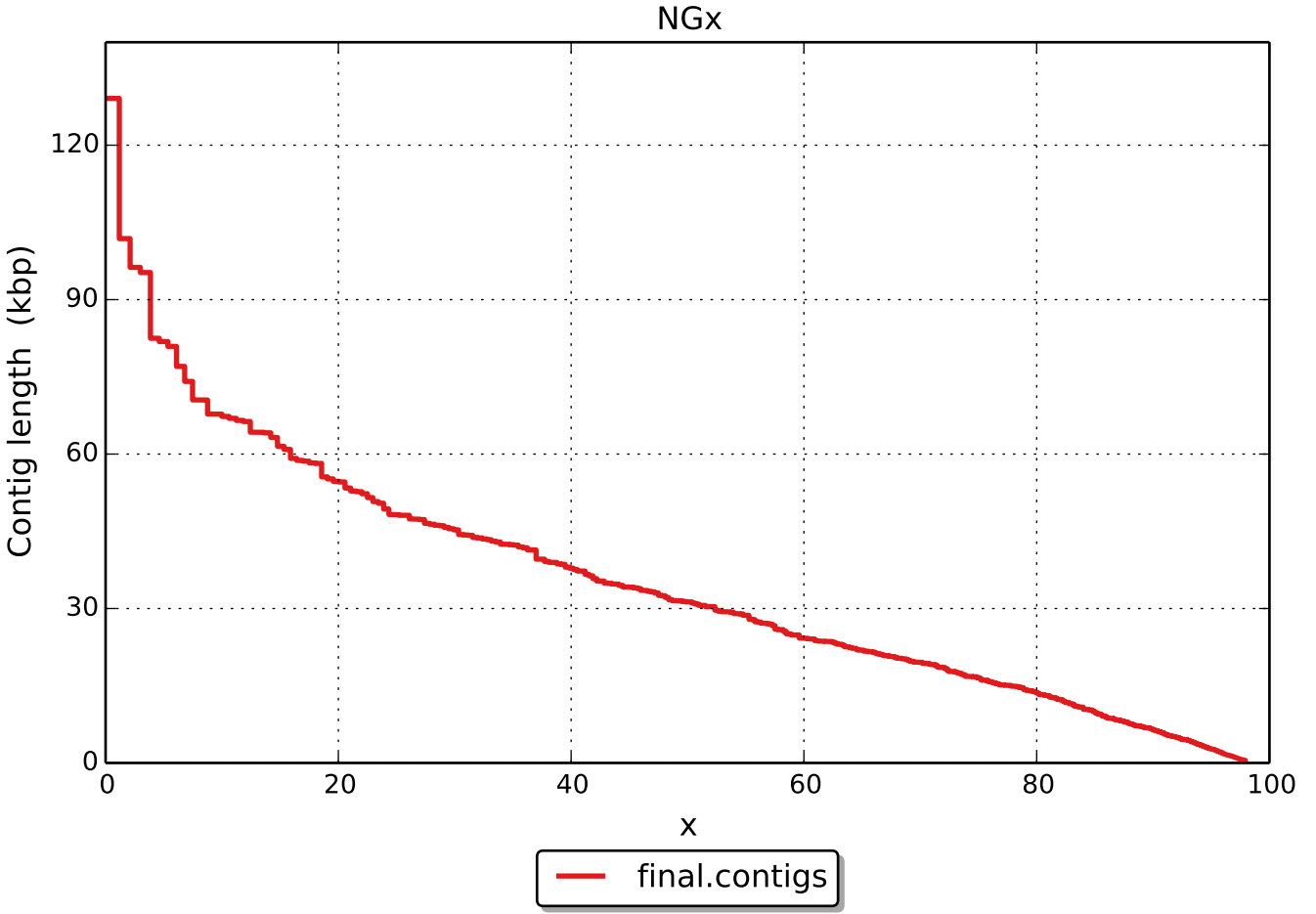
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

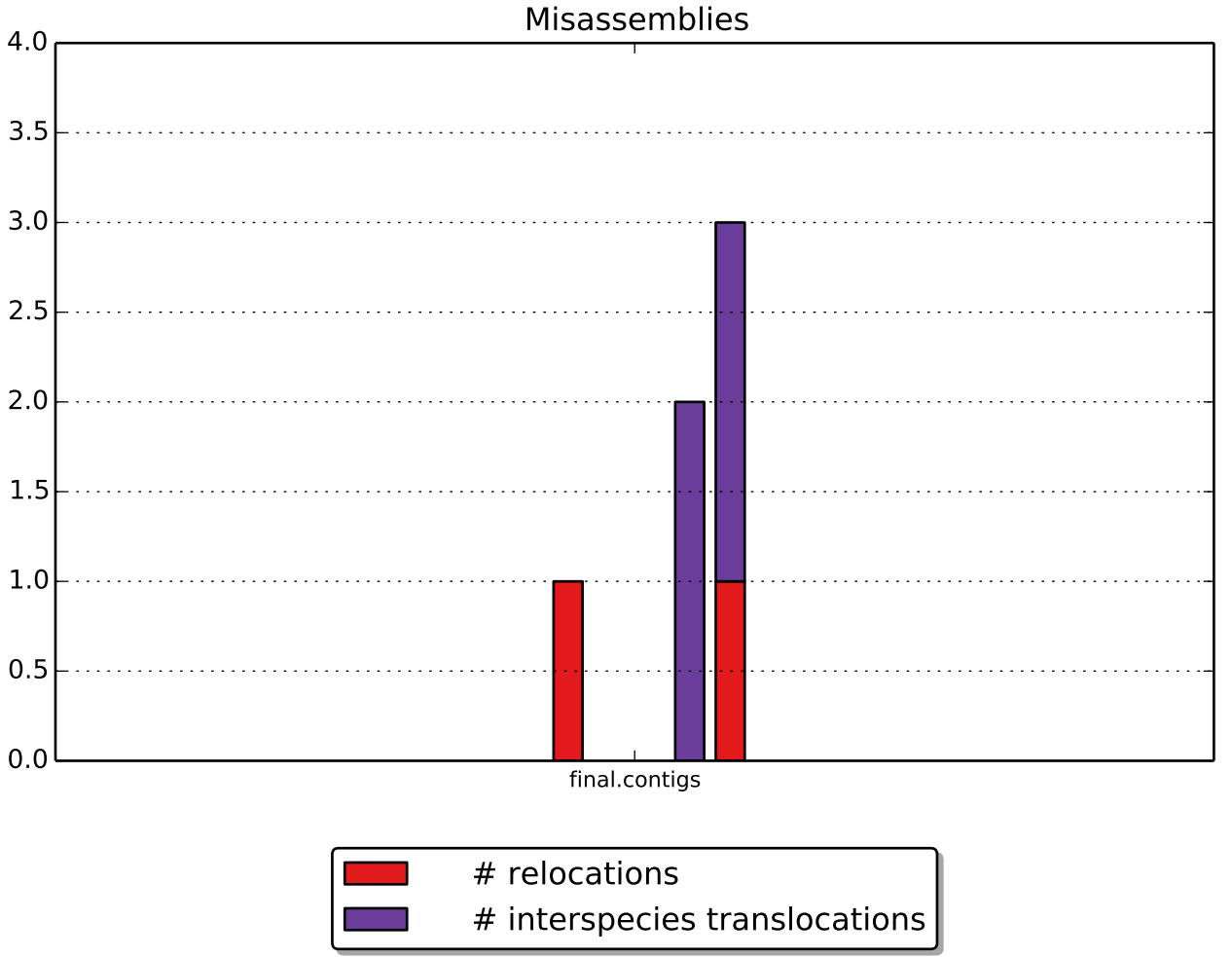
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

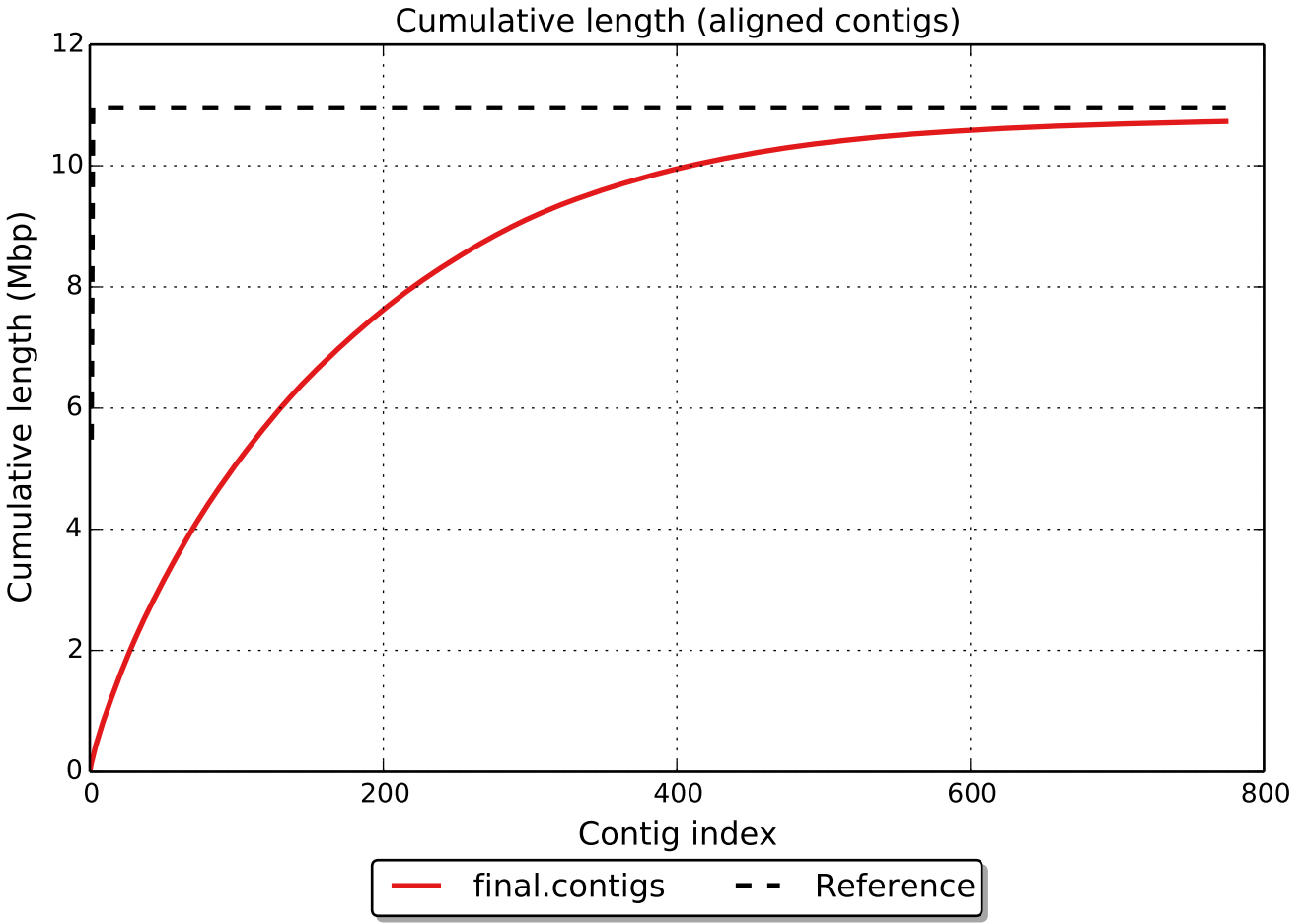

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
200
400
600
800
Contig index
final.contigs
Reference

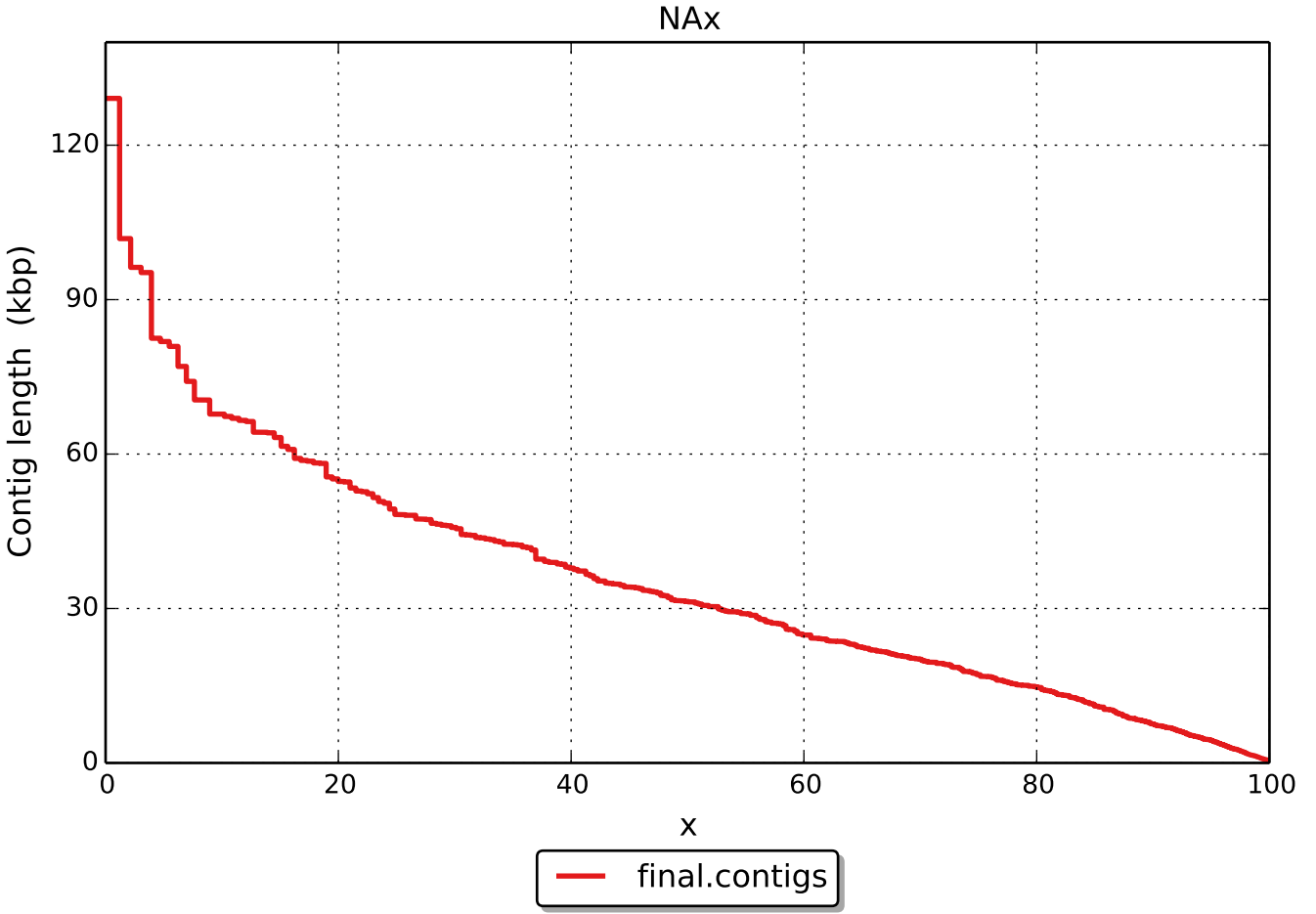

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

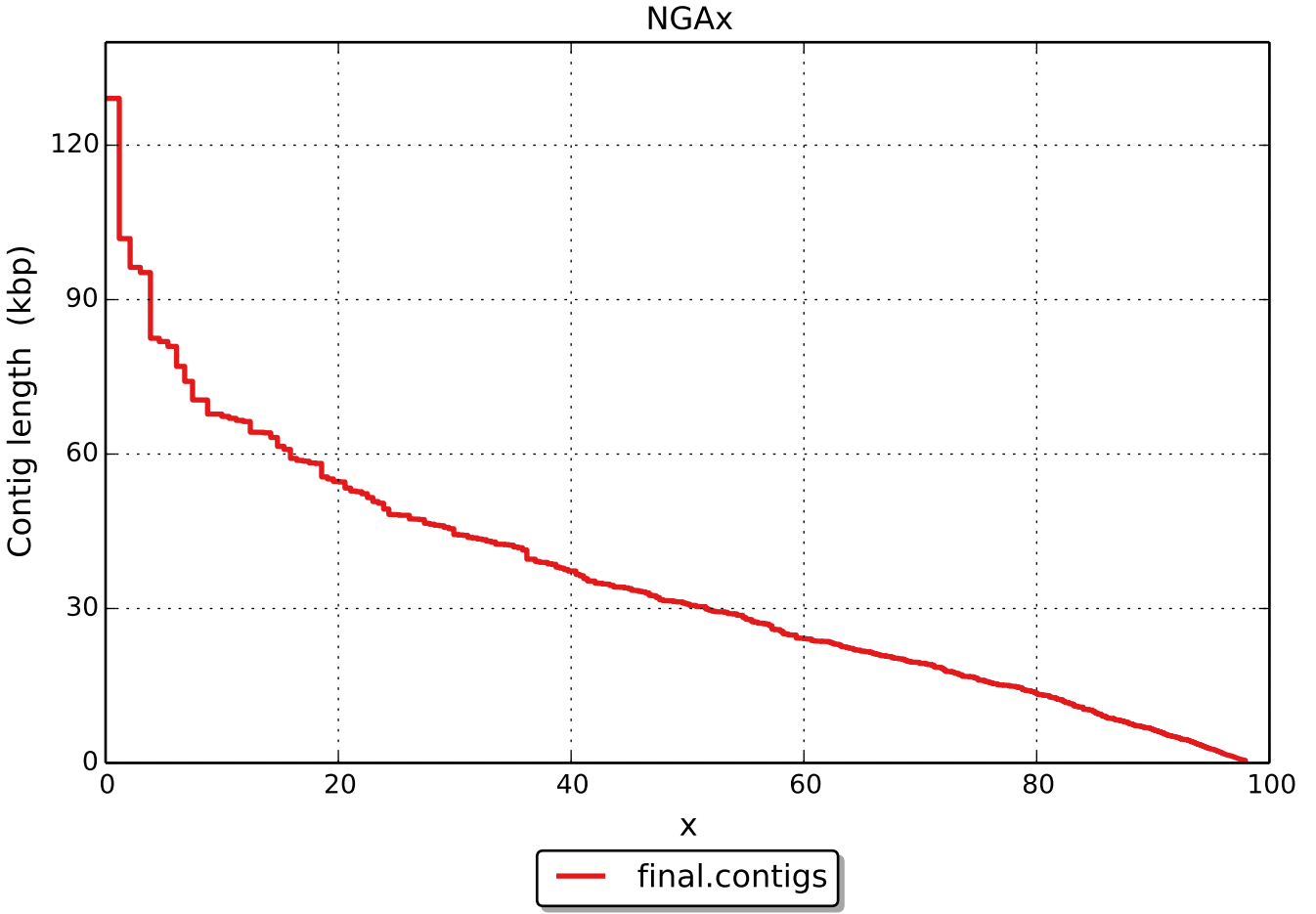

Nx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
120
90
60
30
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)
Contig index
0
2
4
6
8
10
12
0
200
400
600
800
final.contigs
Reference


NAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
120
90
60
30
0
0
20
40
60
80
100
x
final.contigs