Report

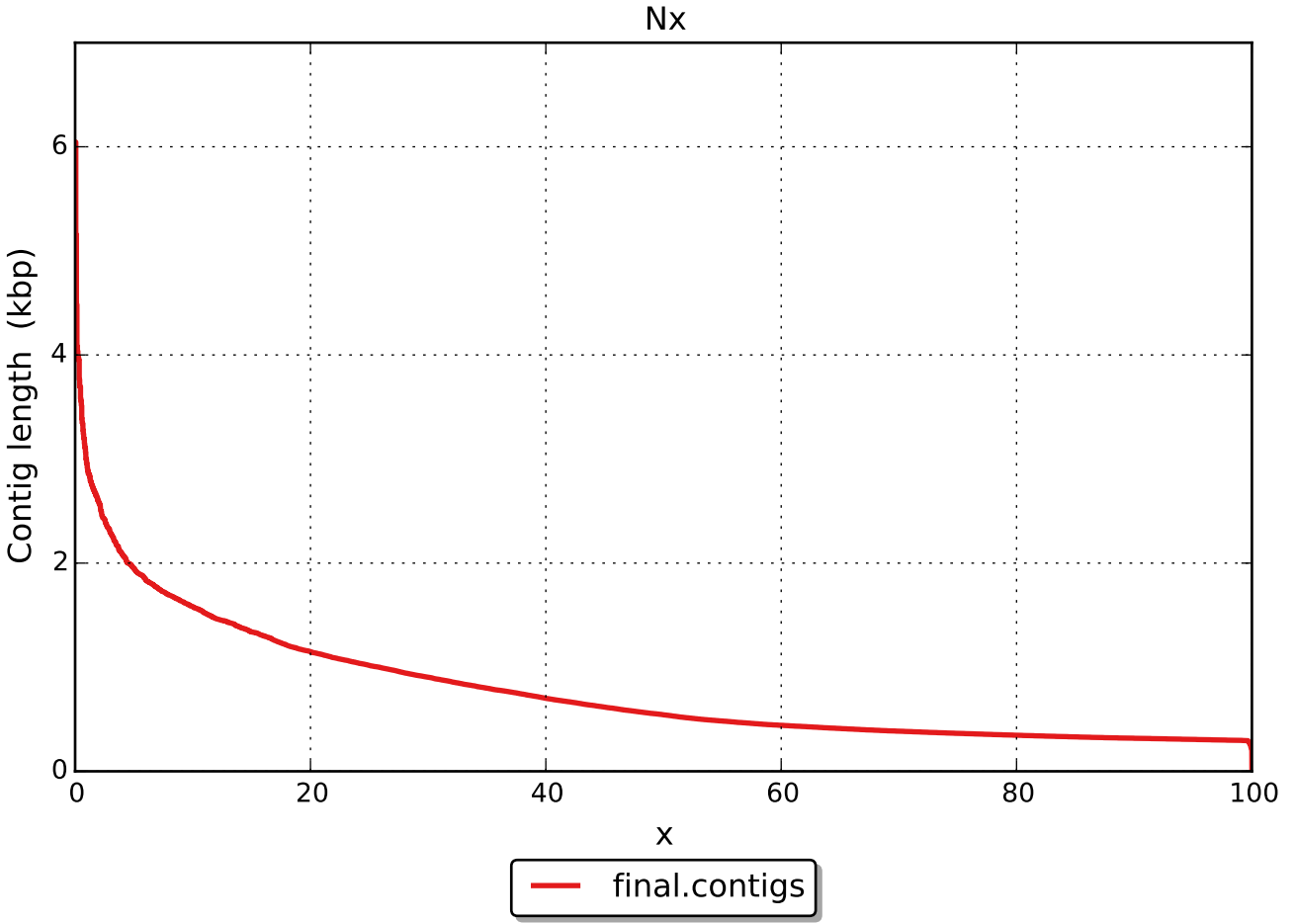
	final.contigs
# contigs (>= 0 bp)	19079
# contigs (>= 1000 bp)	1825
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	10223444
Total length (>= 1000 bp)	2641490
Total length (>= 5000 bp)	11201
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	19079
Largest contig	6045
Total length	10223444
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	542
NG50	1074
N75	365
NG75	817
L50	5221
LG50	1516
L75	11186
LG75	2756
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	17600 + 51 part
Unaligned length	8481546
Genome fraction (%)	36.616
Duplication ratio	1.025
# N's per 100 kbp	0.00
# mismatches per 100 kbp	635.39
# indels per 100 kbp	0.18
Largest alignment	6045
NGA50	-

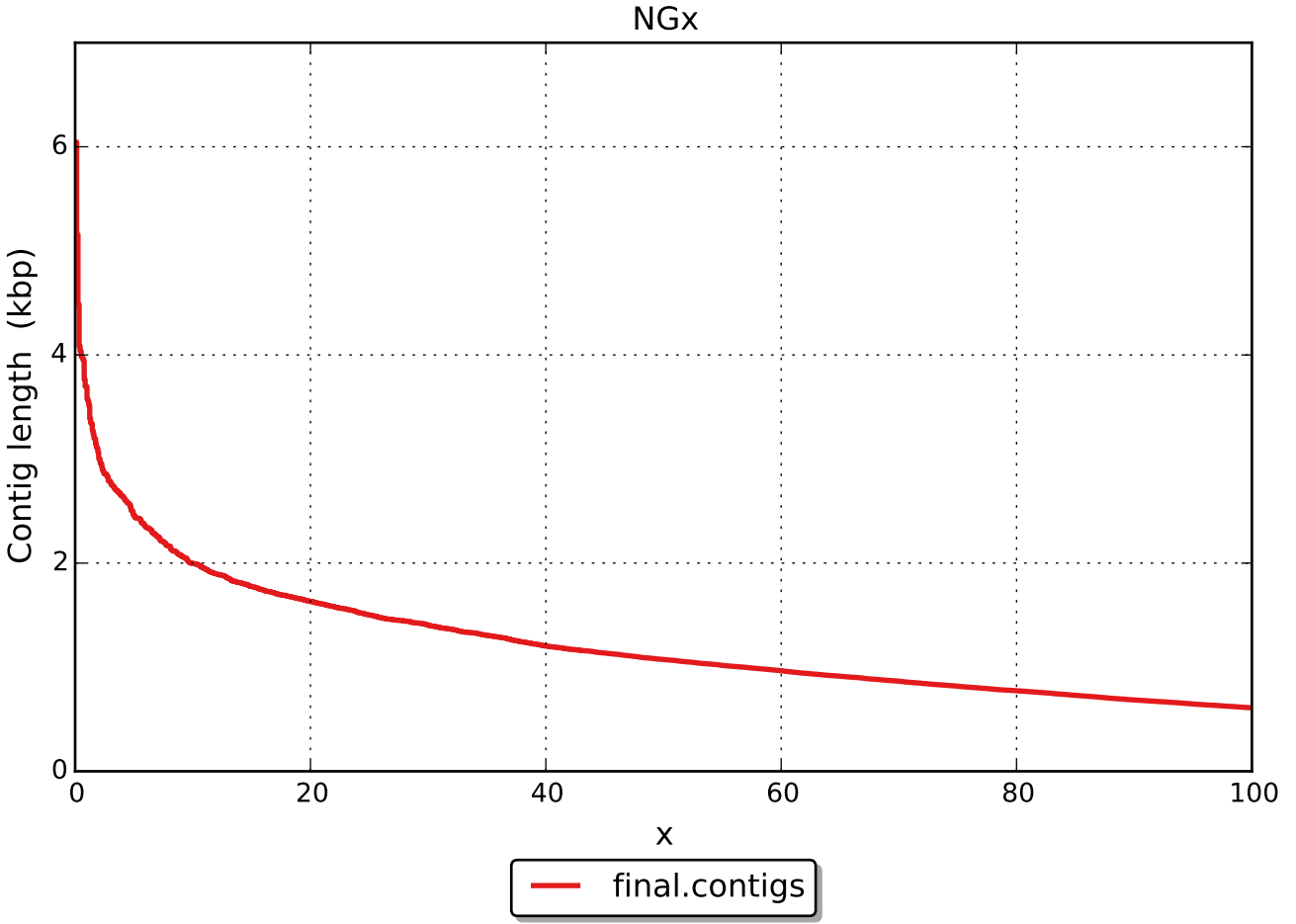
Misassemblies report

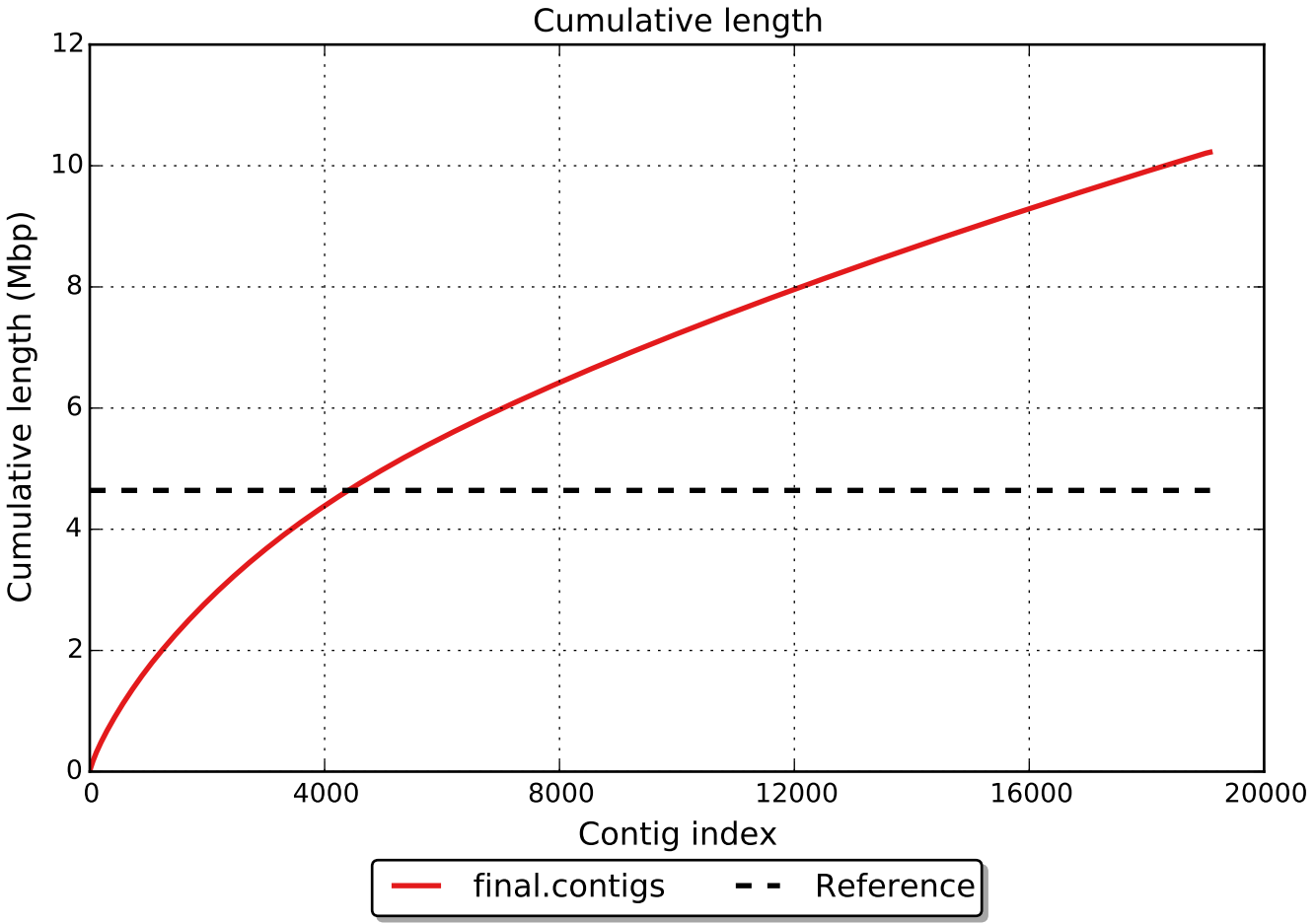
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	10799
# indels	3
# short indels	3
# long indels	0
Indels length	3

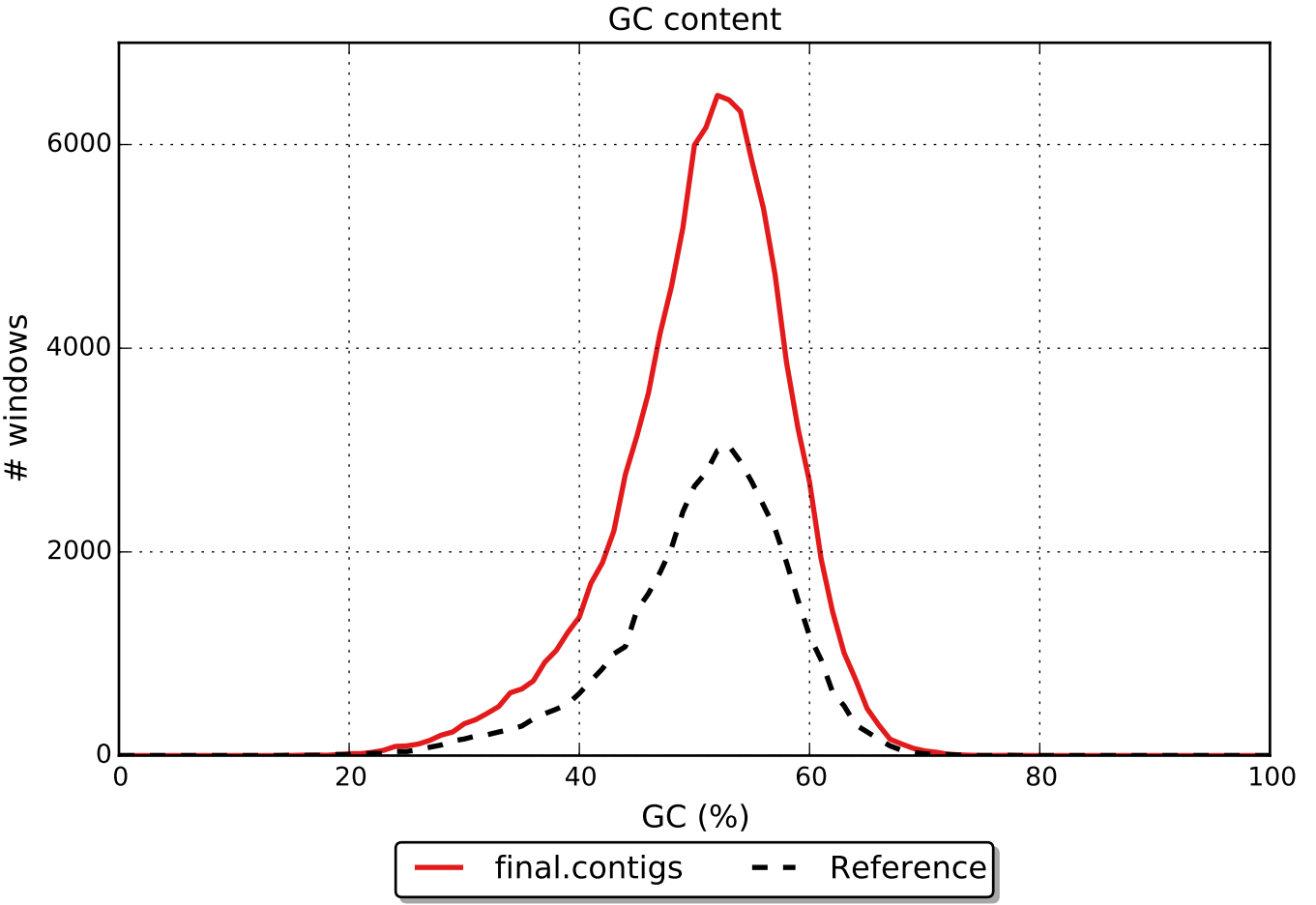
Unaligned report

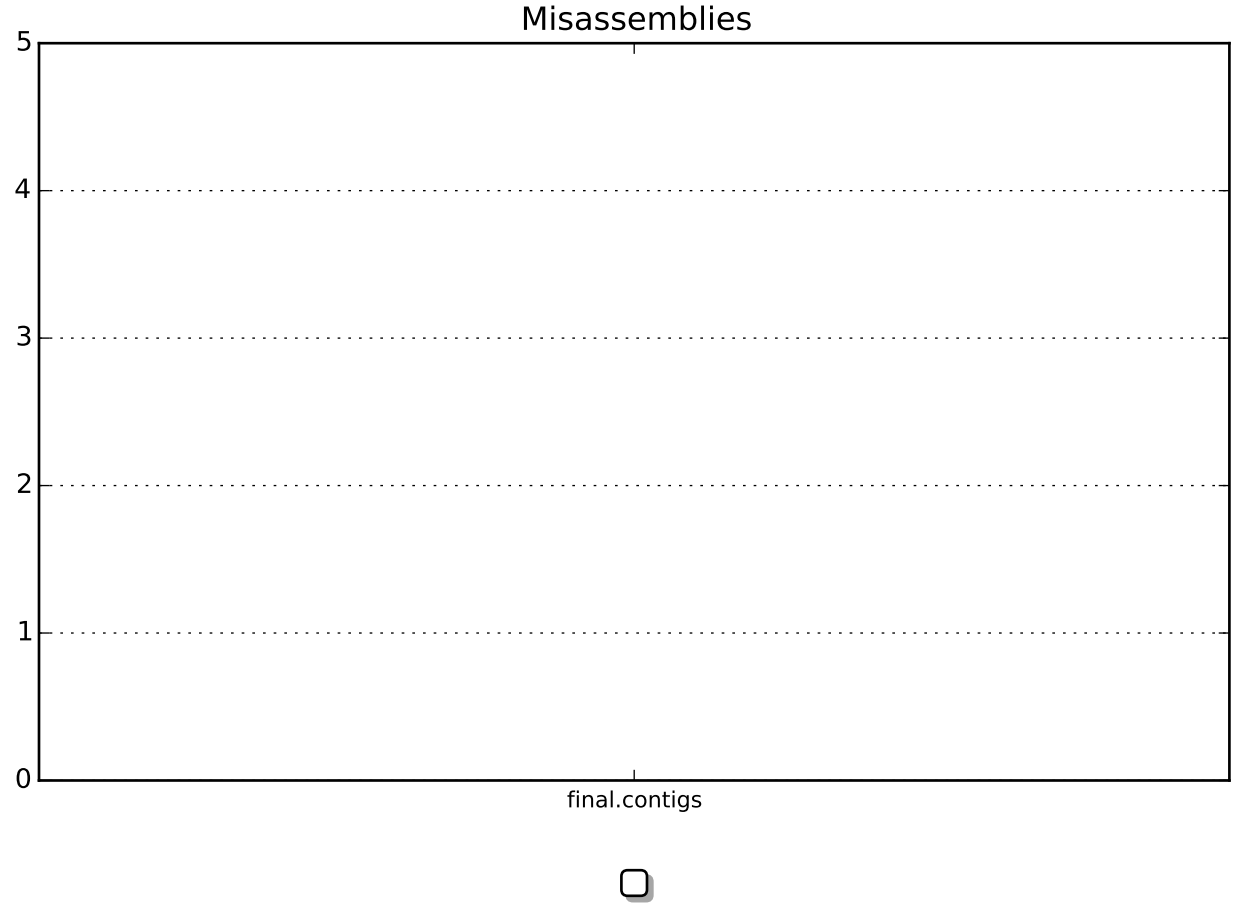
	final.contigs
# fully unaligned contigs	17600
Fully unaligned length	8460845
# partially unaligned contigs	51
# with misassembly	2
# both parts are significant	51
Partially unaligned length	20701
# N's	0

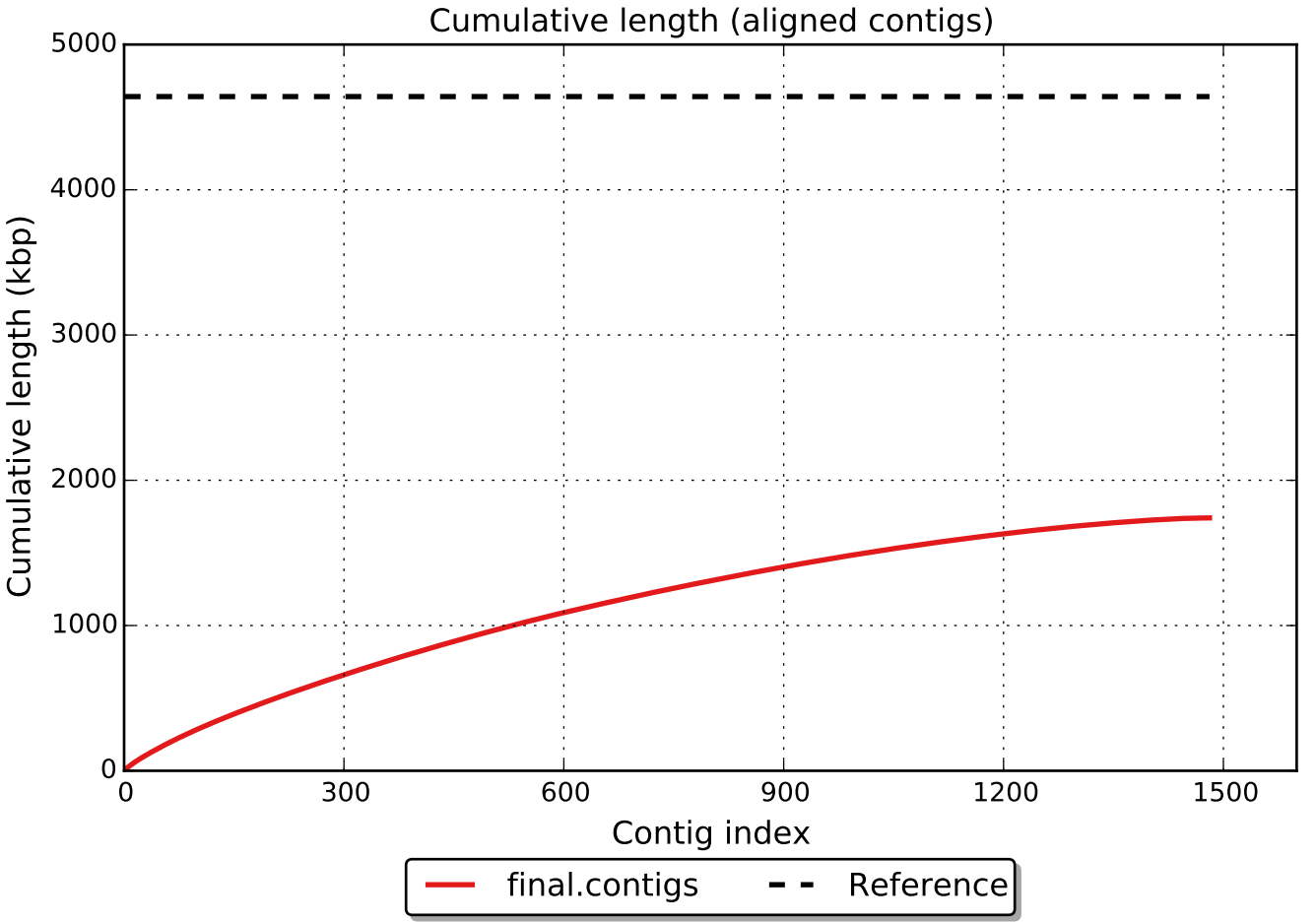

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

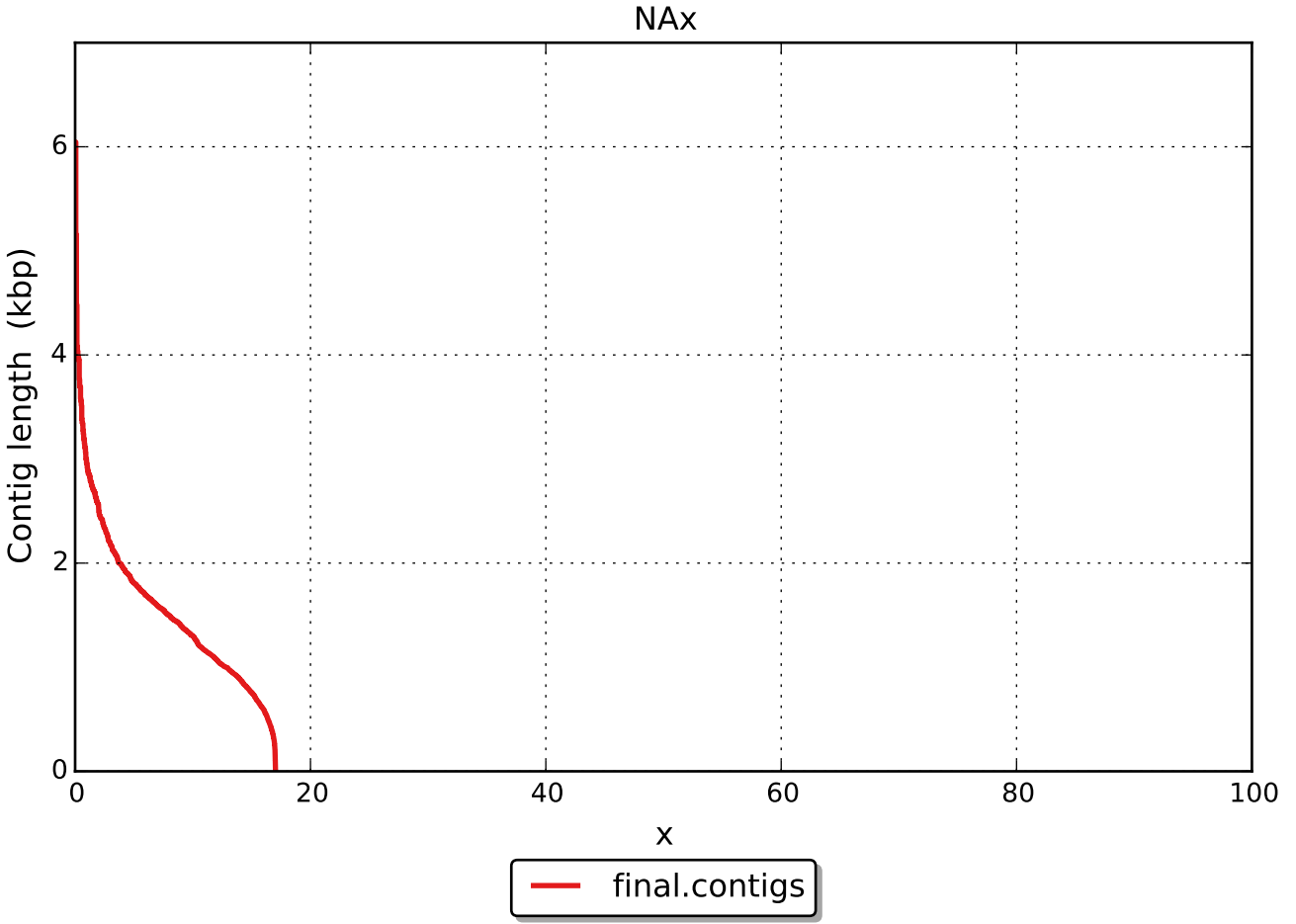

NGx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

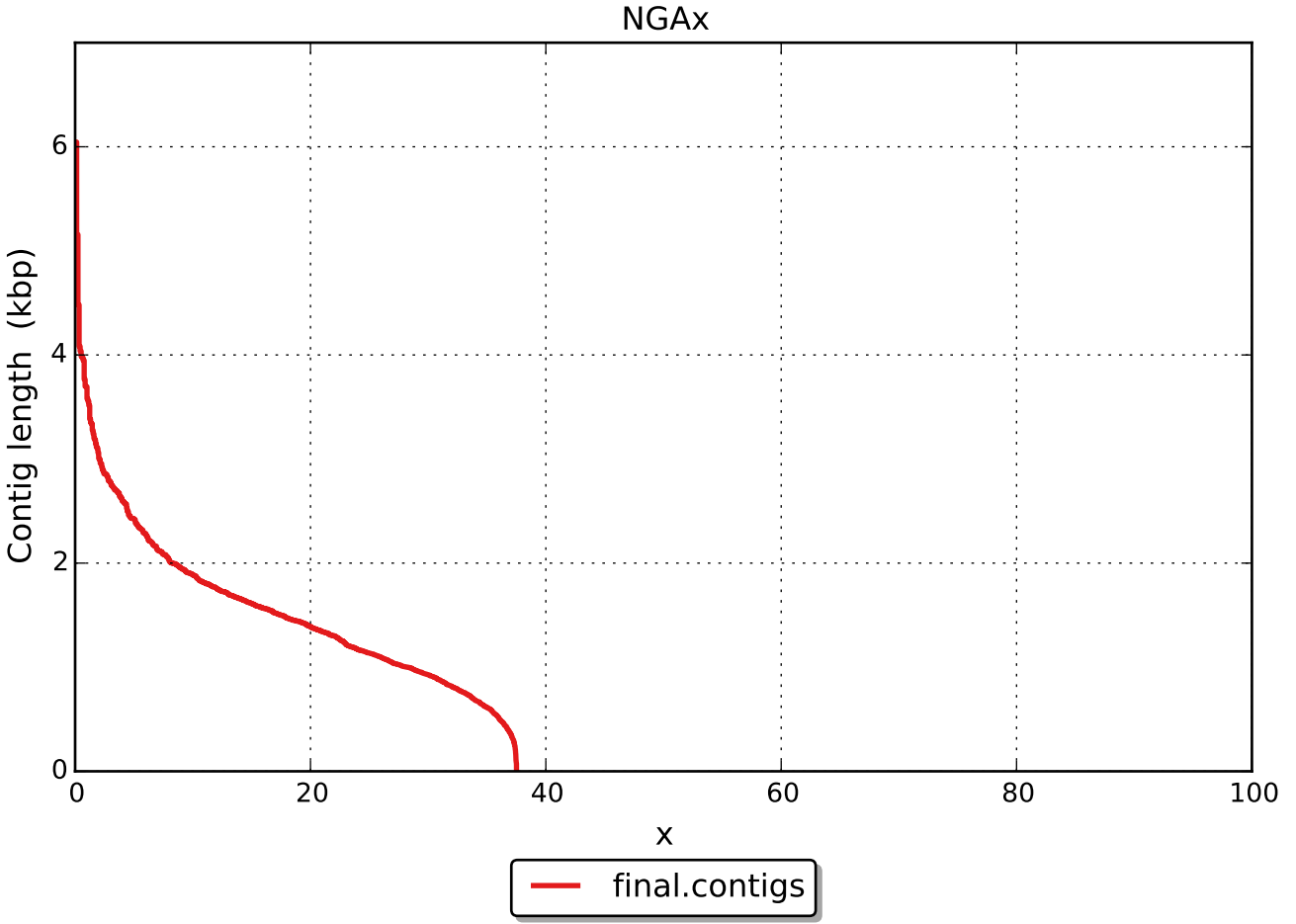

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
4000
8000
12000
16000
20000
Contig index
final.contigs
Reference


GC content
windows
6000
4000
2000
0
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
300
600
900
1200
1500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs