

Report

	final.contigs
# contigs (>= 1000 bp)	1511
# contigs (>= 5000 bp)	108
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3903367
Total length (>= 5000 bp)	709559
Total length (>= 10000 bp)	48458
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2044
Largest contig	14149
Total length	4302638
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	2830
NG50	2637
N75	1666
NG75	1433
L50	500
LG50	562
L75	997
LG75	1161
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	30951
# local misassemblies	10
# unaligned contigs	0 + 4 part
Unaligned length	169
Genome fraction (℥)	91.983
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	207.35
# indels per 100 kbp	9.84
Largest alignment	14149
NA50	2825
NGA50	2636
NA75	1662
NGA75	1427
LA50	502
LGA50	564
LA75	1000
LGA75	1165

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

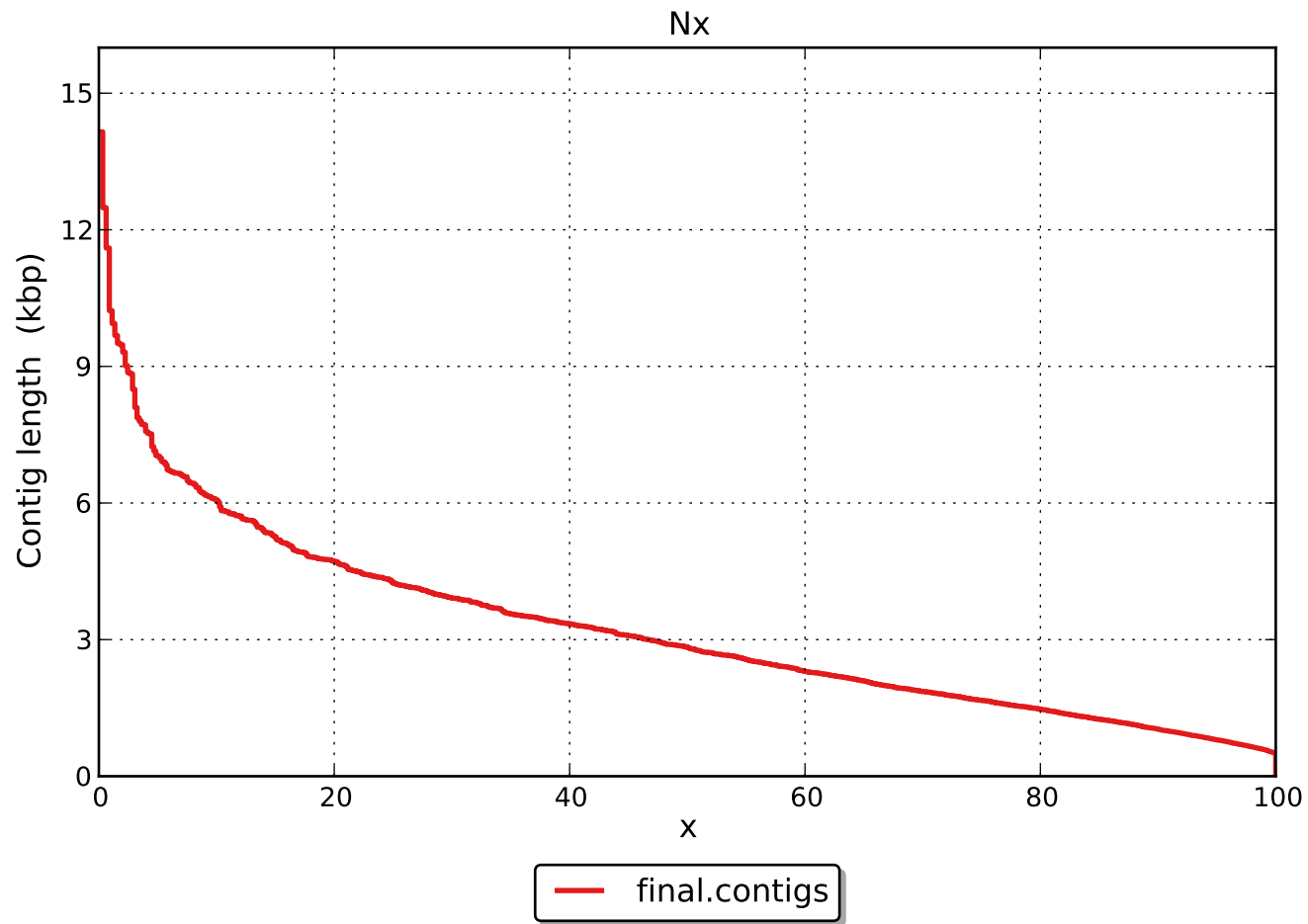
	final.contigs
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	7
Misassembled contigs length	30951
# local misassemblies	10
# mismatches	8853
# indels	420
# short indels	416
# long indels	4
Indels length	714

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

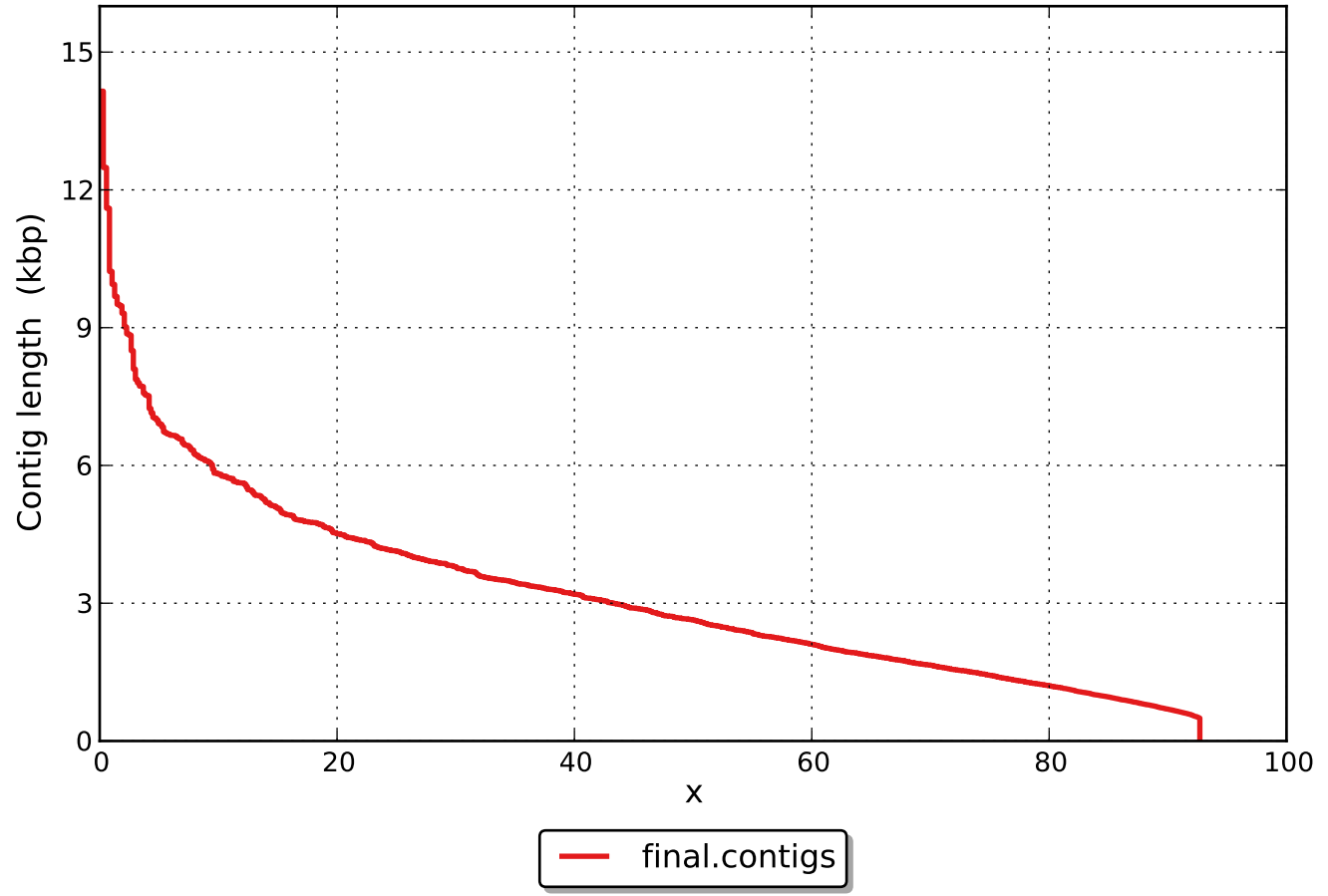
## Unaligned report

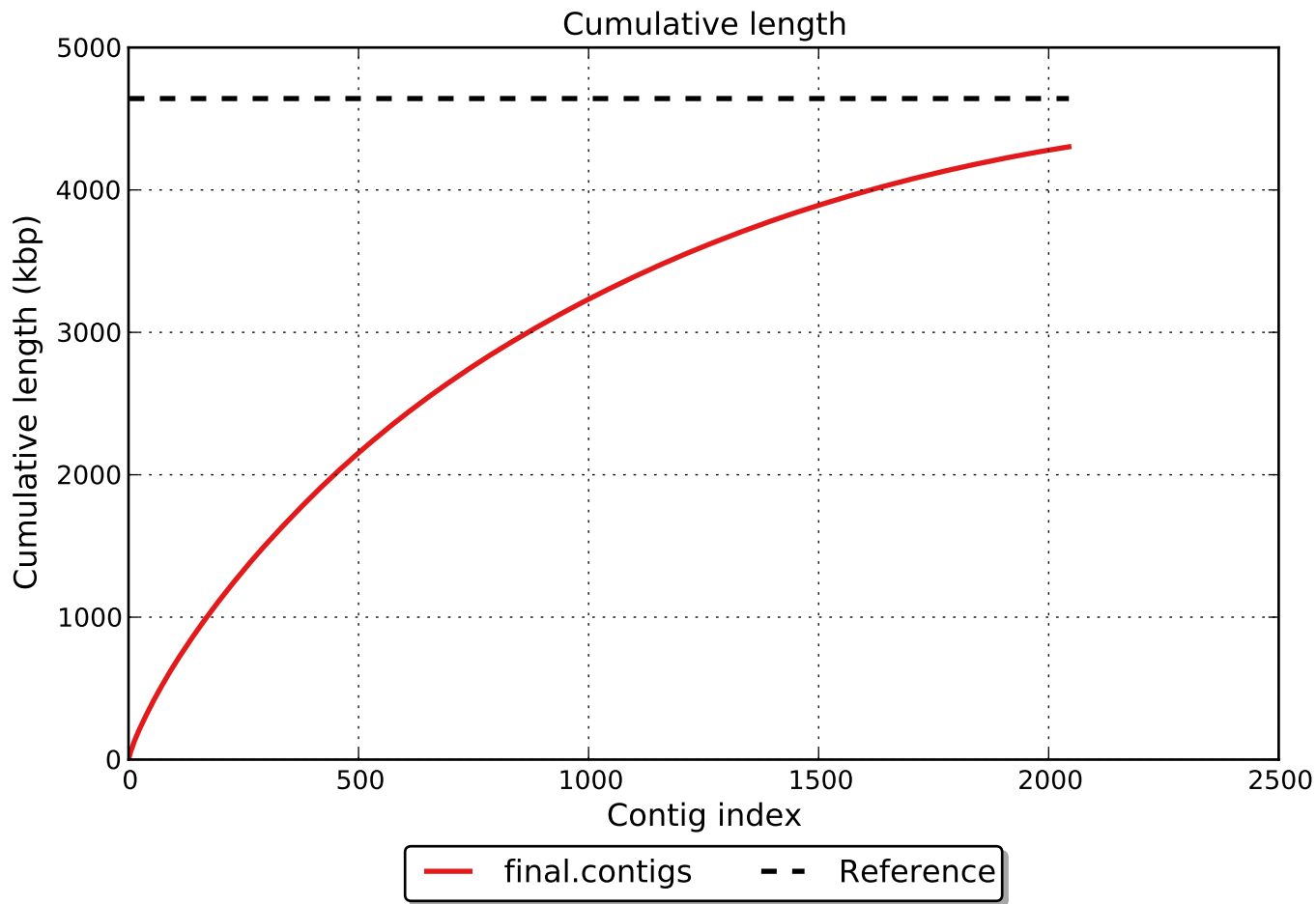
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	169
# N's	0

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

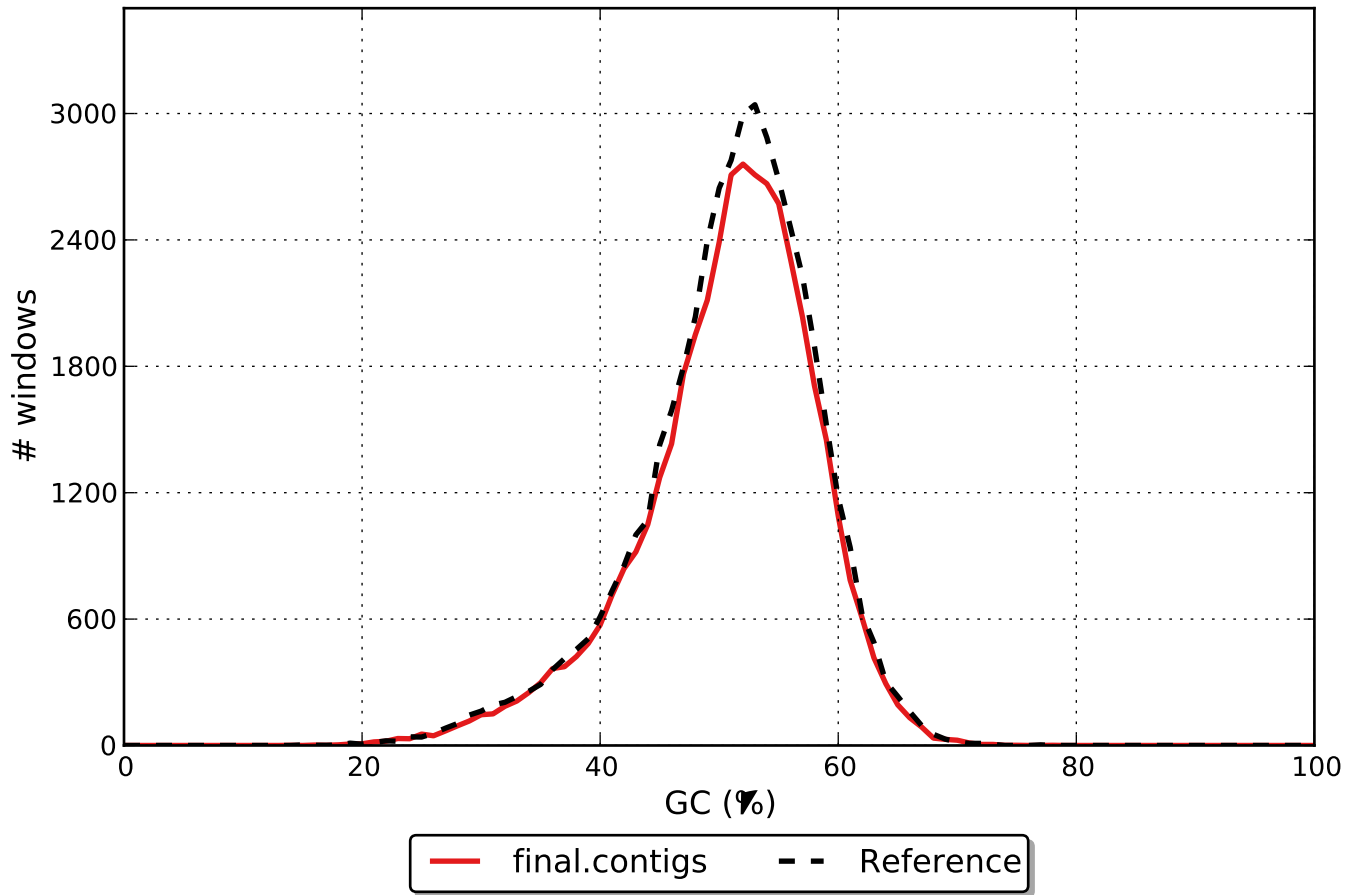


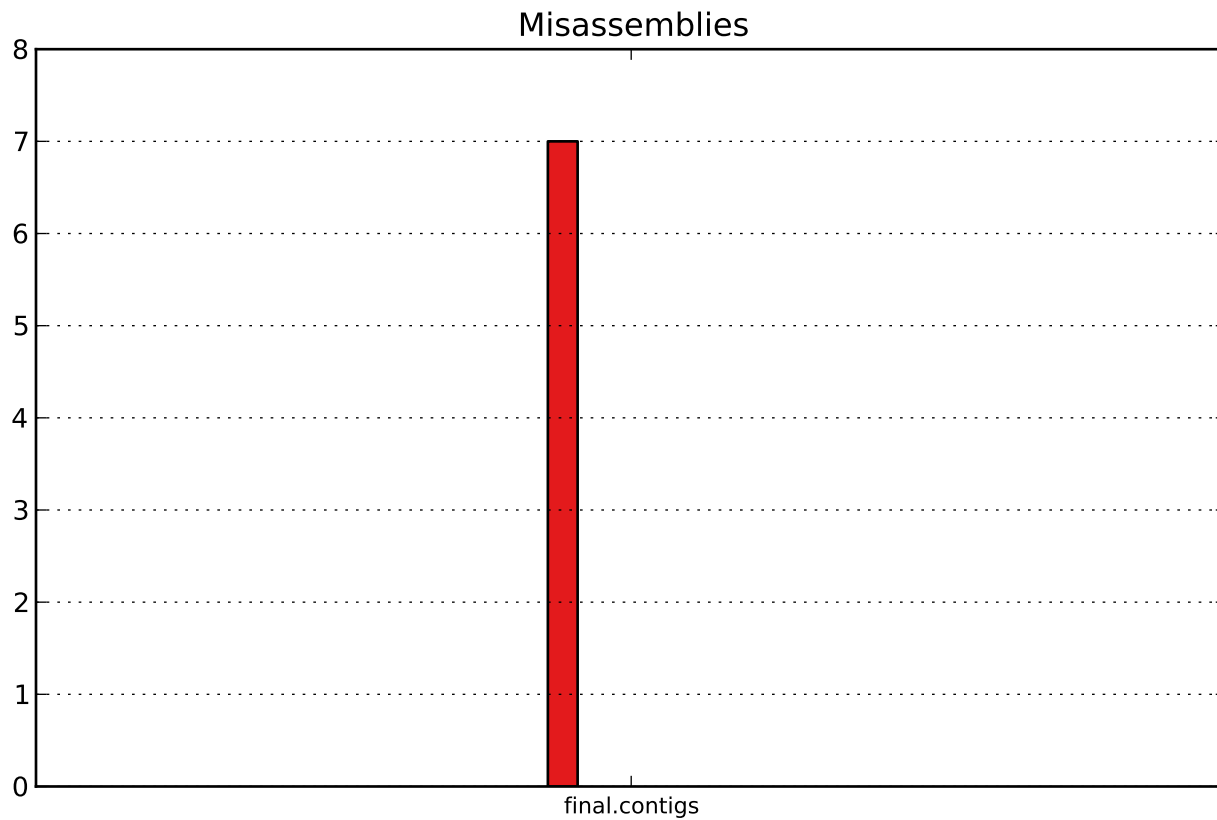
NGx





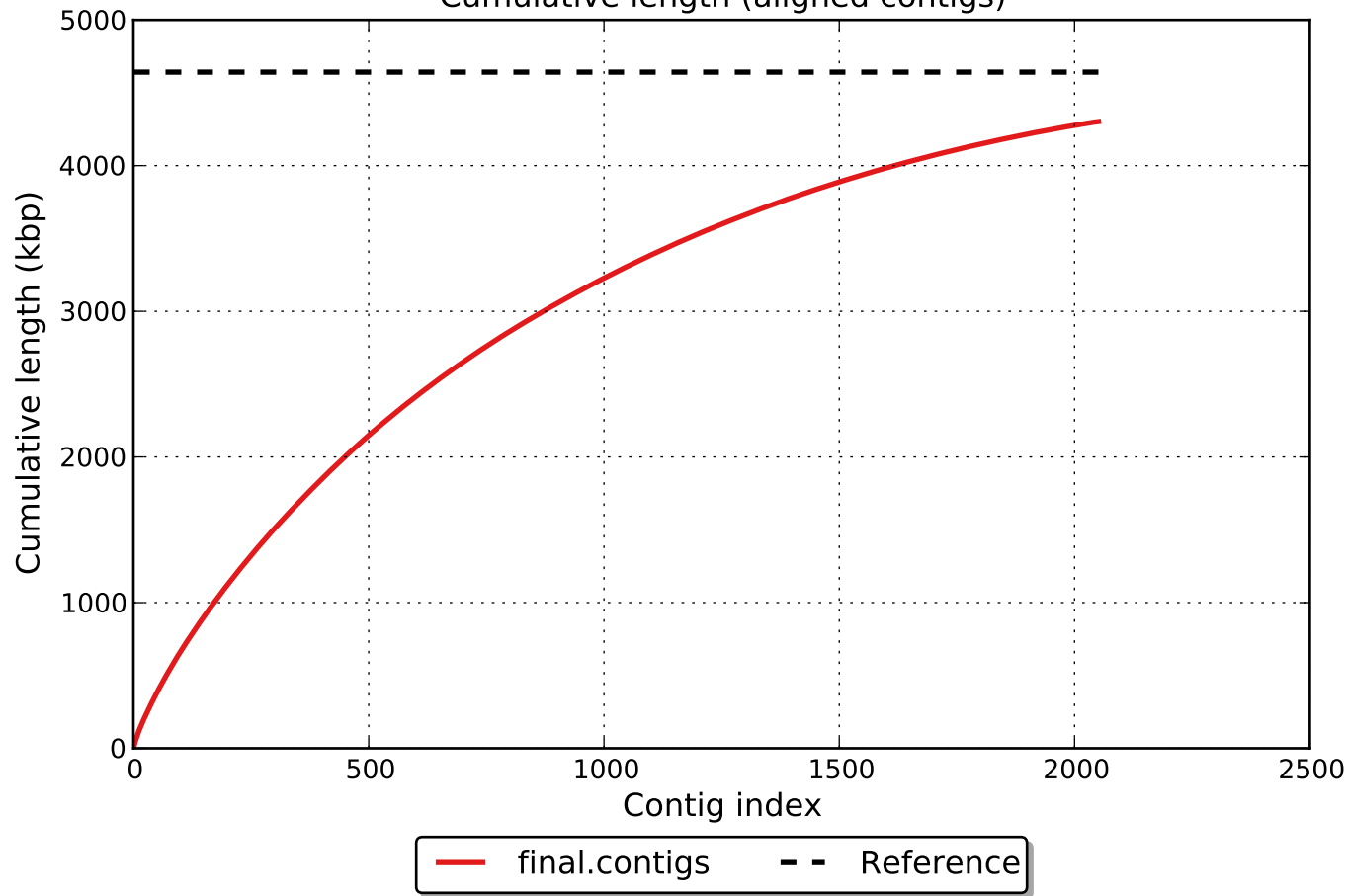
# GC content



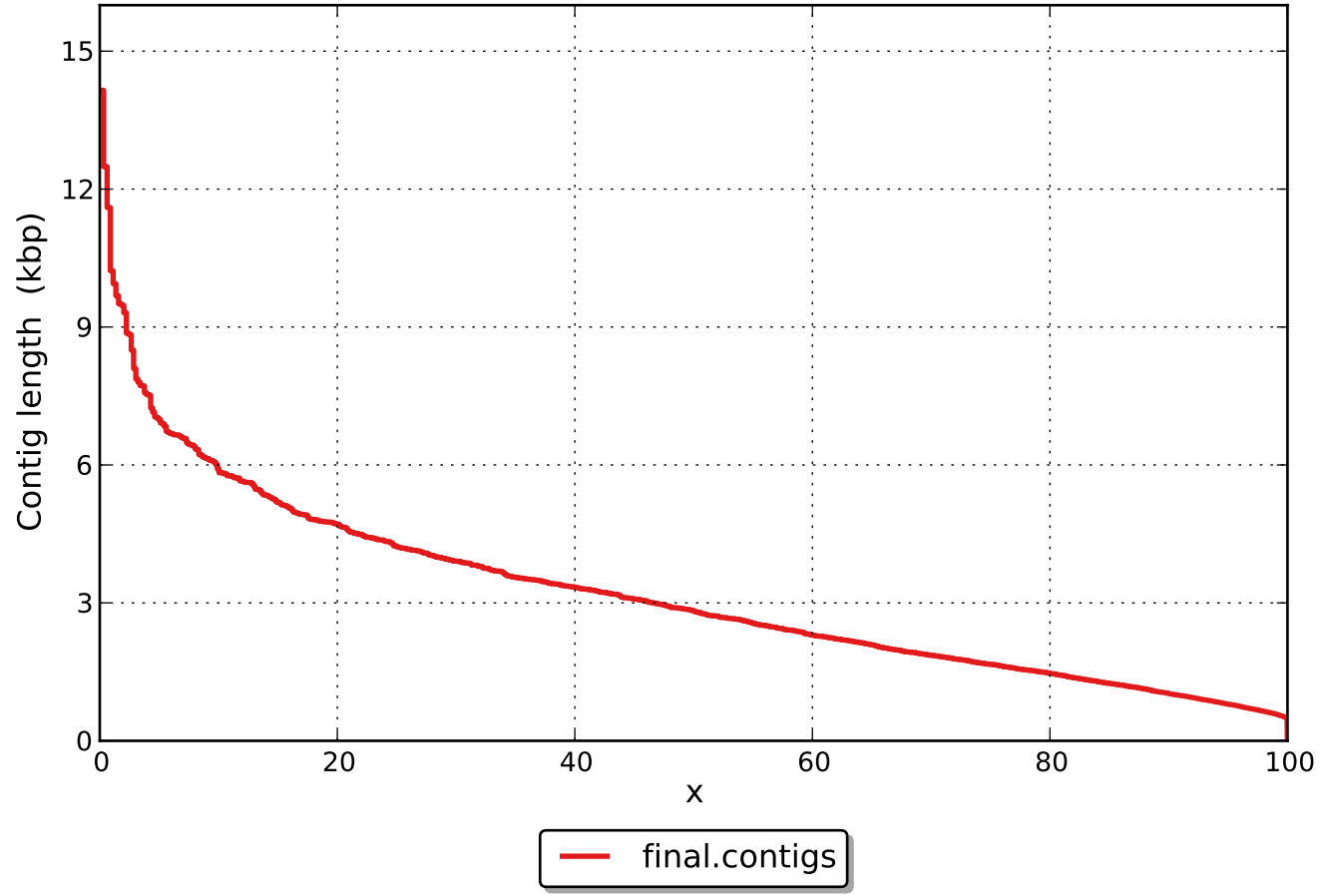




Cumulative length (aligned contigs)



NAx



NGAx

