

## Report

	final.contigs
# contigs ( $\geq 1000$ bp)	132
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	167143
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	1342
Largest contig	3469
Total length	956930
Reference length	4641652
GC (%)	50.55
Reference GC (%)	50.79
N50	692
N75	579
L50	517
L75	897
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	6799
# local misassemblies	2
# unaligned contigs	0 + 7 part
Unaligned length	566
Genome fraction (%)	20.427
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1382.25
# indels per 100 kbp	2.32
Largest alignment	3469
NA50	690
NGA50	-
NA75	578
LA50	518
LA75	900

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).

## Misassemblies report

	final.contigs
# misassemblies	6
# relocations	6
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	6799
# local misassemblies	2
# mismatches	13106
# indels	22
# short indels	22
# long indels	0
Indels length	30

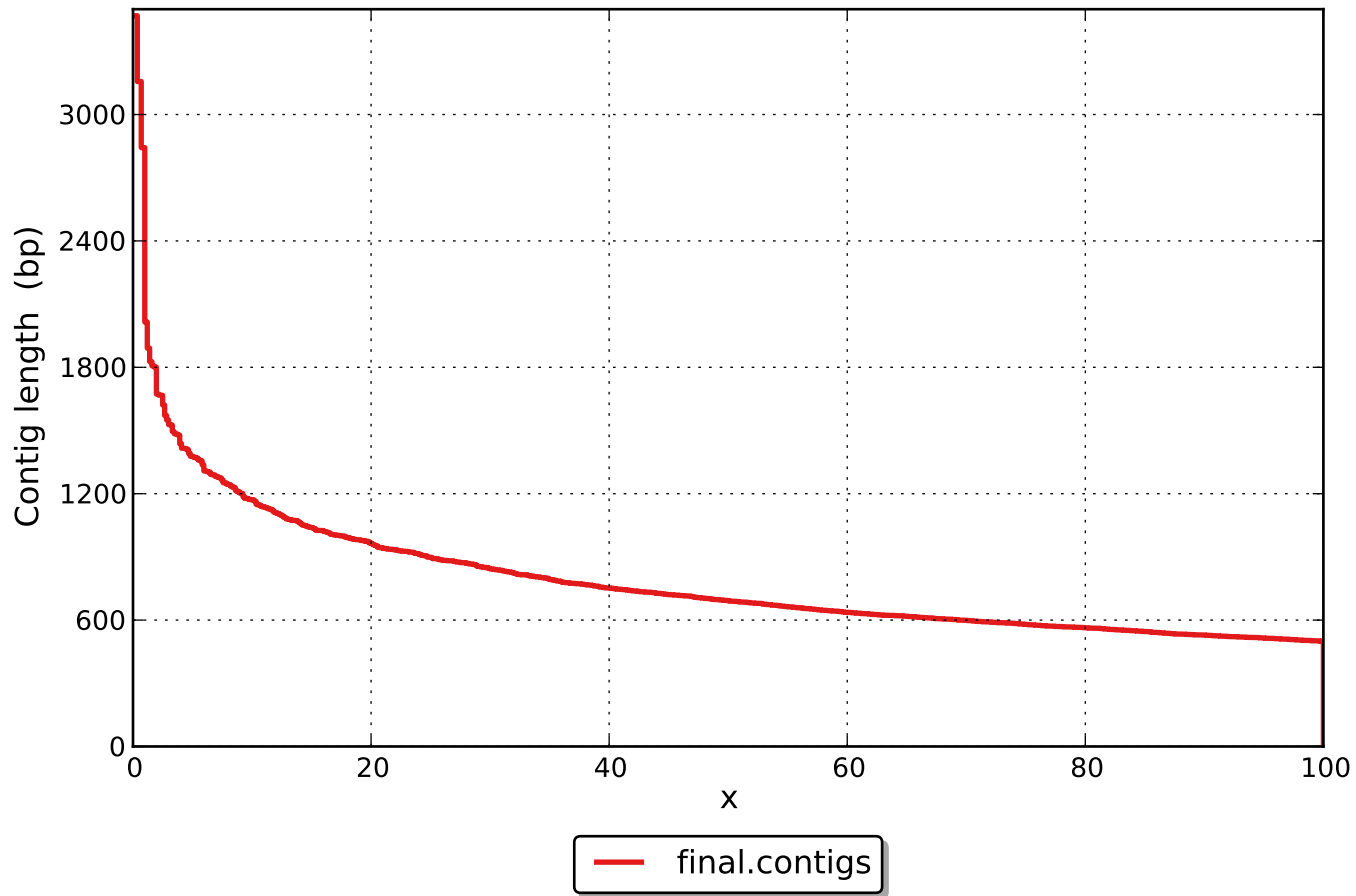
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

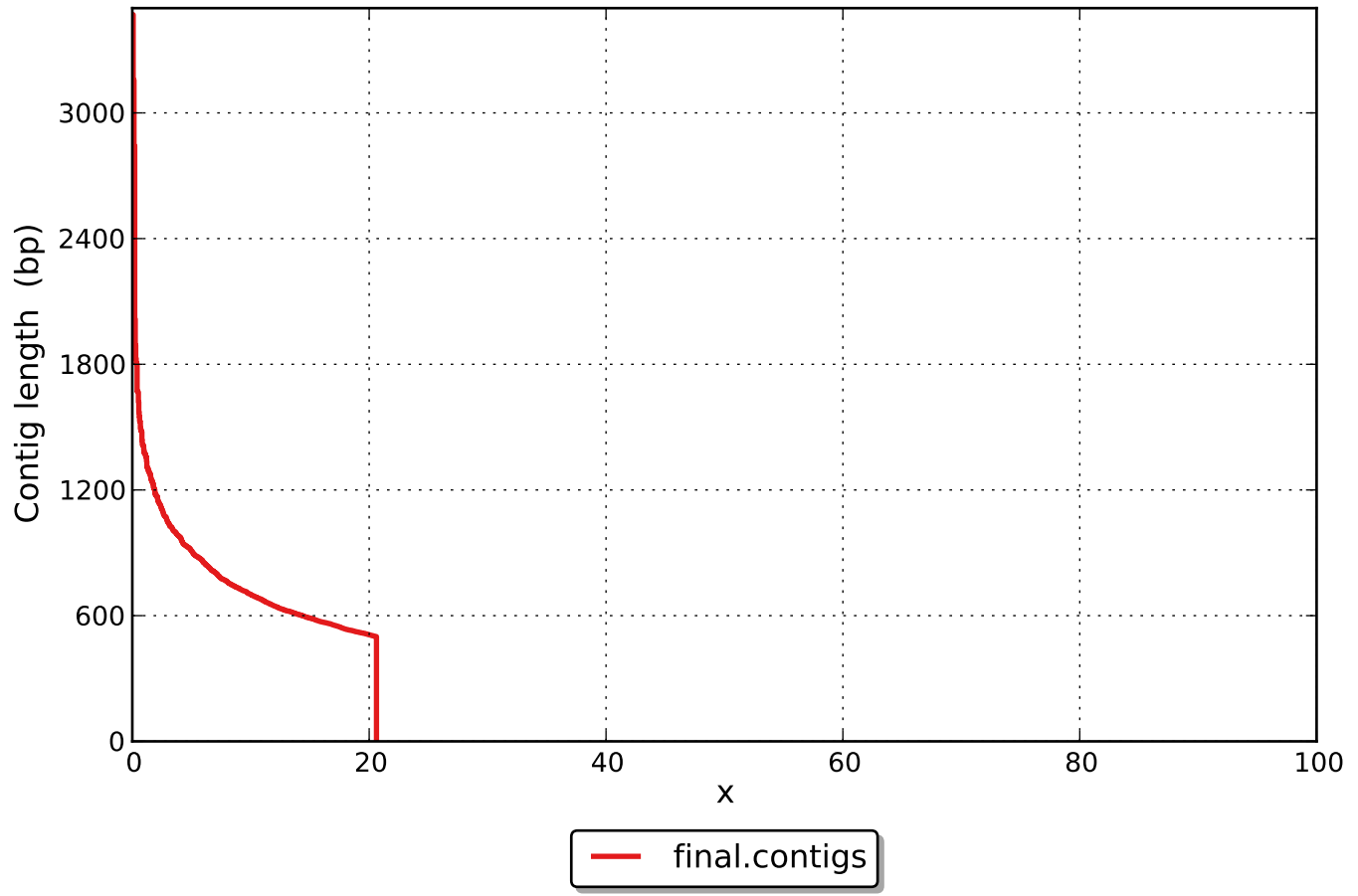
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	566
# N's	0

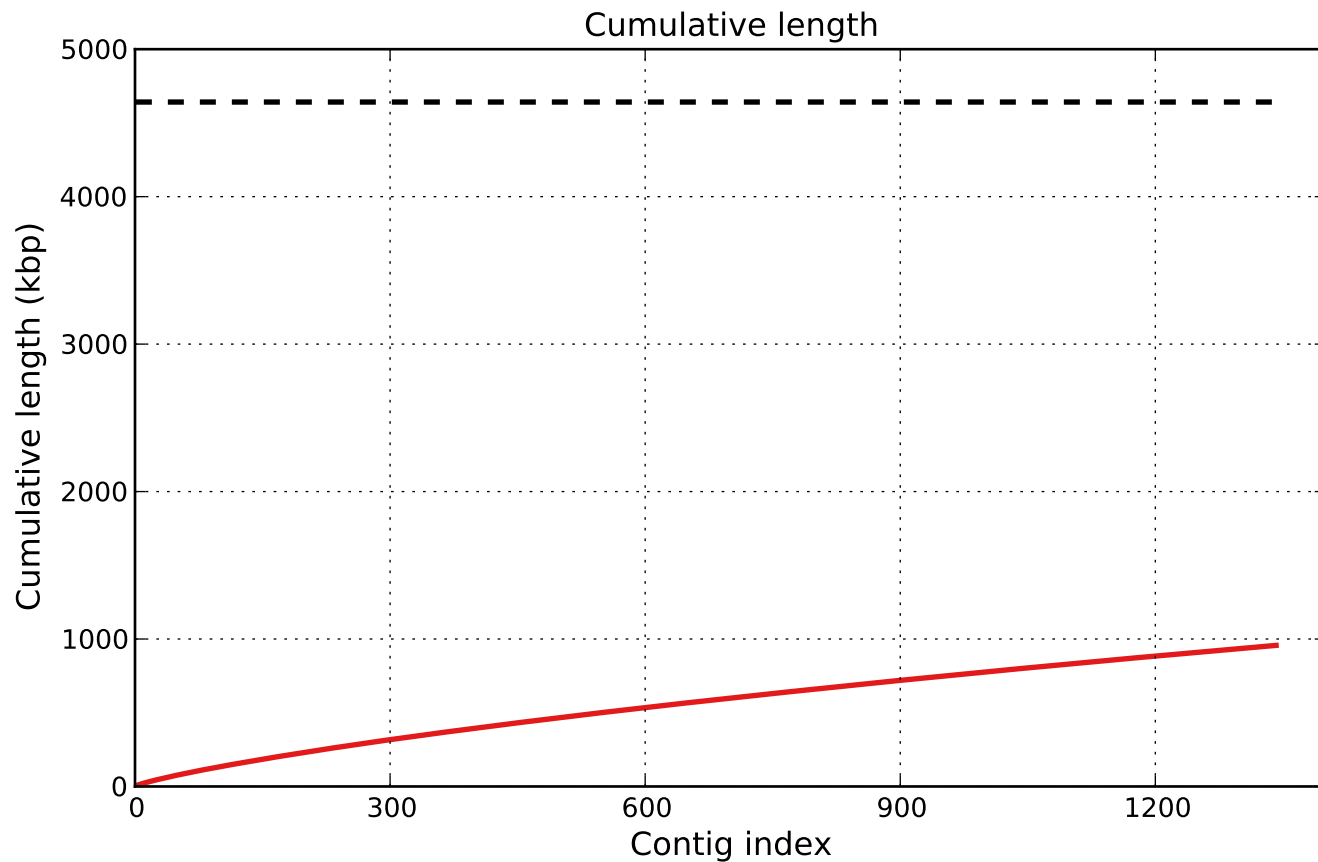
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

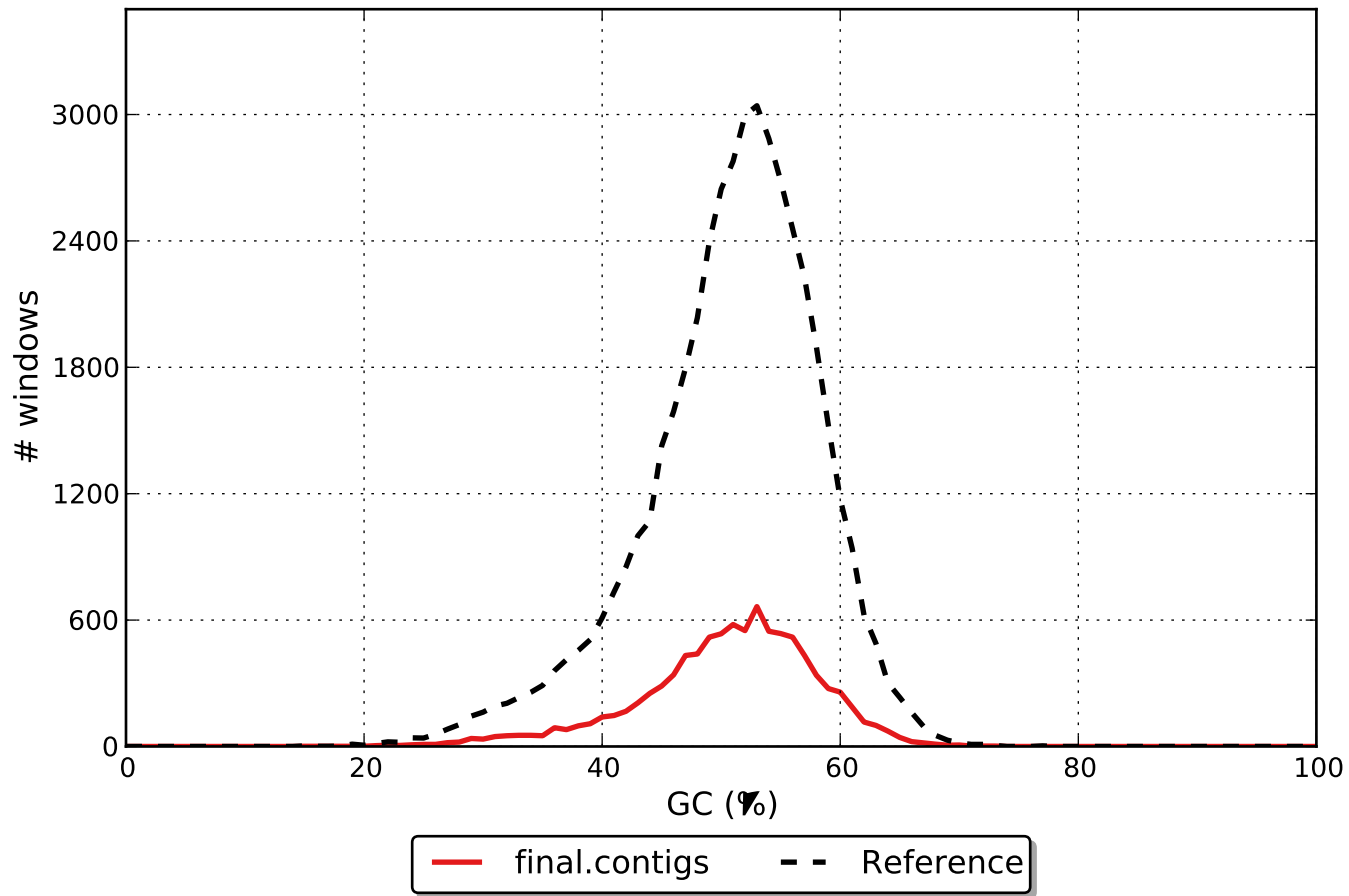


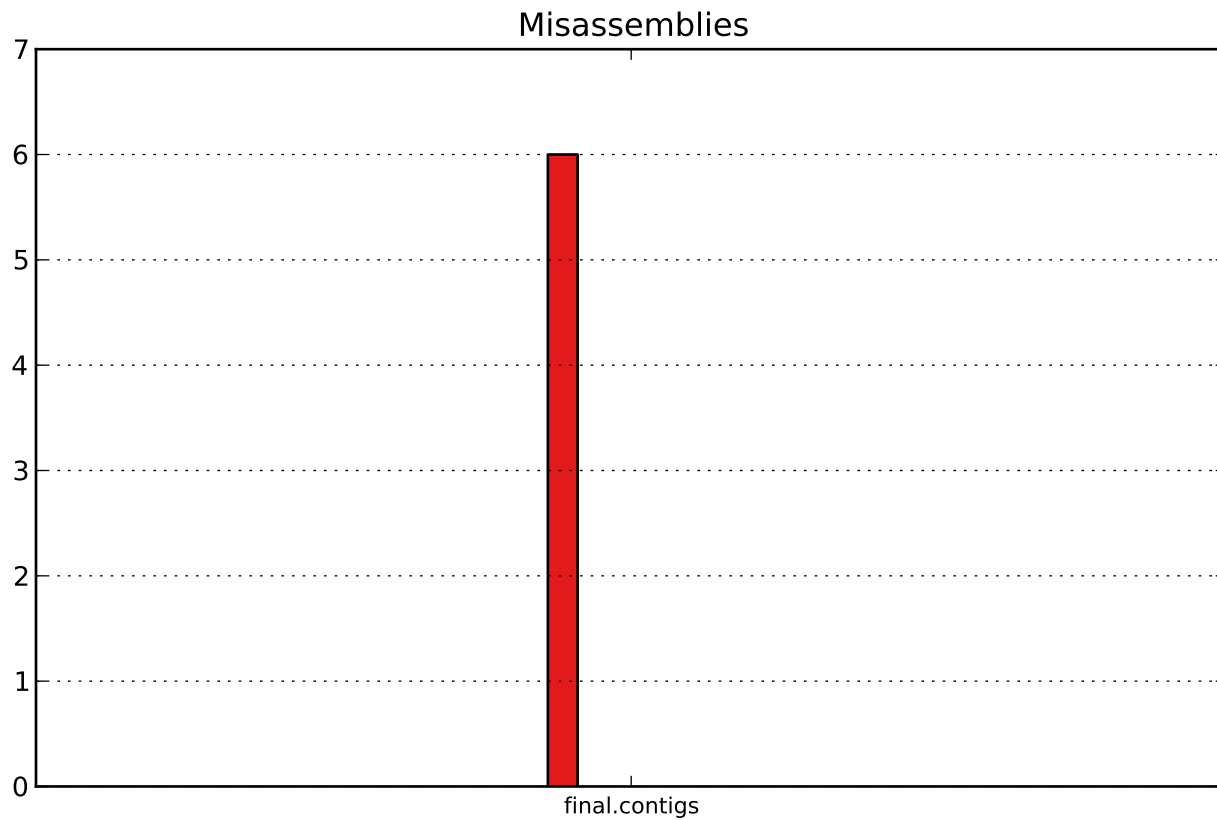
NGx





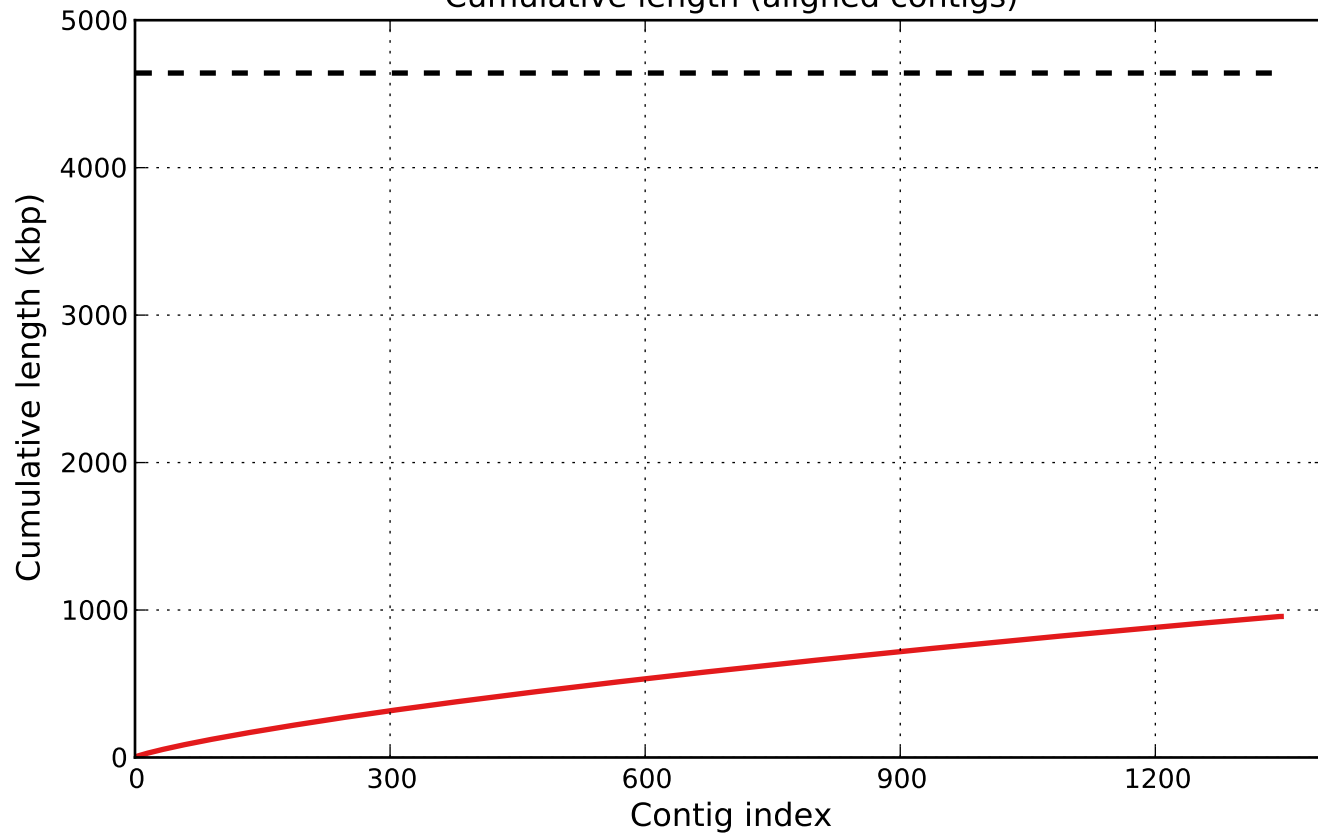
GC content





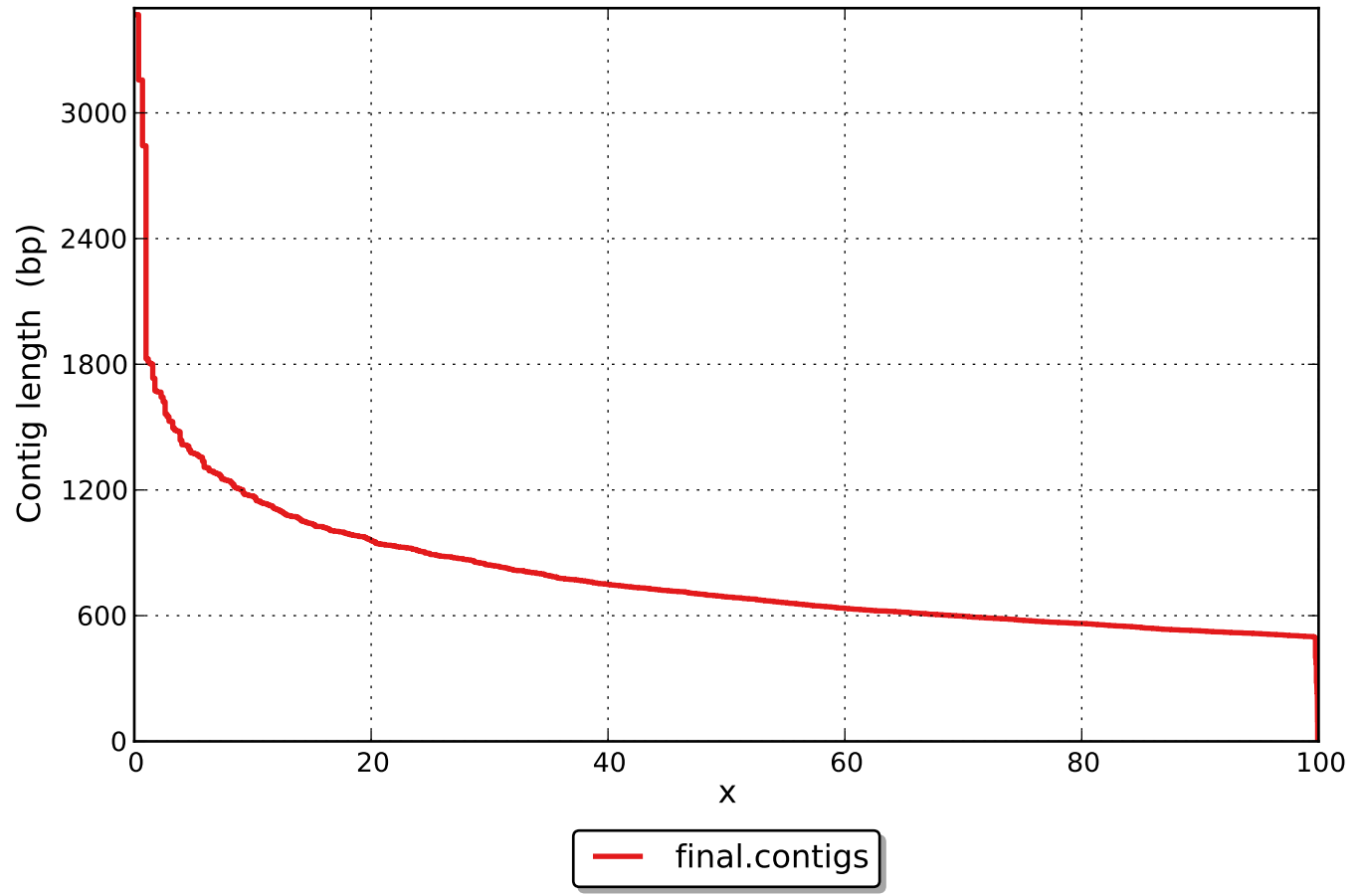


Cumulative length (aligned contigs)



— final.contigs      - - Reference

NAx



NGAx

