

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1530
# contigs ( $\geq 1000$ bp)	286
Total length ( $\geq 0$ bp)	1102952
Total length ( $\geq 1000$ bp)	416895
# contigs	975
Largest contig	4410
Total length	898866
Reference length	1231960
GC (%)	25.49
Reference GC (%)	25.35
N50	956
NG50	753
N75	693
L50	320
LG50	517
L75	597
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	69.219
Duplication ratio	1.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	174.26
# indels per 100 kbp	0.00
Largest alignment	4410
NA50	956
NGA50	753
NA75	693
LA50	320
LGA50	517
LA75	597

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	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1486
# indels	0
# short indels	0
# long indels	0
Indels length	0

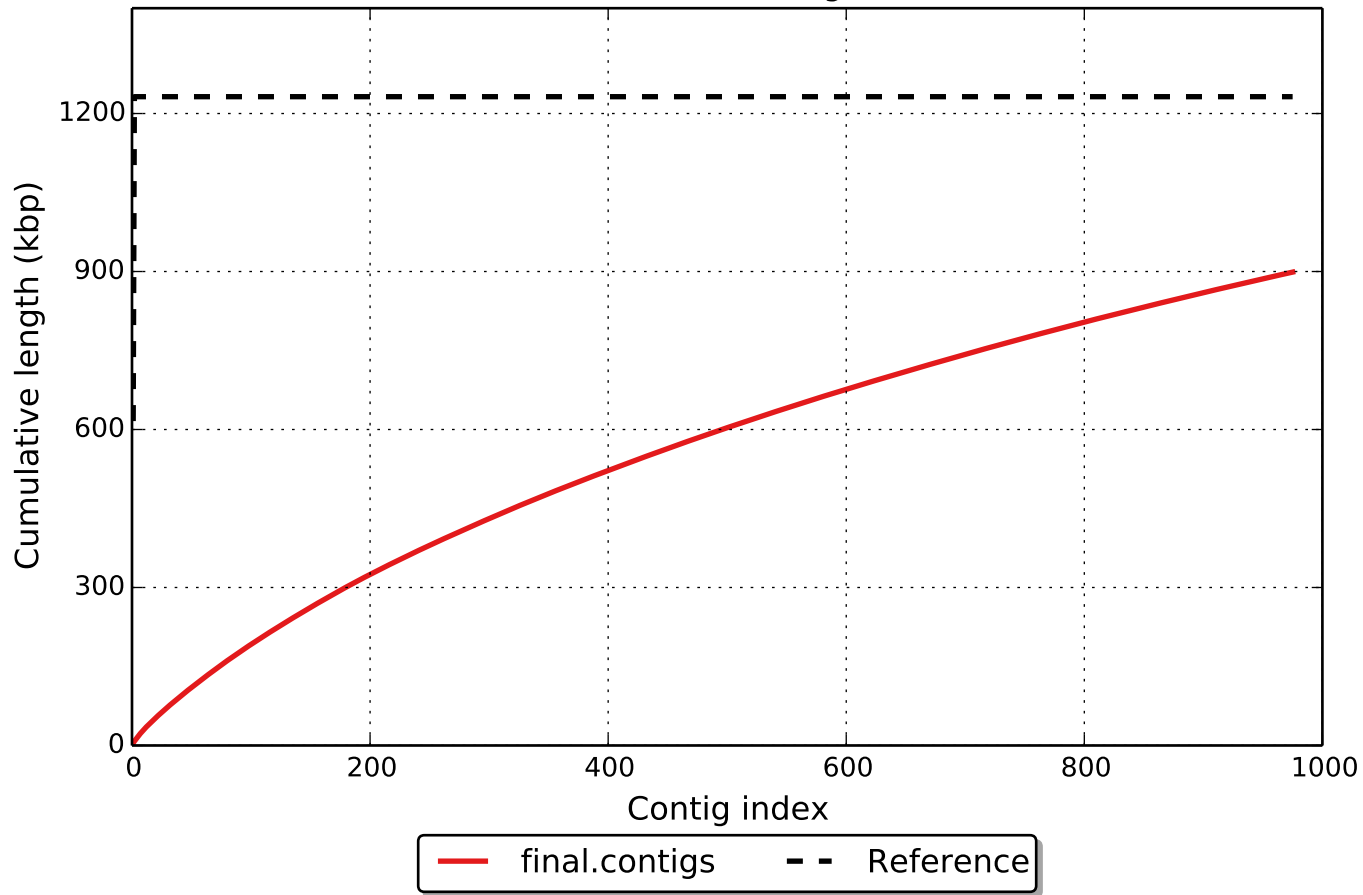
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

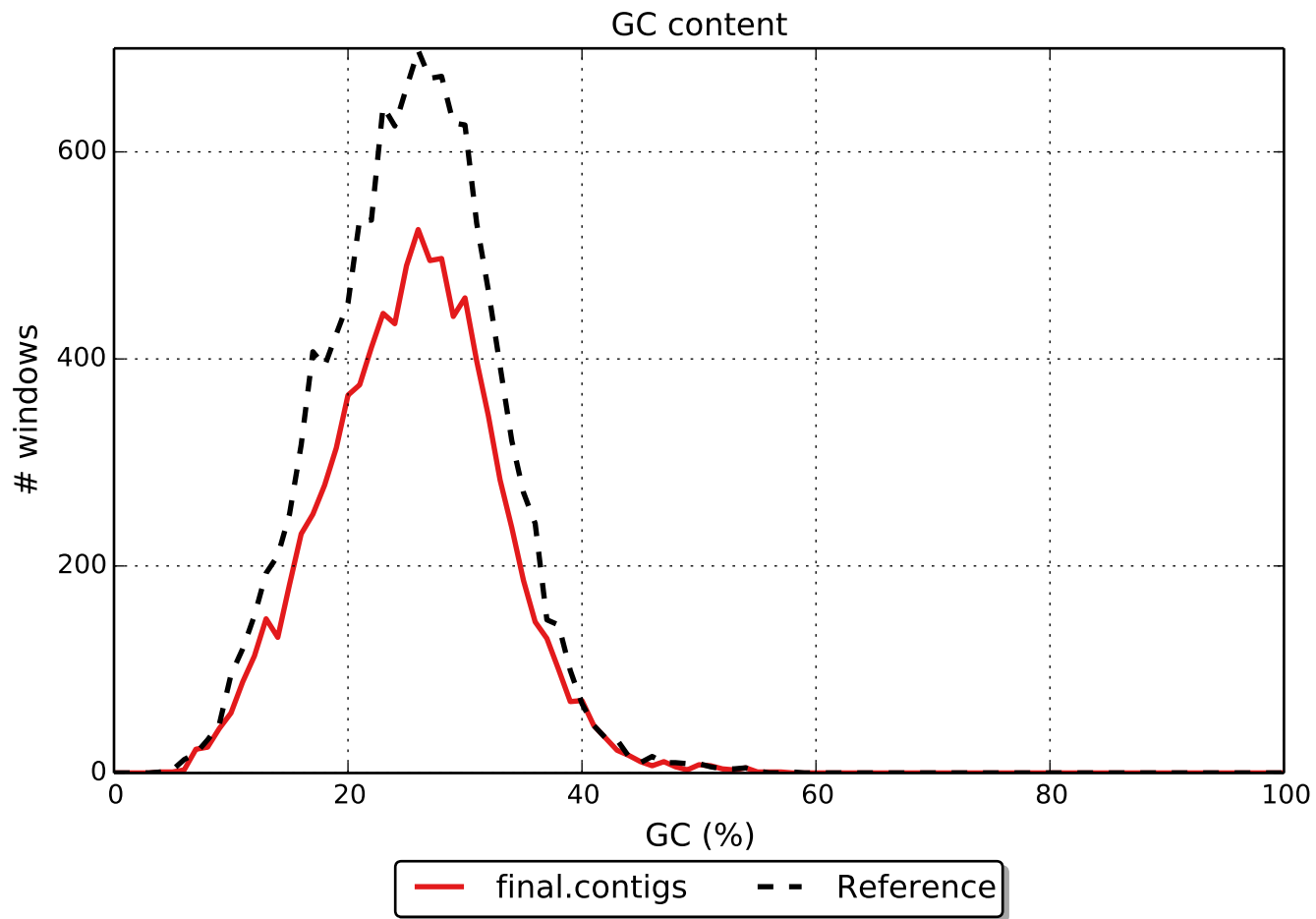
## Unaligned report

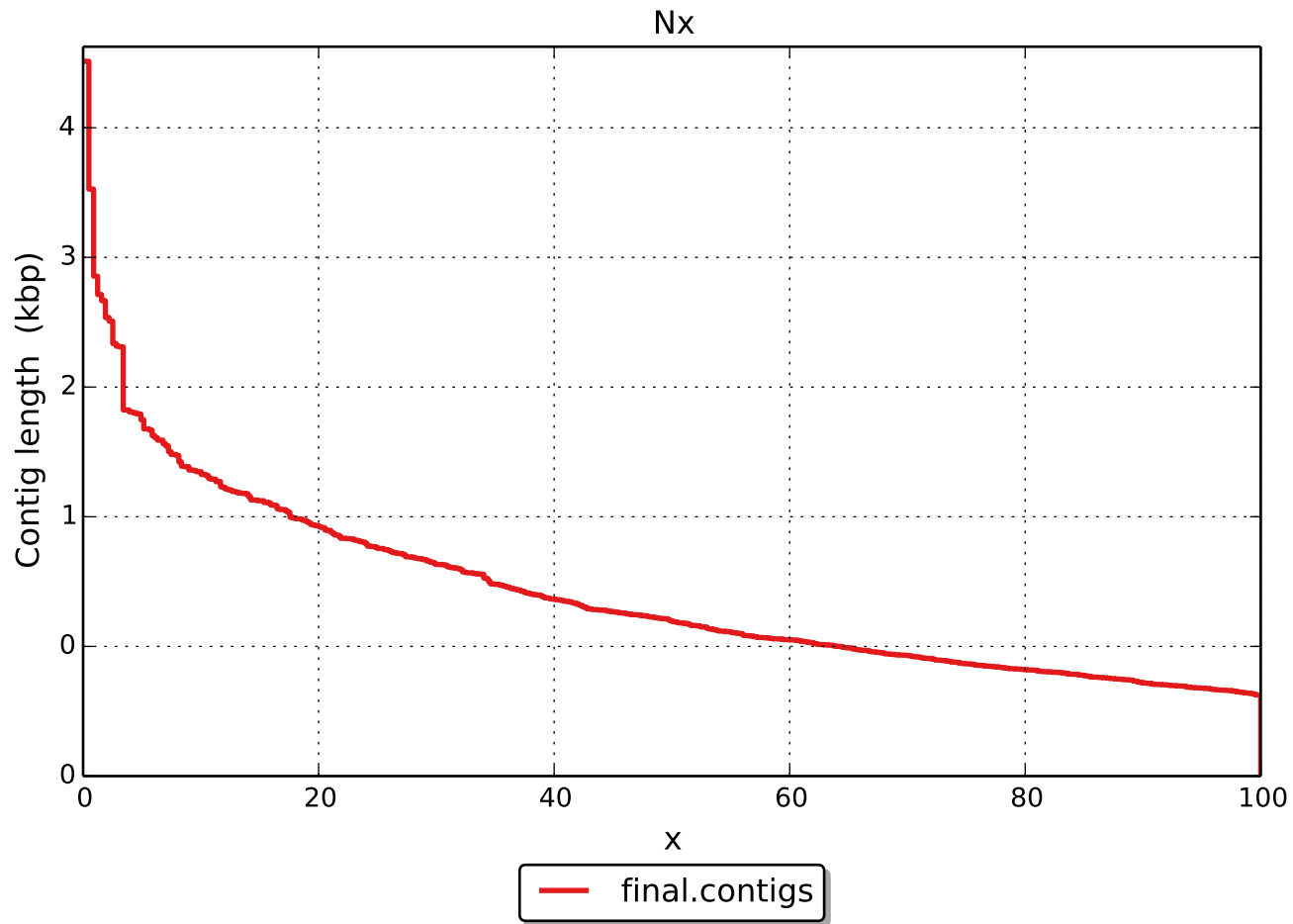
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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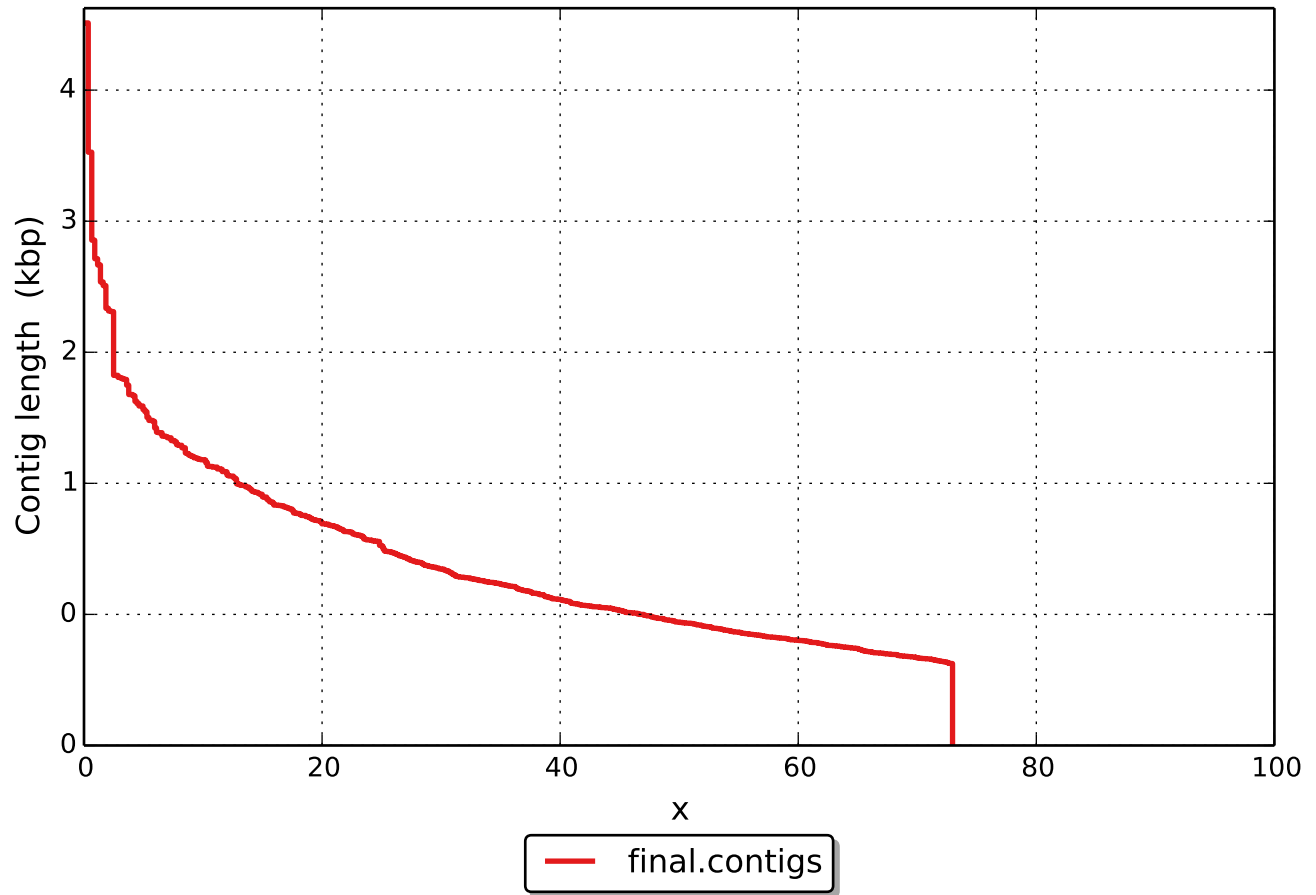
Cumulative length







NGx

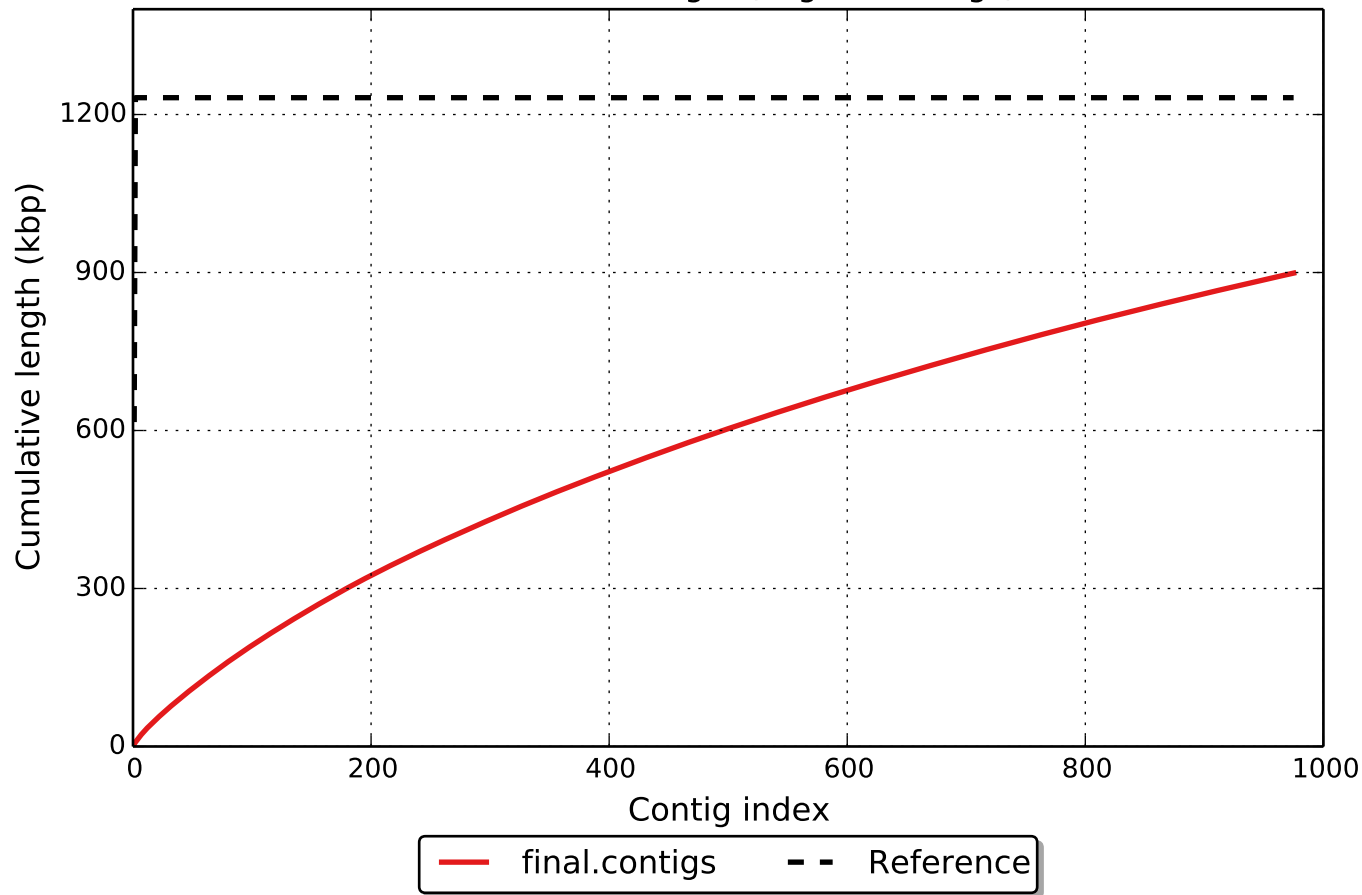


# Misassemblies

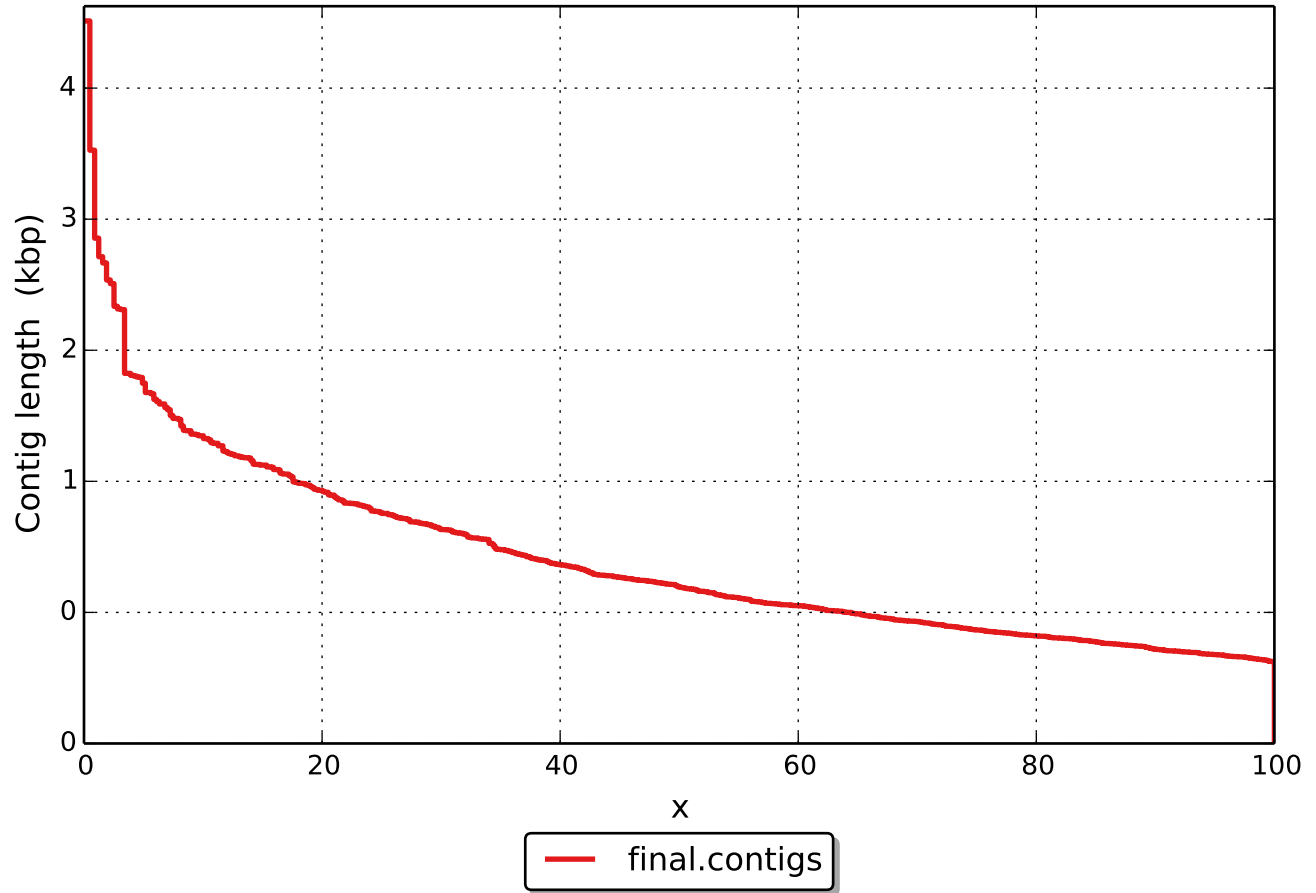




Cumulative length (aligned contigs)



NAx



NGAx

