

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1315
# contigs ( $\geq 1000$ bp)	451
Total length ( $\geq 0$ bp)	1276739
Total length ( $\geq 1000$ bp)	780191
# contigs	950
Largest contig	8192
Total length	1143011
Reference length	1231960
GC (%)	25.44
Reference GC (%)	25.34
N50	1356
NG50	1269
N75	888
NG75	797
L50	271
LG50	305
L75	533
LG75	612
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.150
Duplication ratio	1.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	76.44
# indels per 100 kbp	0.00
Largest alignment	8192
NA50	1356
NGA50	1269
NA75	888
NGA75	797
LA50	271
LGA50	305
LA75	533
LGA75	612

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	849
# indels	0
# short indels	0
# long indels	0
Indels length	0

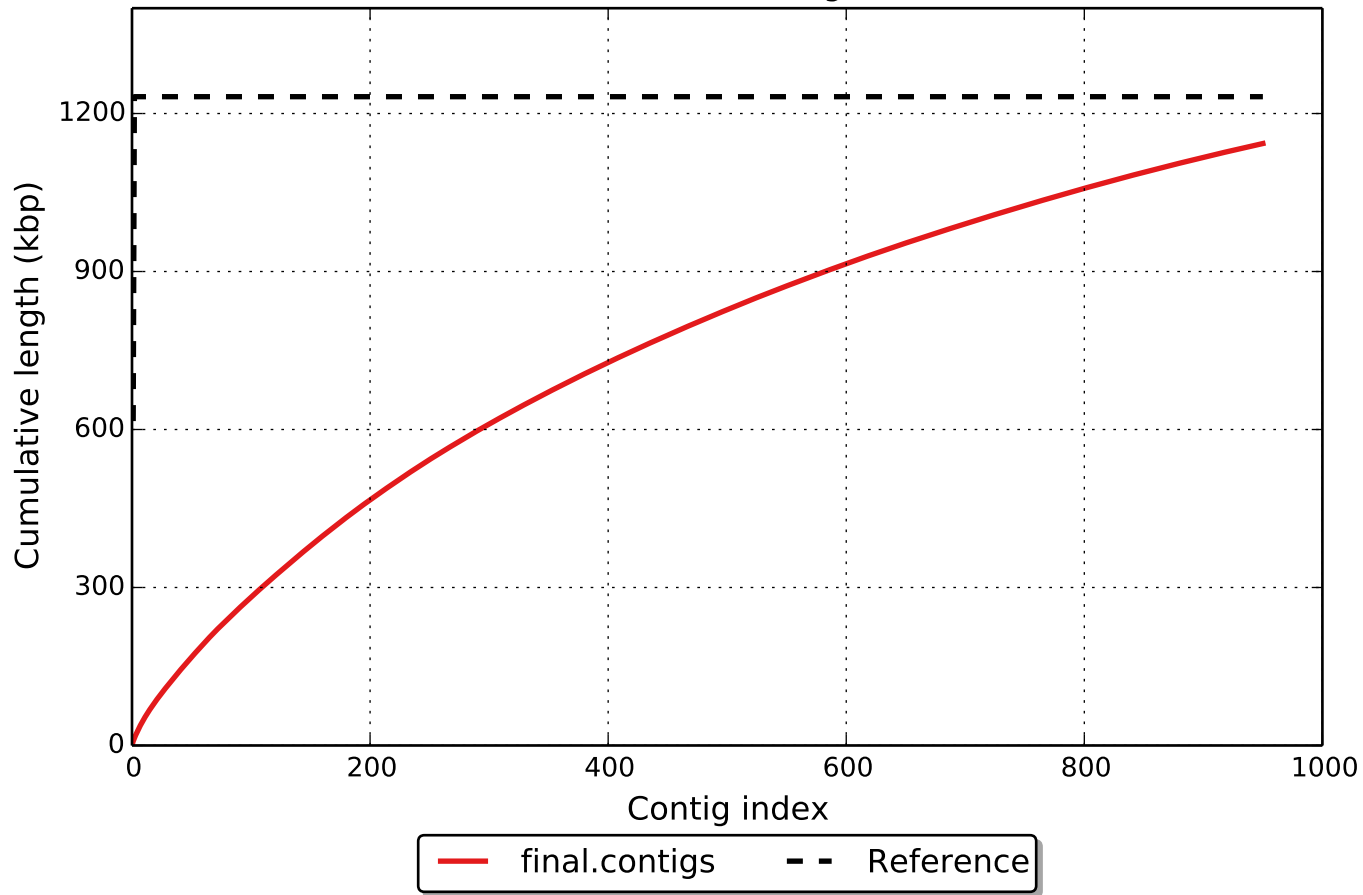
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

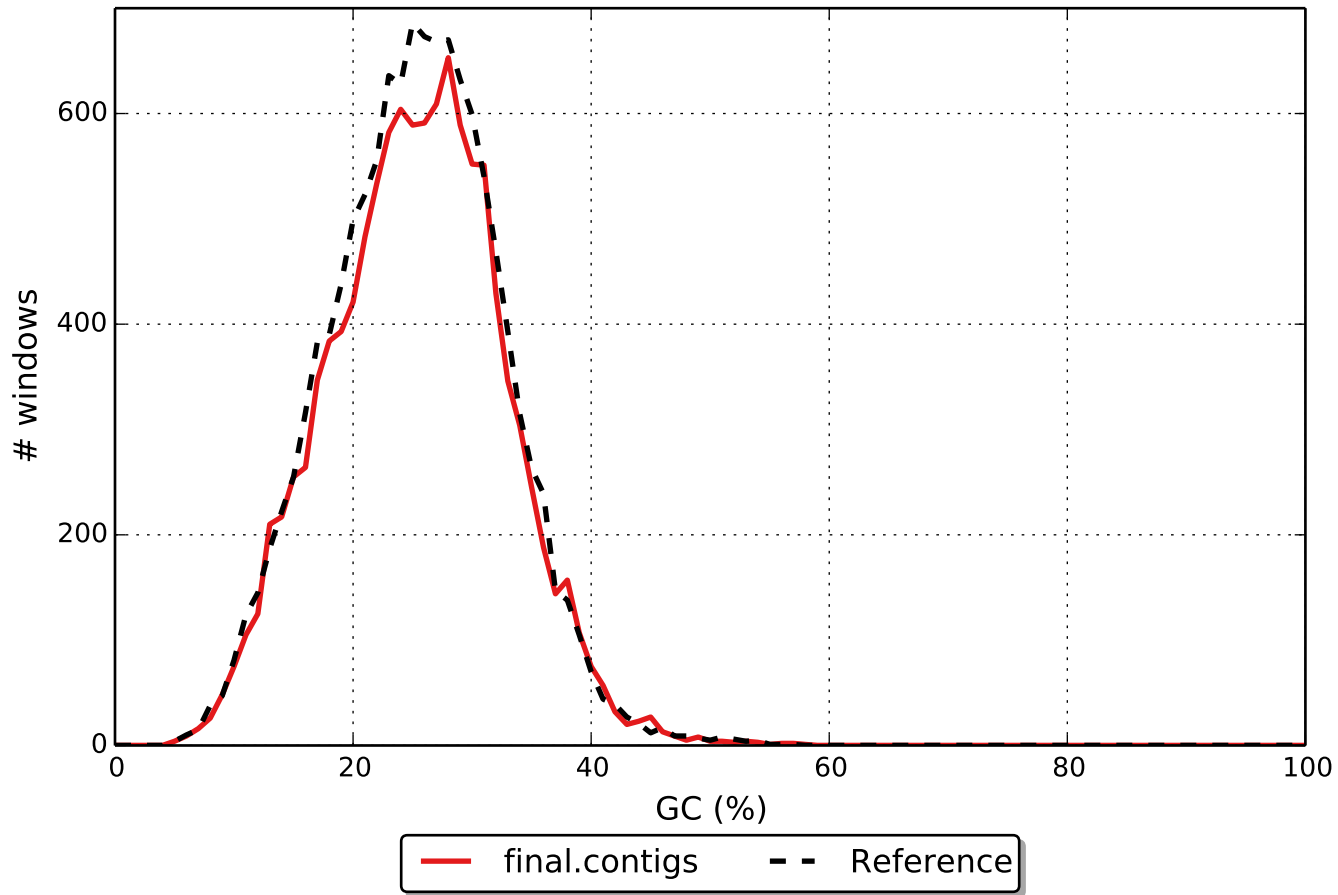
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

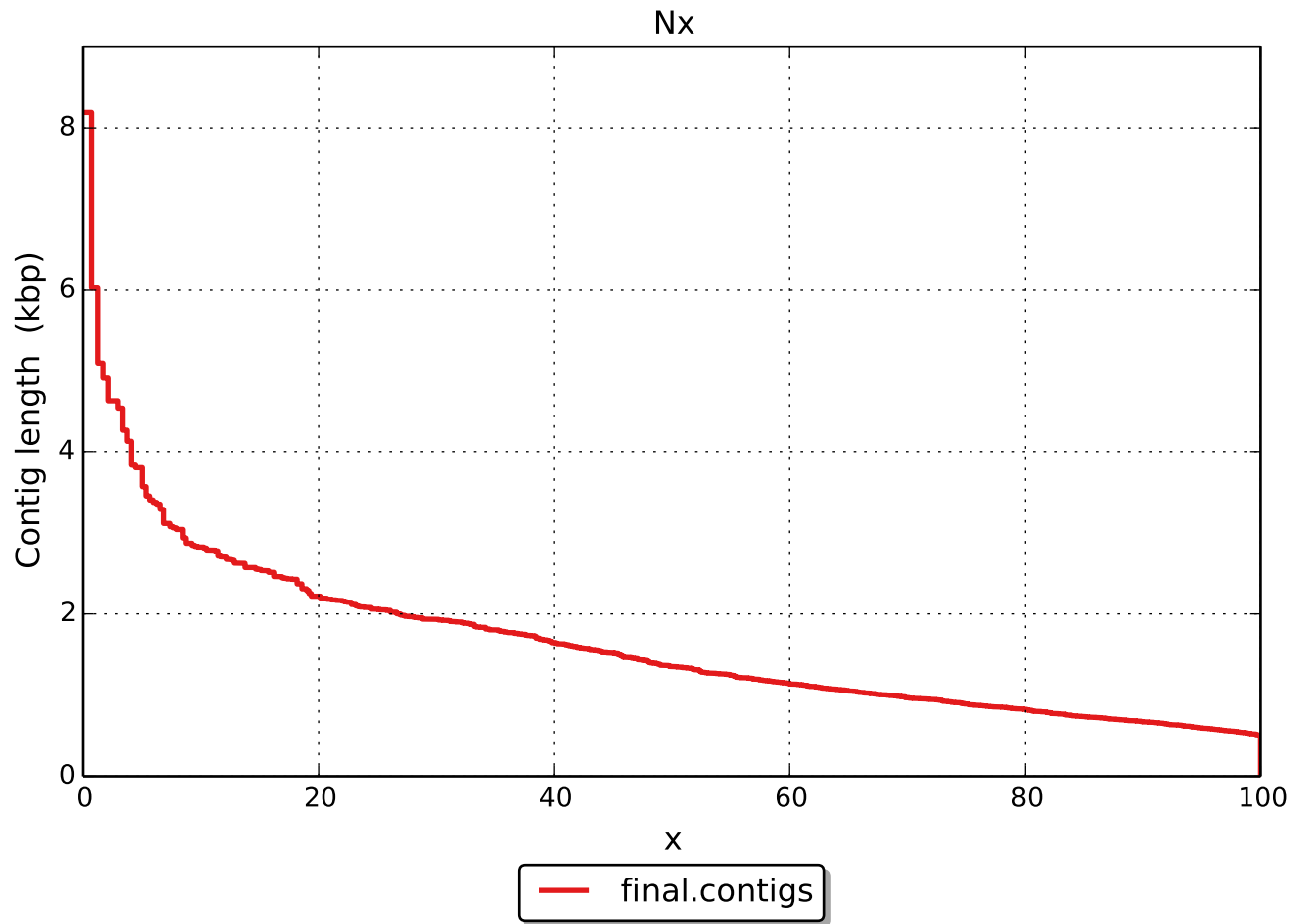
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

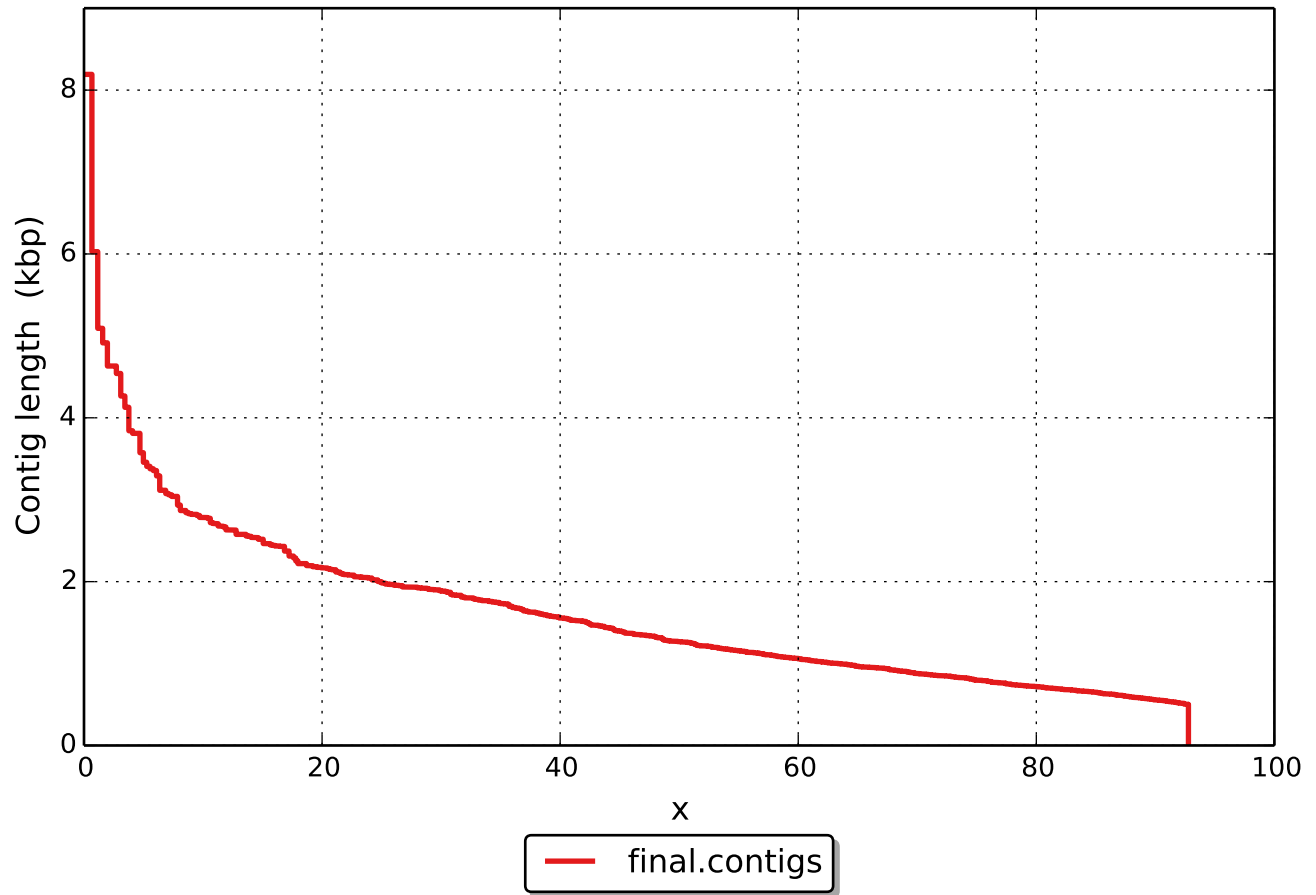


GC content





NGx

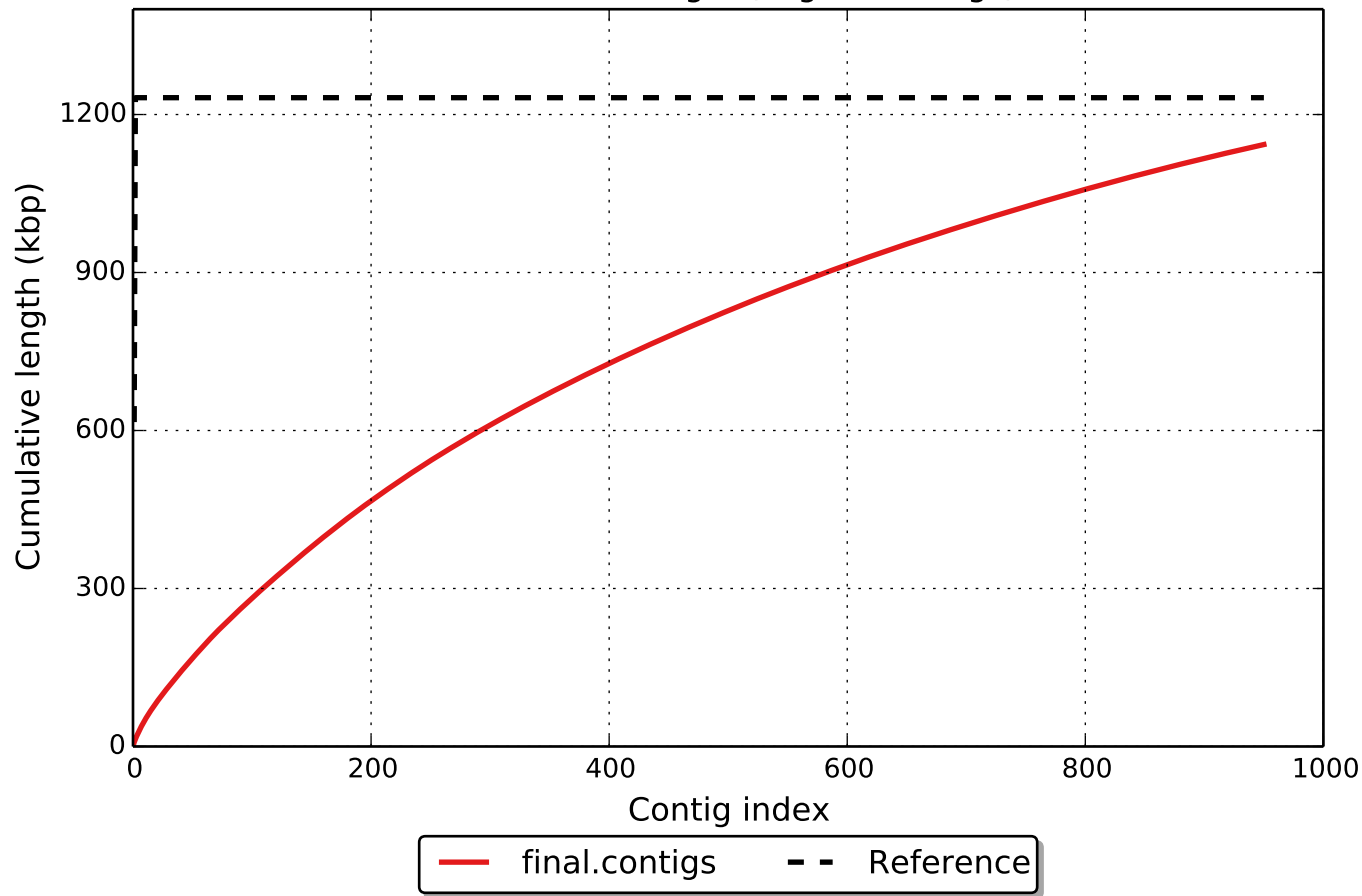


# Misassemblies

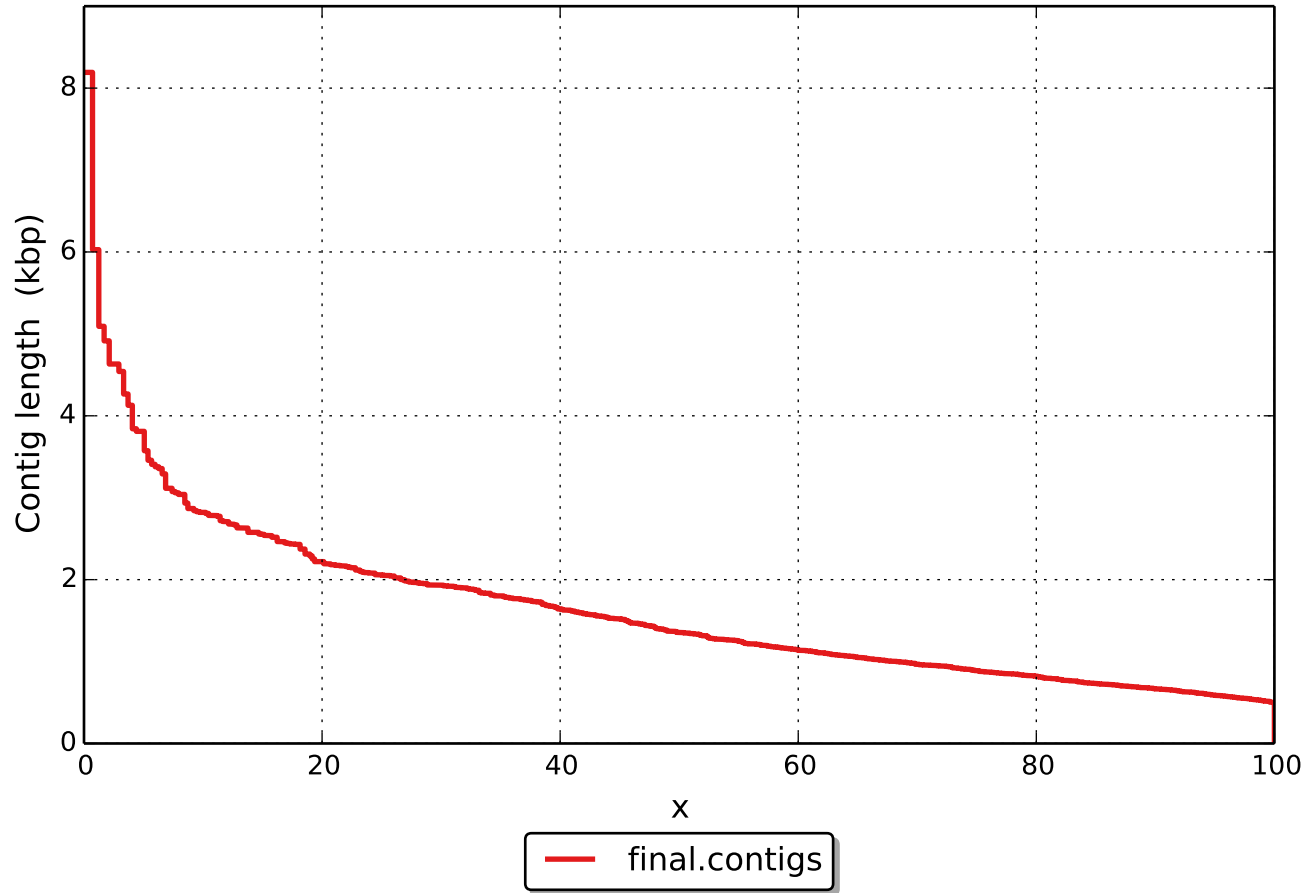




Cumulative length (aligned contigs)



NAx



# NGAx

