

# Report

	final.contigs
# contigs ( $\geq 0$ bp)	216
# contigs ( $\geq 1000$ bp)	196
Total length ( $\geq 0$ bp)	1294222
Total length ( $\geq 1000$ bp)	1278850
# contigs	216
Largest contig	37441
Total length	1294222
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	8699
NG50	12747
N75	5707
NG75	10471
L50	49
LG50	18
L75	96
LG75	32
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	4139
# local misassemblies	0
# unaligned contigs	76 + 17 part
Unaligned length	614922
Genome fraction (%)	99.679
Duplication ratio	1.062
# N's per 100 kbp	0.00
# mismatches per 100 kbp	142.72
# indels per 100 kbp	0.31
Largest alignment	37441
NA50	1451
NGA50	8373
NGA75	5680
LA50	100
LGA50	24
LGA75	47

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	11
# misassembled contigs	1
Misassembled contigs length	4139
# local misassemblies	0
# mismatches	913
# indels	2
# short indels	2
# long indels	0
Indels length	2

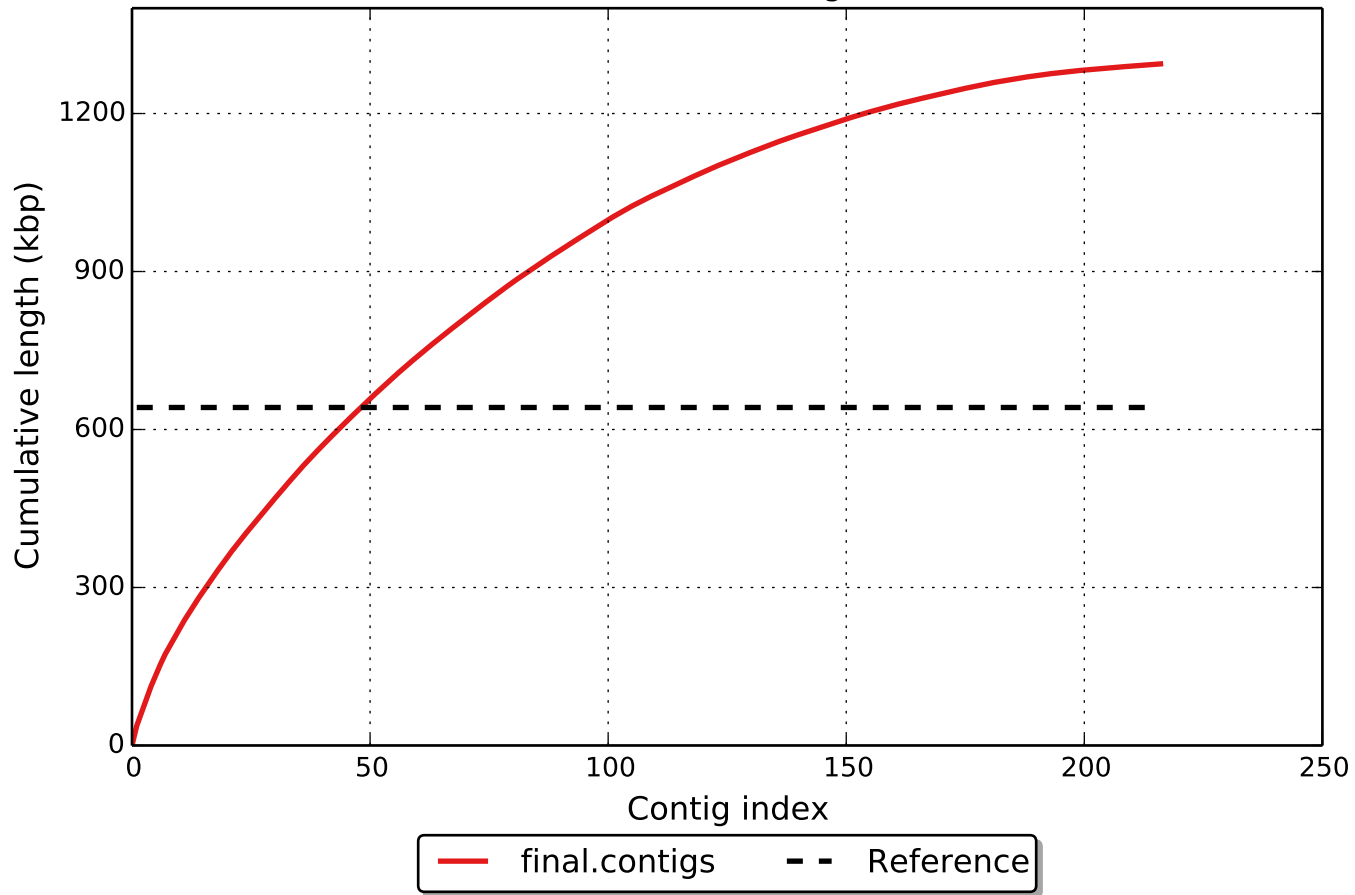
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

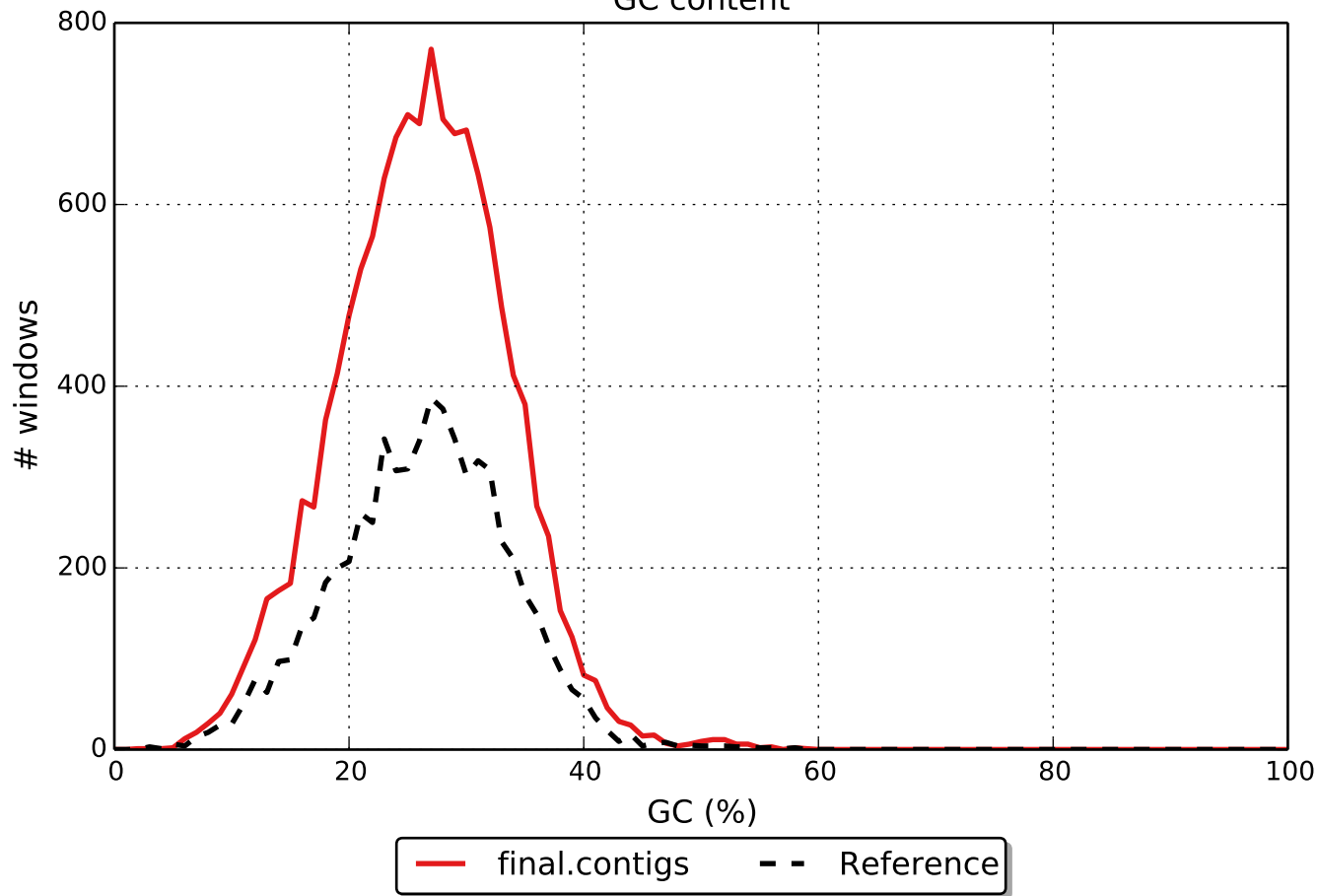
	final.contigs
# fully unaligned contigs	76
Fully unaligned length	509949
# partially unaligned contigs	17
# with misassembly	0
# both parts are significant	11
Partially unaligned length	104973
# N's	0

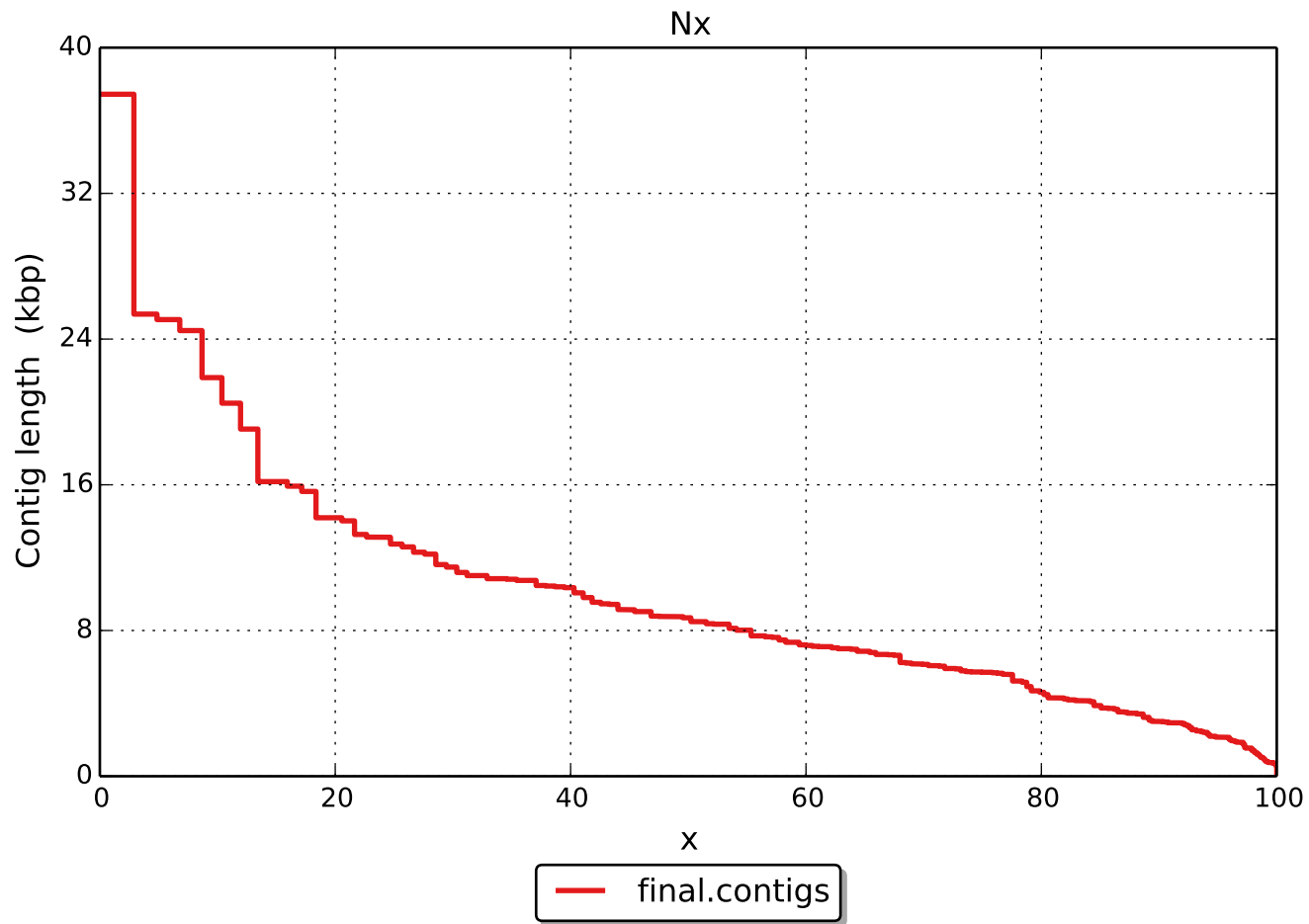
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Cumulative length



GC content





NGx

