

Report

	final.contigs
# contigs (≥ 0 bp)	3864
# contigs (≥ 1000 bp)	842
Total length (≥ 0 bp)	5973678
Total length (≥ 1000 bp)	4880343
# contigs	1286
Largest contig	39846
Total length	5169320
Reference length	11094646
GC (%)	50.27
Reference GC (%)	50.48
N50	8472
N75	4218
L50	183
L75	397
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	46.245
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	423.41
# indels per 100 kbp	0.06
Largest alignment	39846
NA50	8472
NA75	4218
LA50	183
LA75	397

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

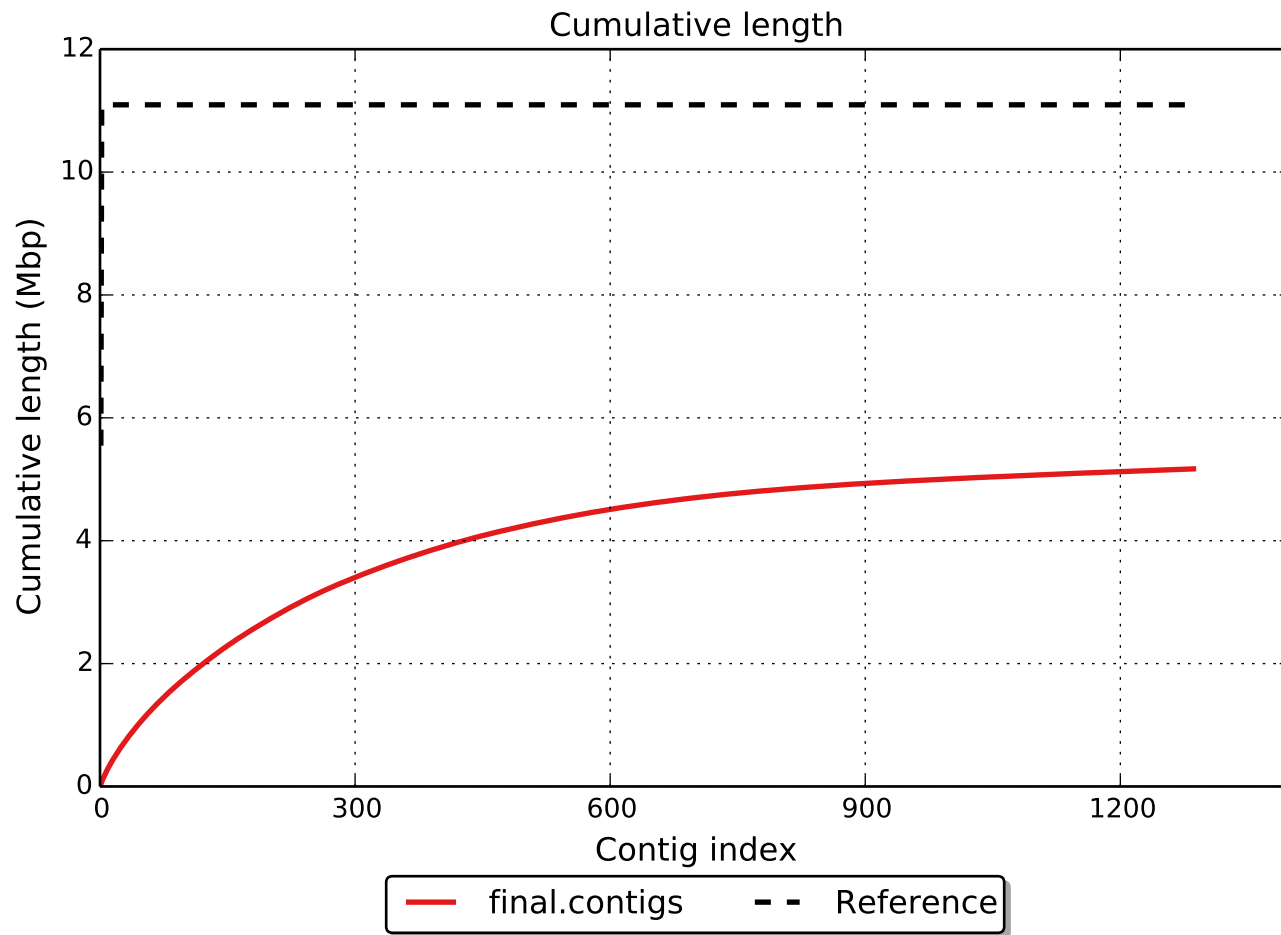
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	21724
# indels	3
# short indels	3
# long indels	0
Indels length	5

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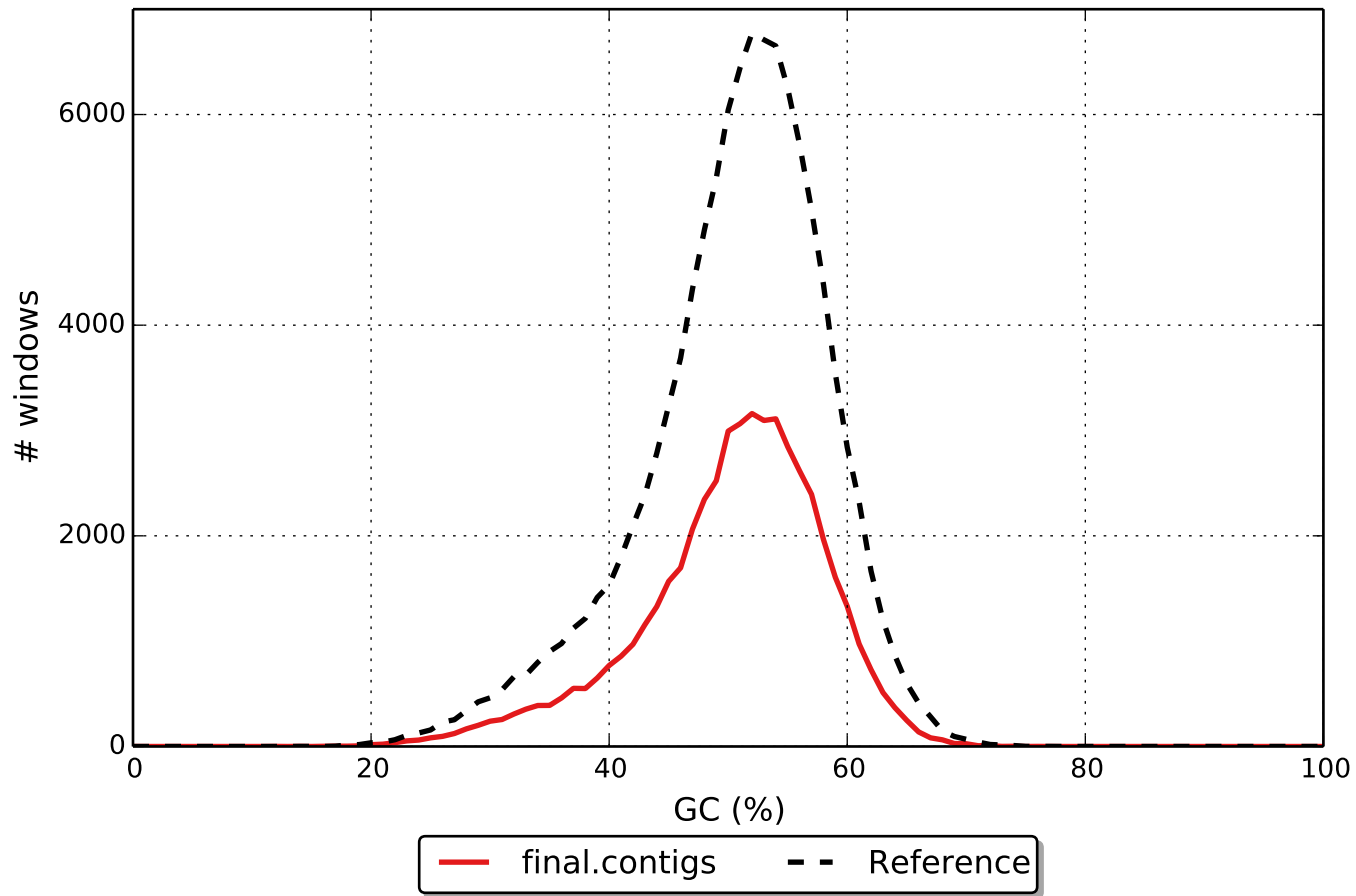
Unaligned report

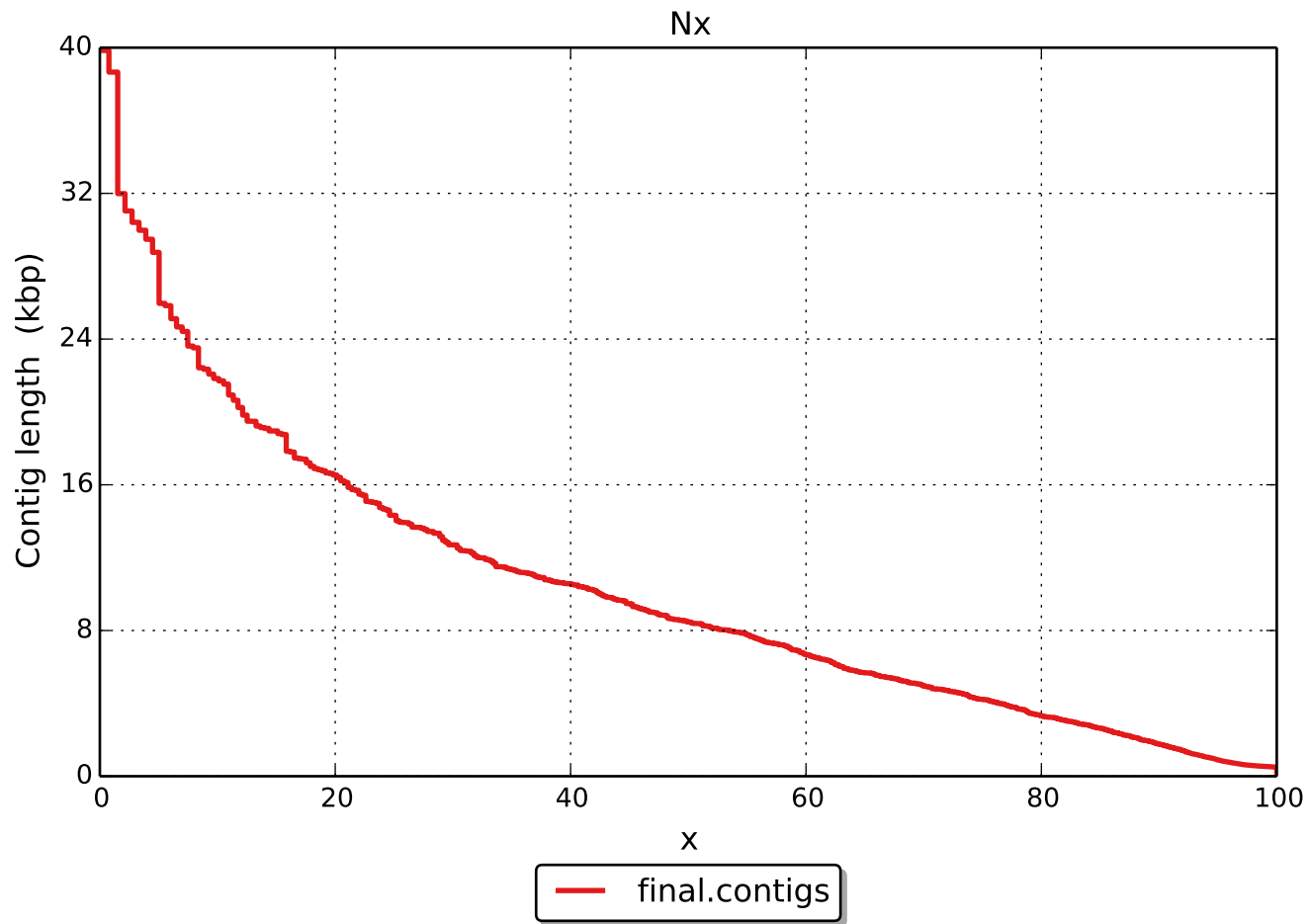
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

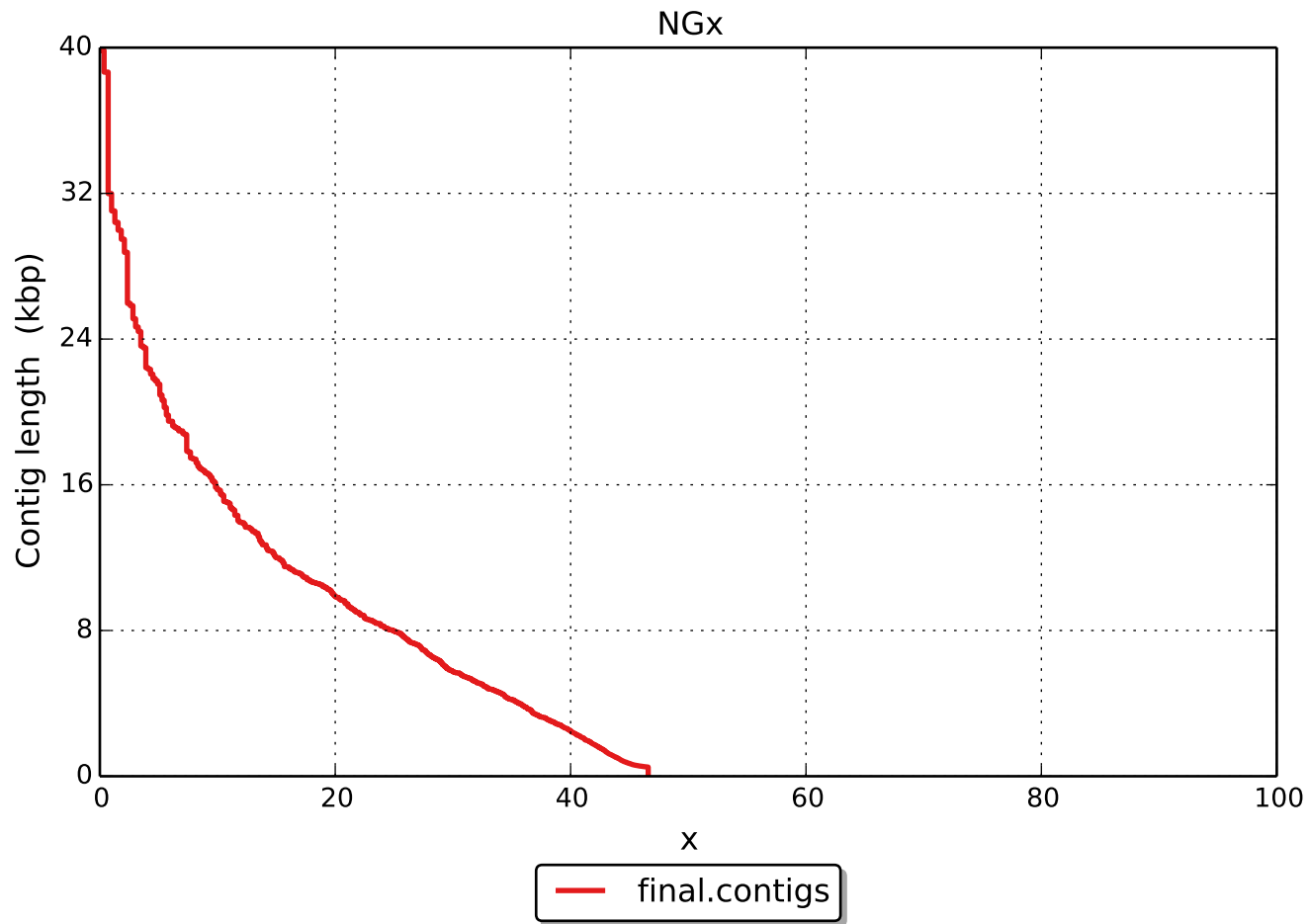
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GC content







Misassemblies



