

Report

	final.contigs
# contigs (≥ 0 bp)	3186
# contigs (≥ 1000 bp)	1401
Total length (≥ 0 bp)	3849558
Total length (≥ 1000 bp)	2837658
# contigs	2417
Largest contig	7824
Total length	3576845
Reference length	3785550
GC (%)	32.30
Reference GC (%)	32.26
N50	1844
NG50	1754
N75	1098
NG75	995
L50	629
LG50	687
L75	1253
LG75	1403
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.732
Duplication ratio	1.041
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.51
# indels per 100 kbp	0.00
Largest alignment	7824
NA50	1844
NGA50	1754
NA75	1098
NGA75	995
LA50	629
LGA50	687
LA75	1253
LGA75	1403

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

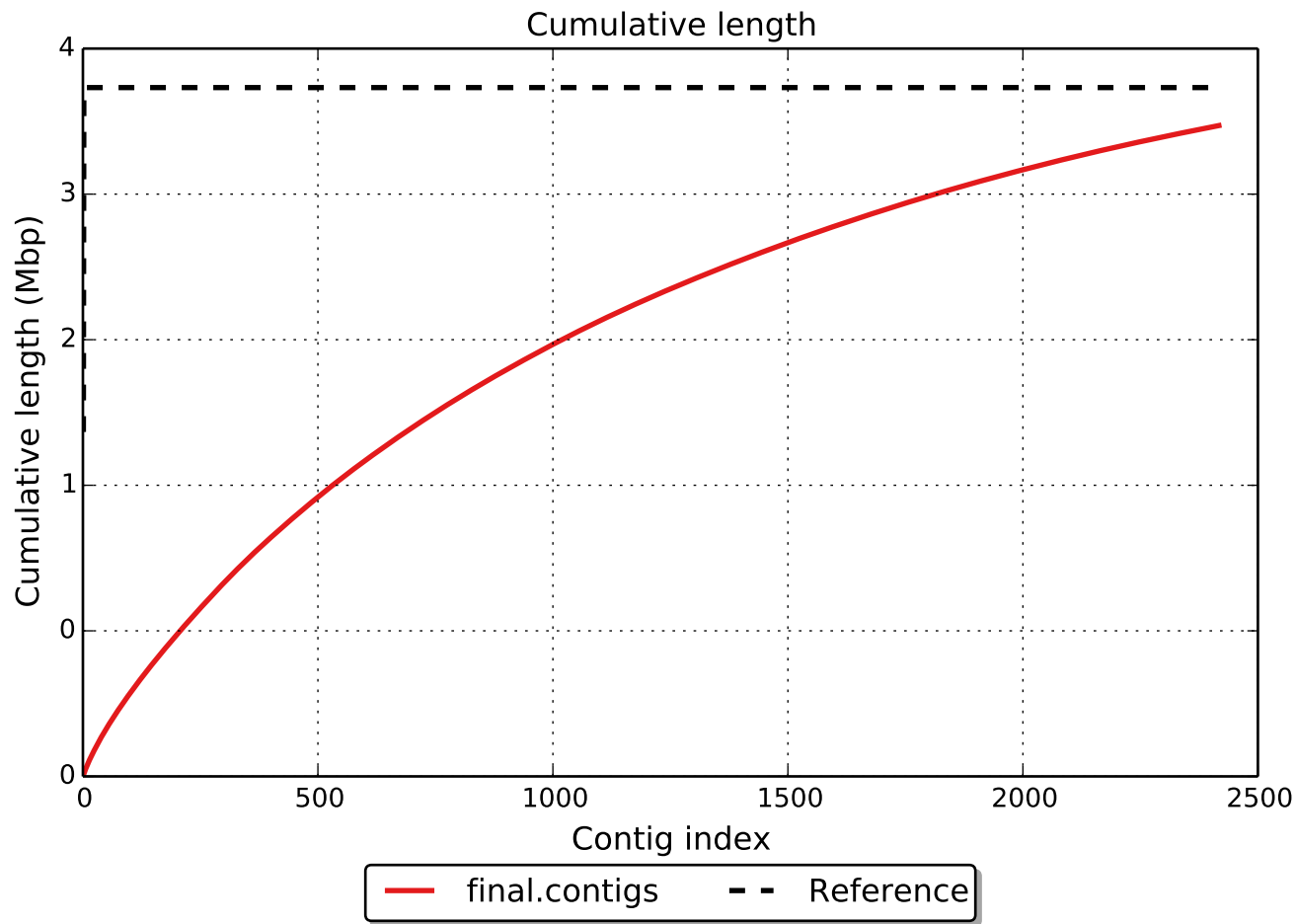
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1357
# indels	0
# short indels	0
# long indels	0
Indels length	0

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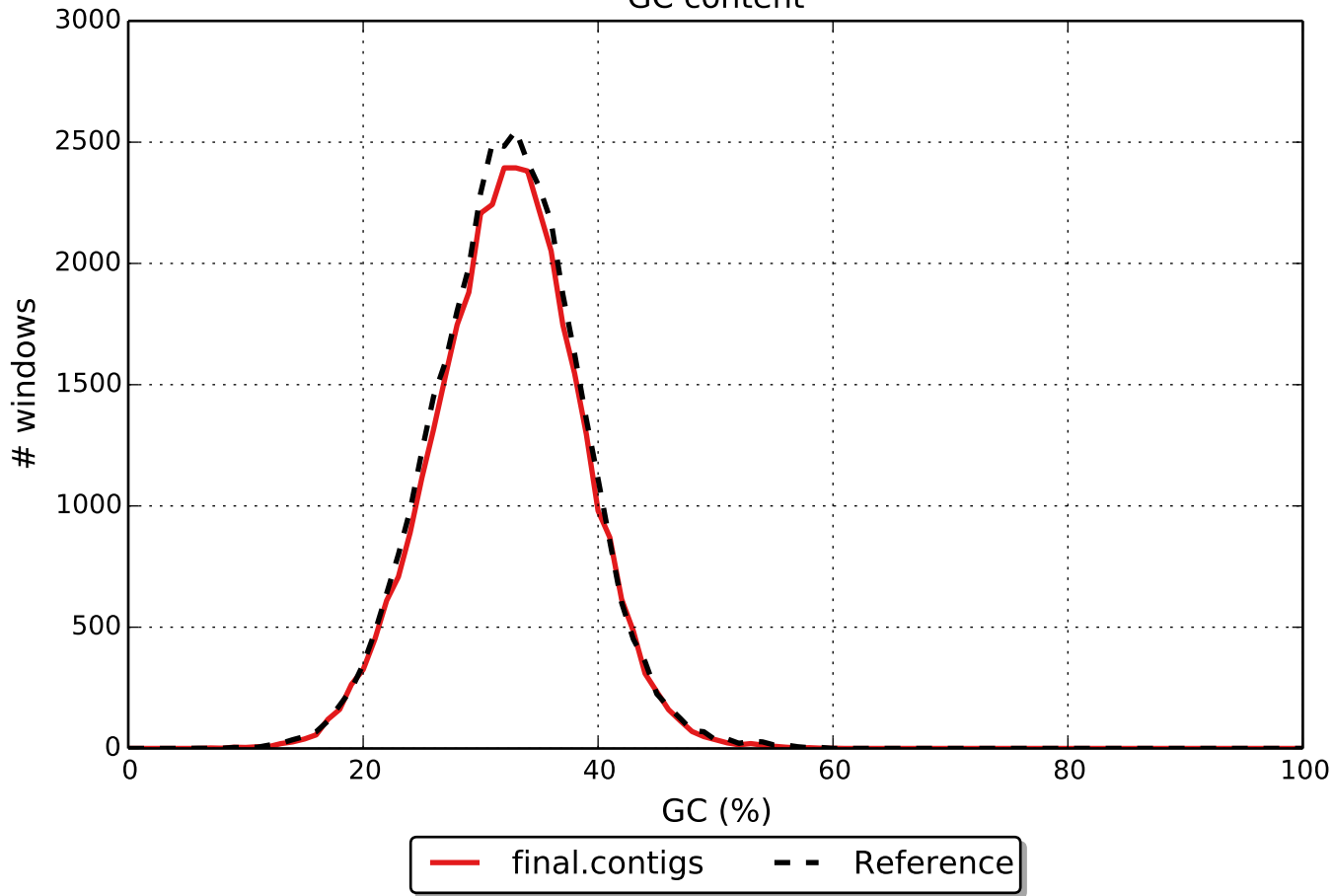
Unaligned report

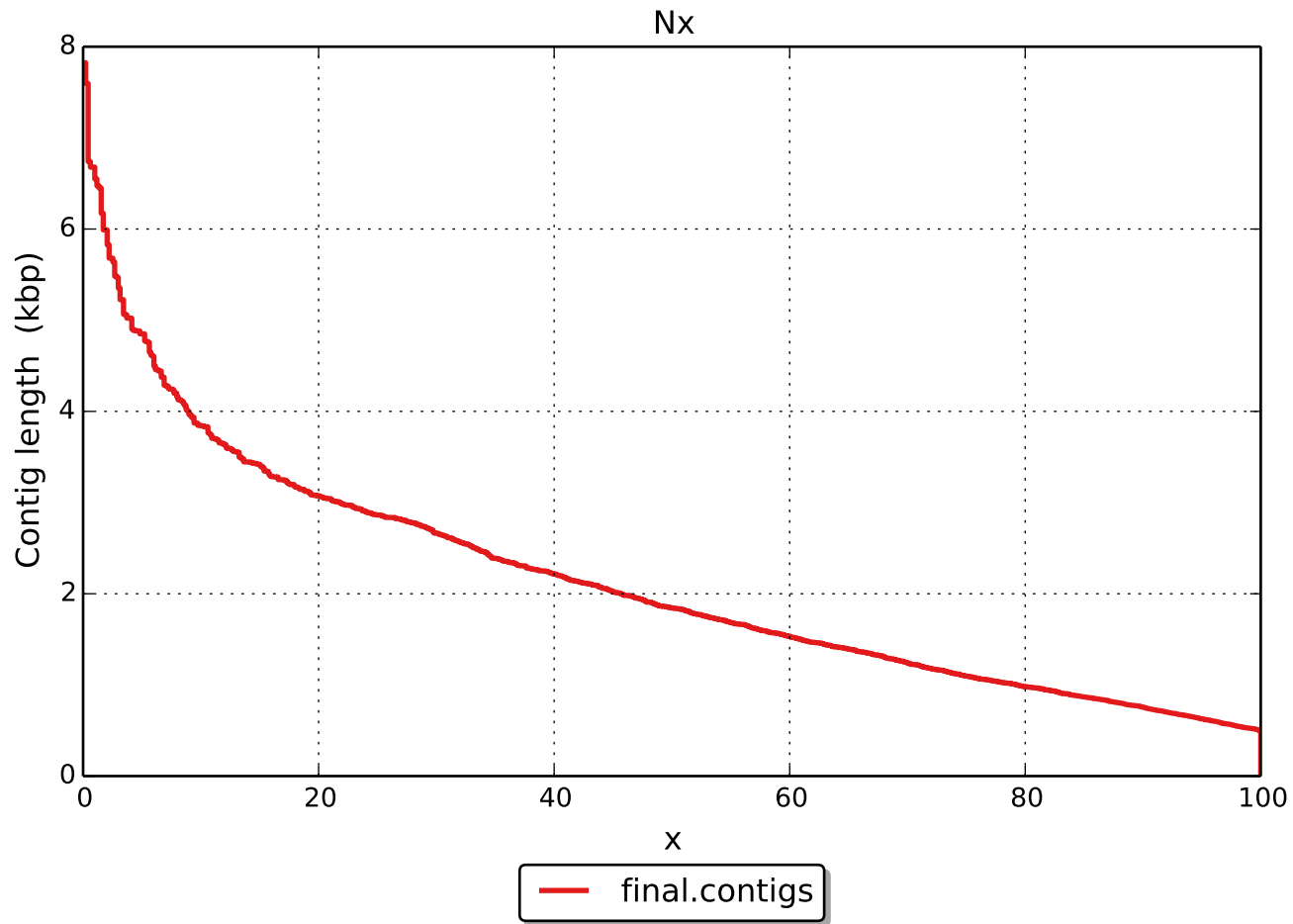
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

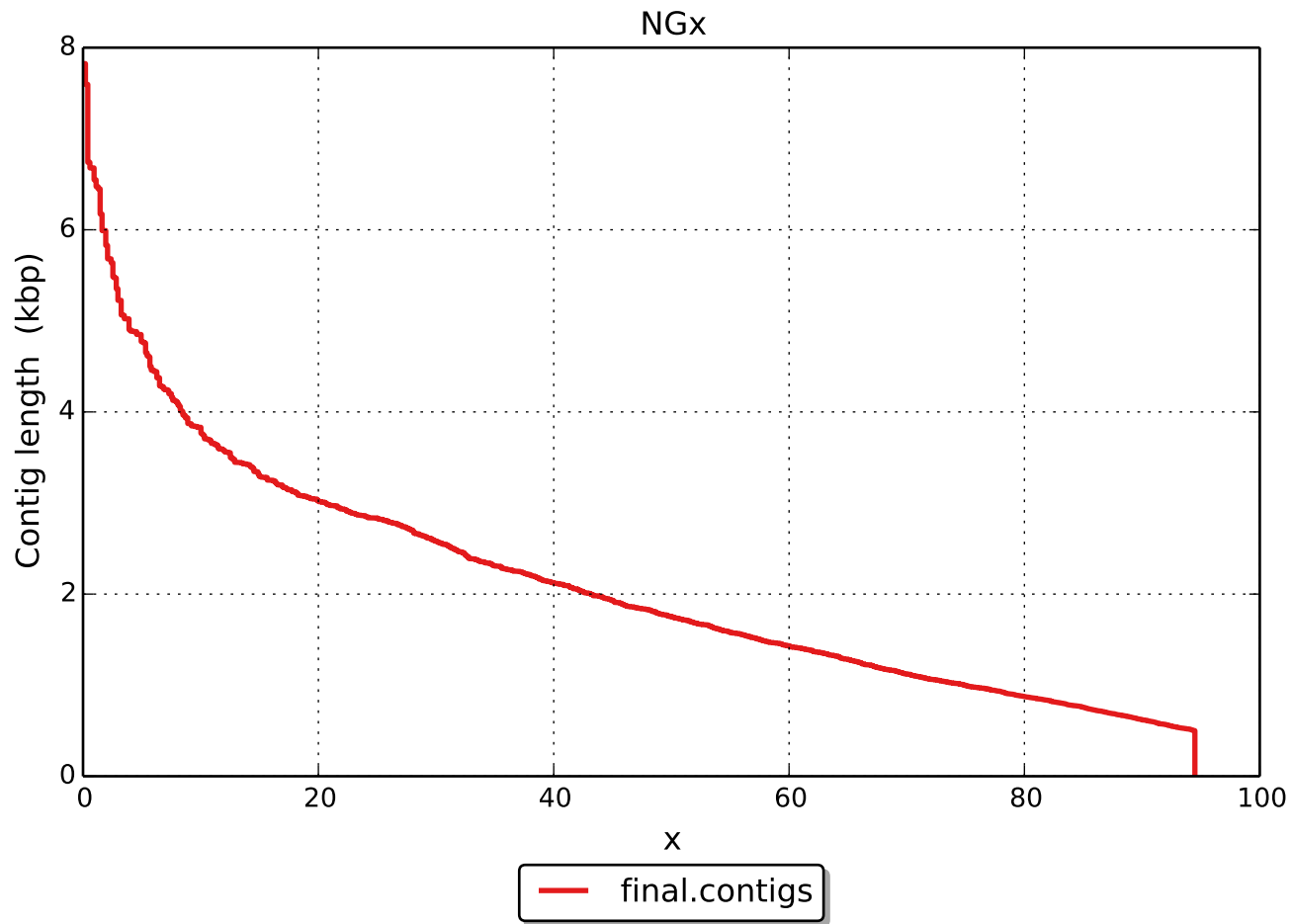
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



