

Report

	final.contigs
# contigs (>= 0 bp)	4576
# contigs (>= 1000 bp)	1160
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3667786
Total length (>= 1000 bp)	1727902
Total length (>= 5000 bp)	7027
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3057
Largest contig	7027
Total length	3066549
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	1077
NG50	759
N75	767
L50	974
LG50	1845
L75	1817
# misassemblies	15
# misassembled contigs	15
Misassembled contigs length	20715
# local misassemblies	3
# unaligned contigs	2 + 10 part
Unaligned length	2098
Genome fraction (%)	65.018
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	922.93
# indels per 100 kbp	1.46
Largest alignment	7027
NA50	1074
NGA50	757
NA75	764
LA50	976
LGA50	1850
LA75	1823

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

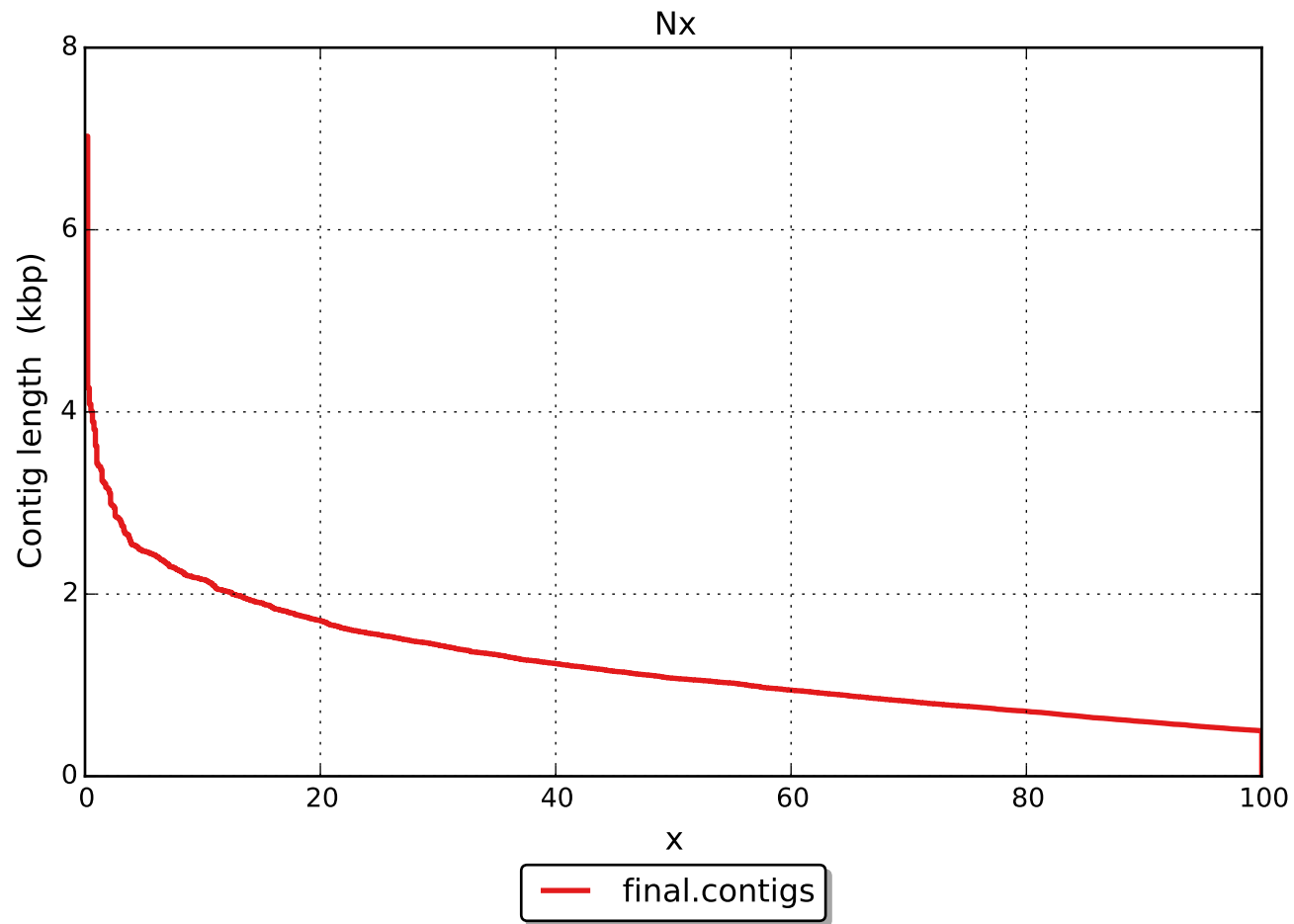
	final.contigs
# misassemblies	15
# relocations	15
# translocations	0
# inversions	0
# misassembled contigs	15
Misassembled contigs length	20715
# local misassemblies	3
# mismatches	27853
# indels	44
# short indels	43
# long indels	1
Indels length	92

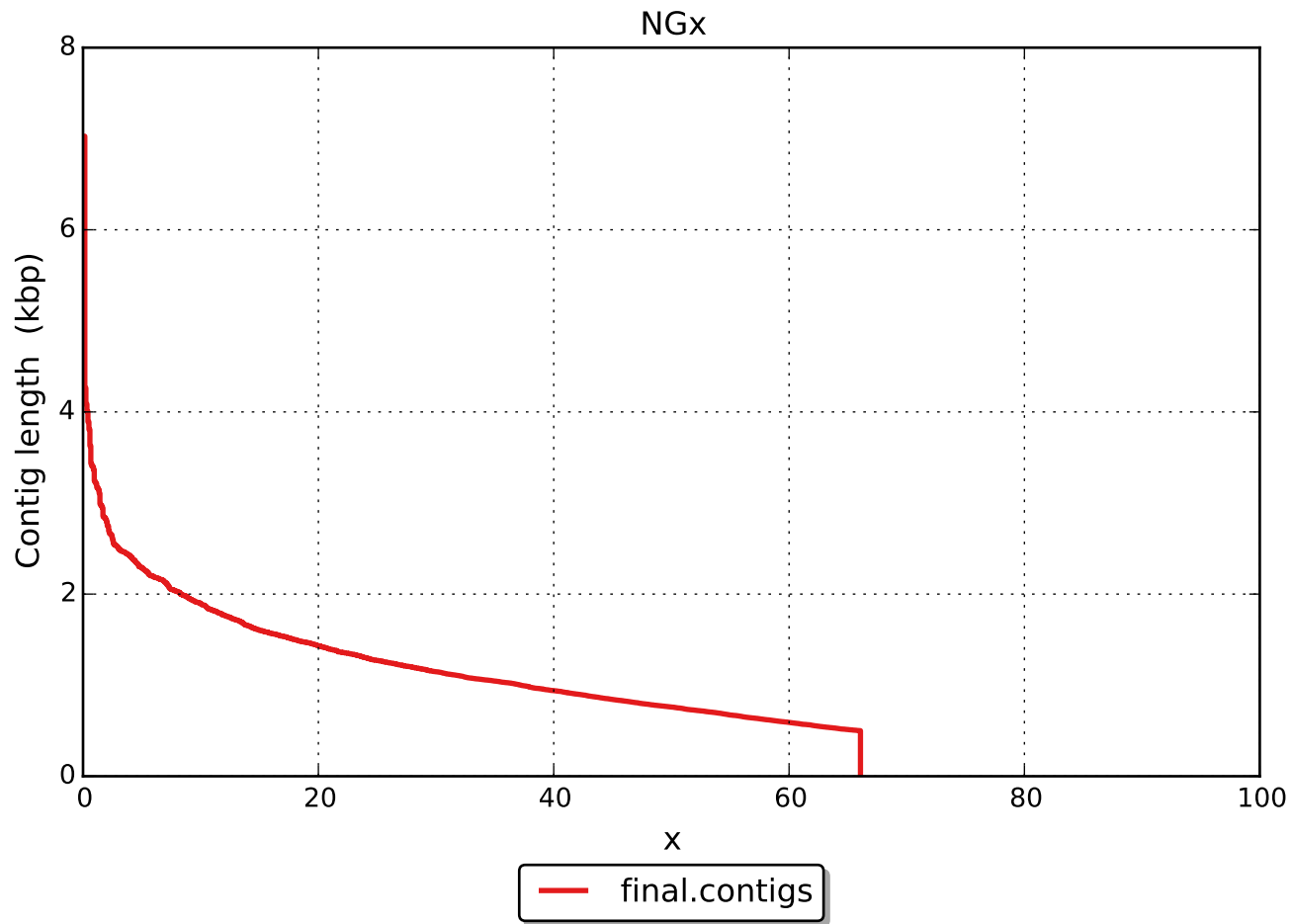
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

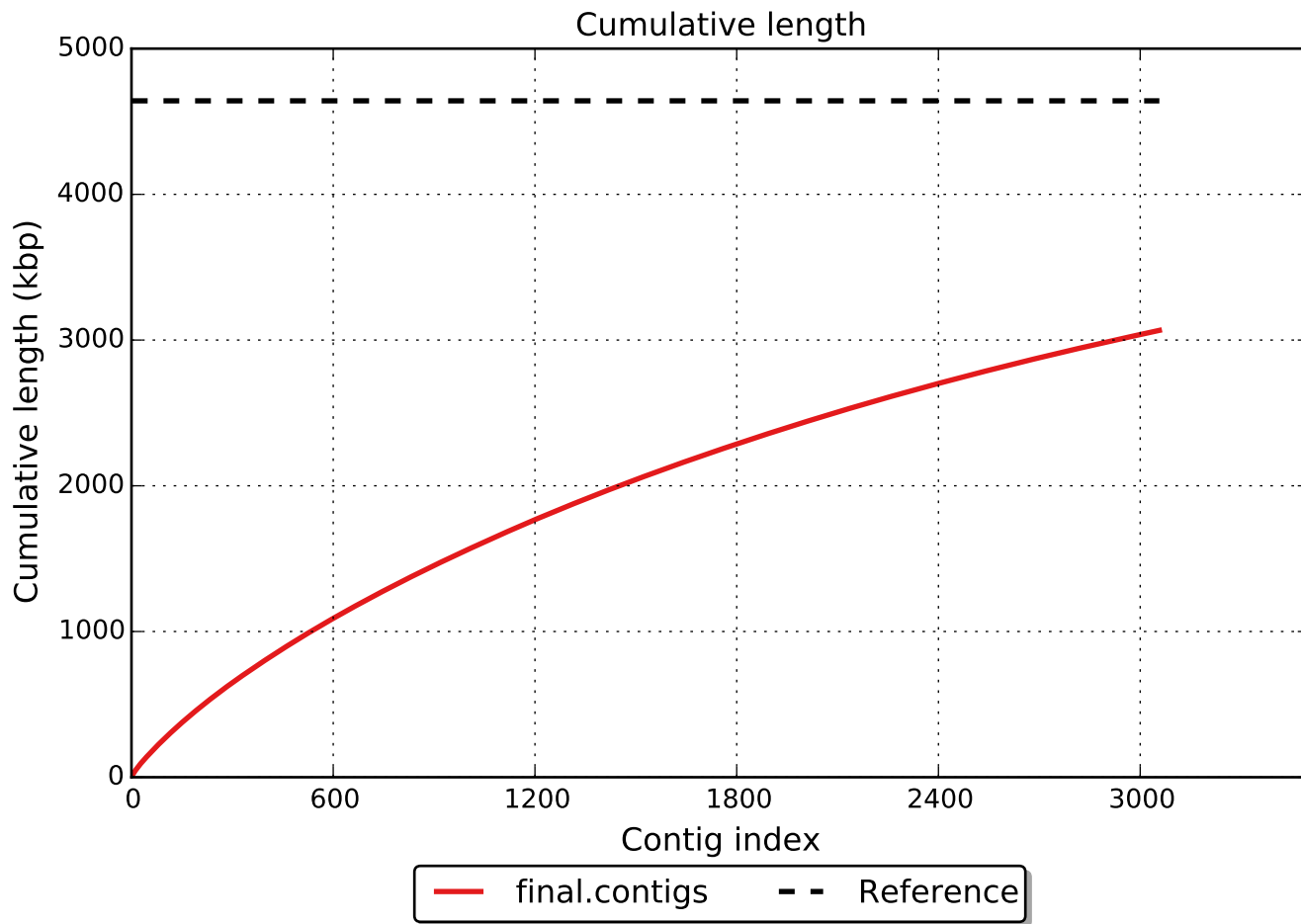
Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1693
# partially unaligned contigs	10
# with misassembly	0
# both parts are significant	0
Partially unaligned length	405
# N's	0

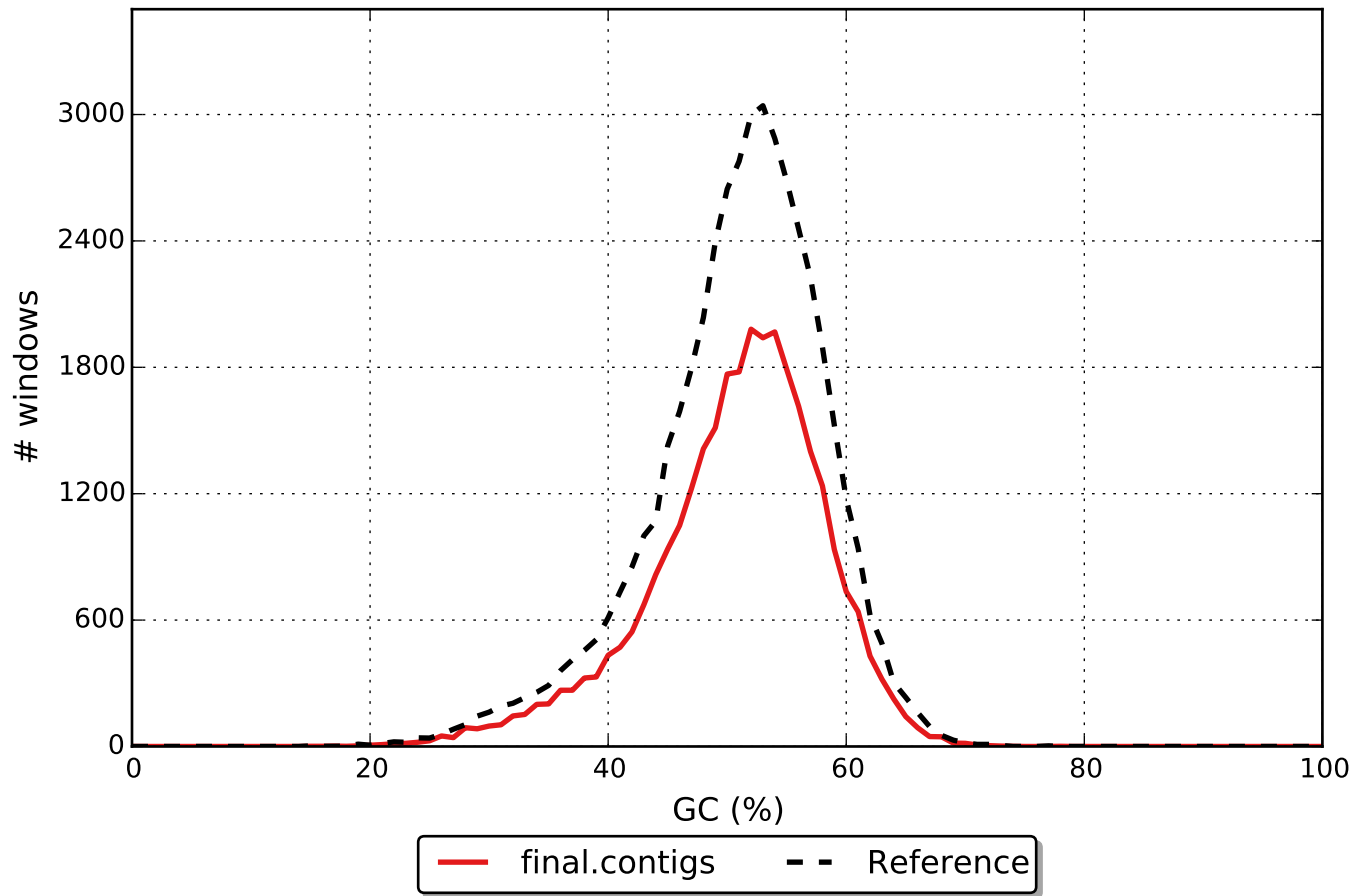
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



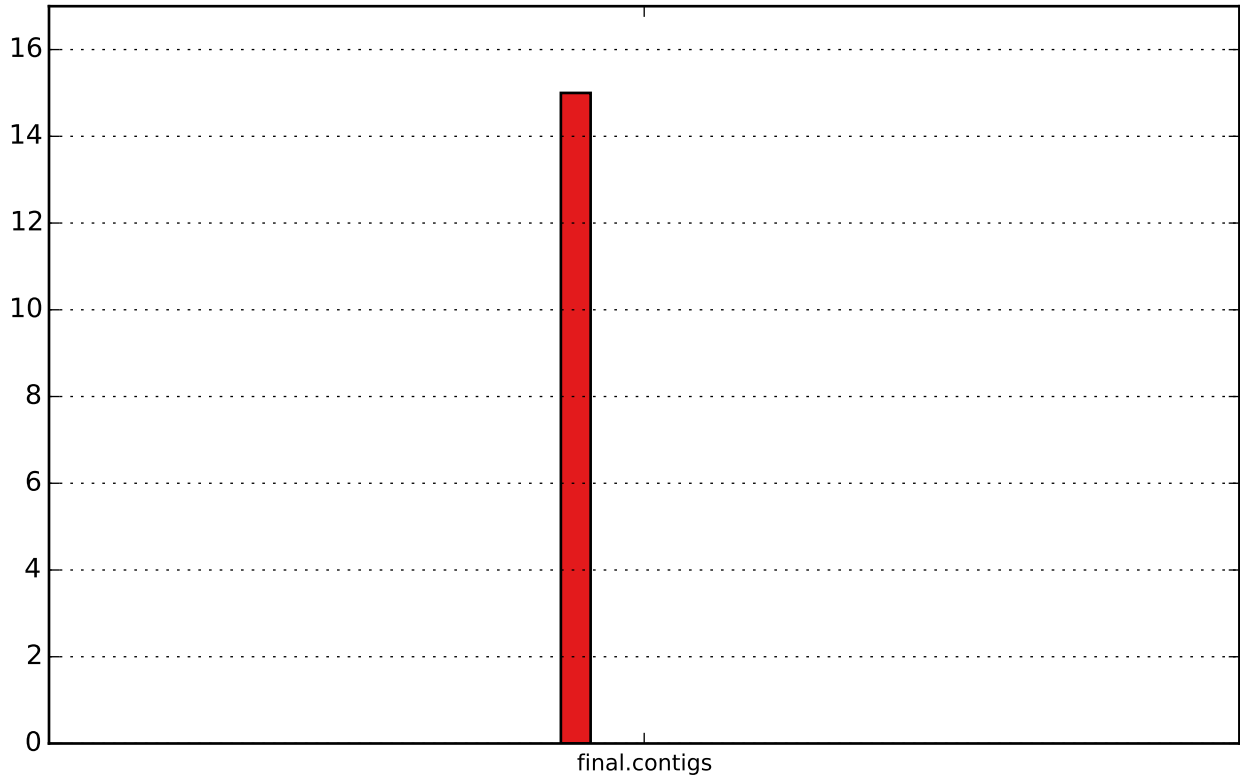




GC content



Misassemblies



Cumulative length (aligned contigs)

