

Report

	final.contigs
# contigs (≥ 0 bp)	1031
# contigs (≥ 1000 bp)	475
Total length (≥ 0 bp)	1197829
Total length (≥ 1000 bp)	793833
# contigs	1031
Largest contig	7521
Total length	1197829
Reference length	641799
GC (%)	26.32
Reference GC (%)	26.30
N50	1270
NG50	1916
N75	876
NG75	1483
L50	302
LG50	121
L75	587
LG75	218
# misassemblies	30
# misassembled contigs	30
Misassembled contigs length	48591
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.782
Duplication ratio	1.990
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1458.89
# indels per 100 kbp	1.33
Largest alignment	7521
NA50	1237
NGA50	1861
NA75	866
NGA75	1460
LA50	309
LGA50	124
LA75	599
LGA75	222

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

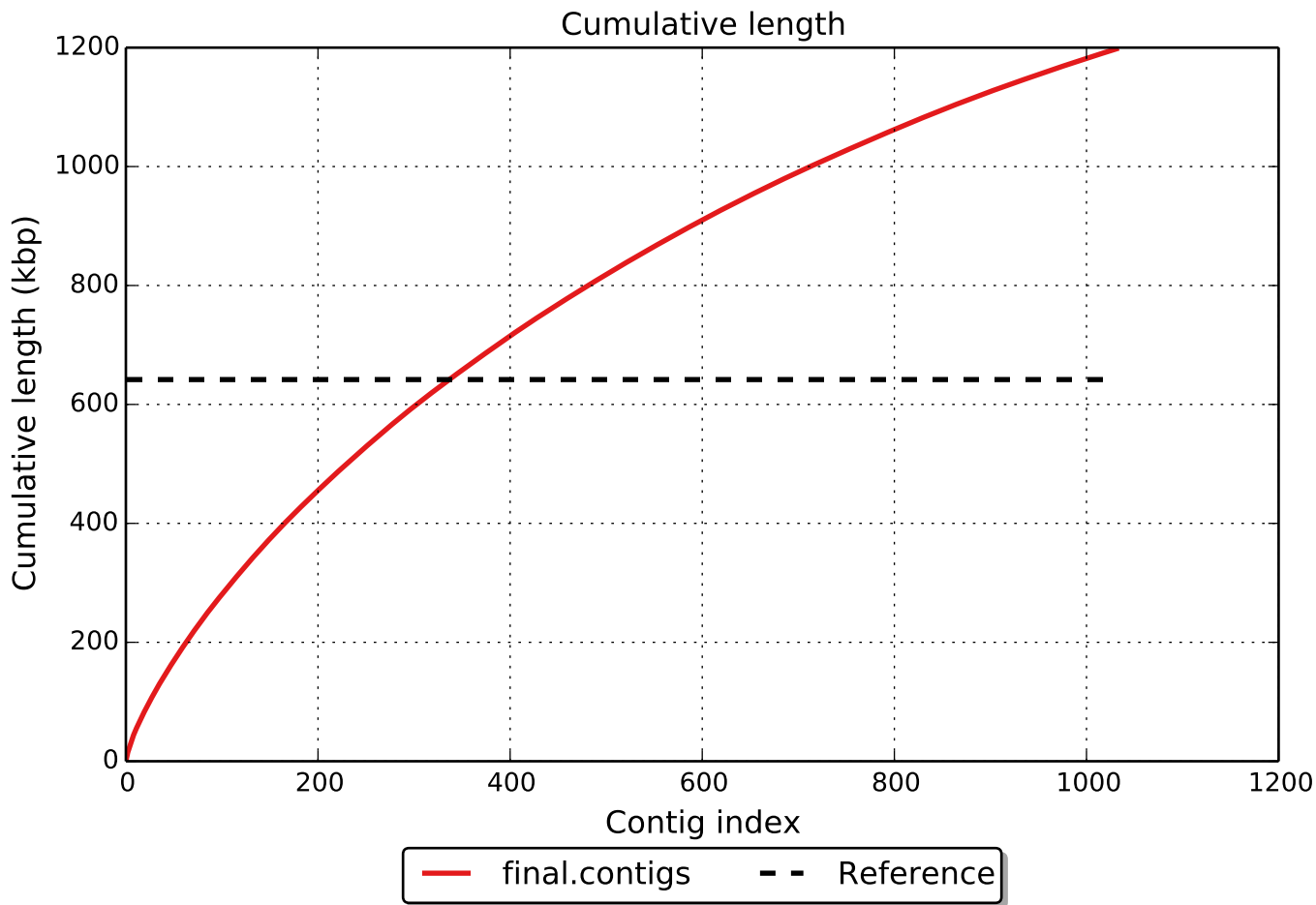
	final.contigs
# misassemblies	30
# relocations	30
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	30
Misassembled contigs length	48591
# local misassemblies	0
# mismatches	8781
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).

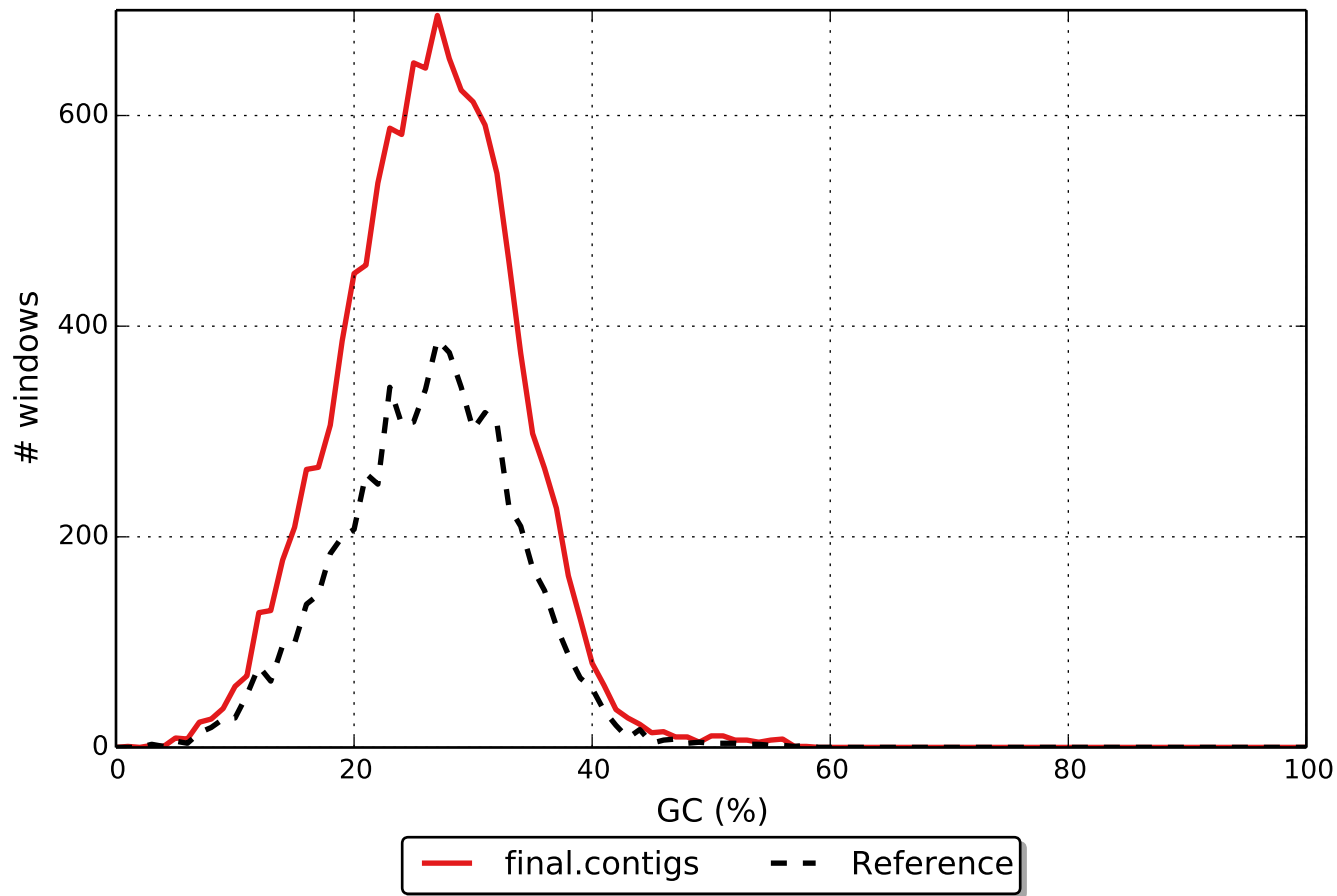
Unaligned report

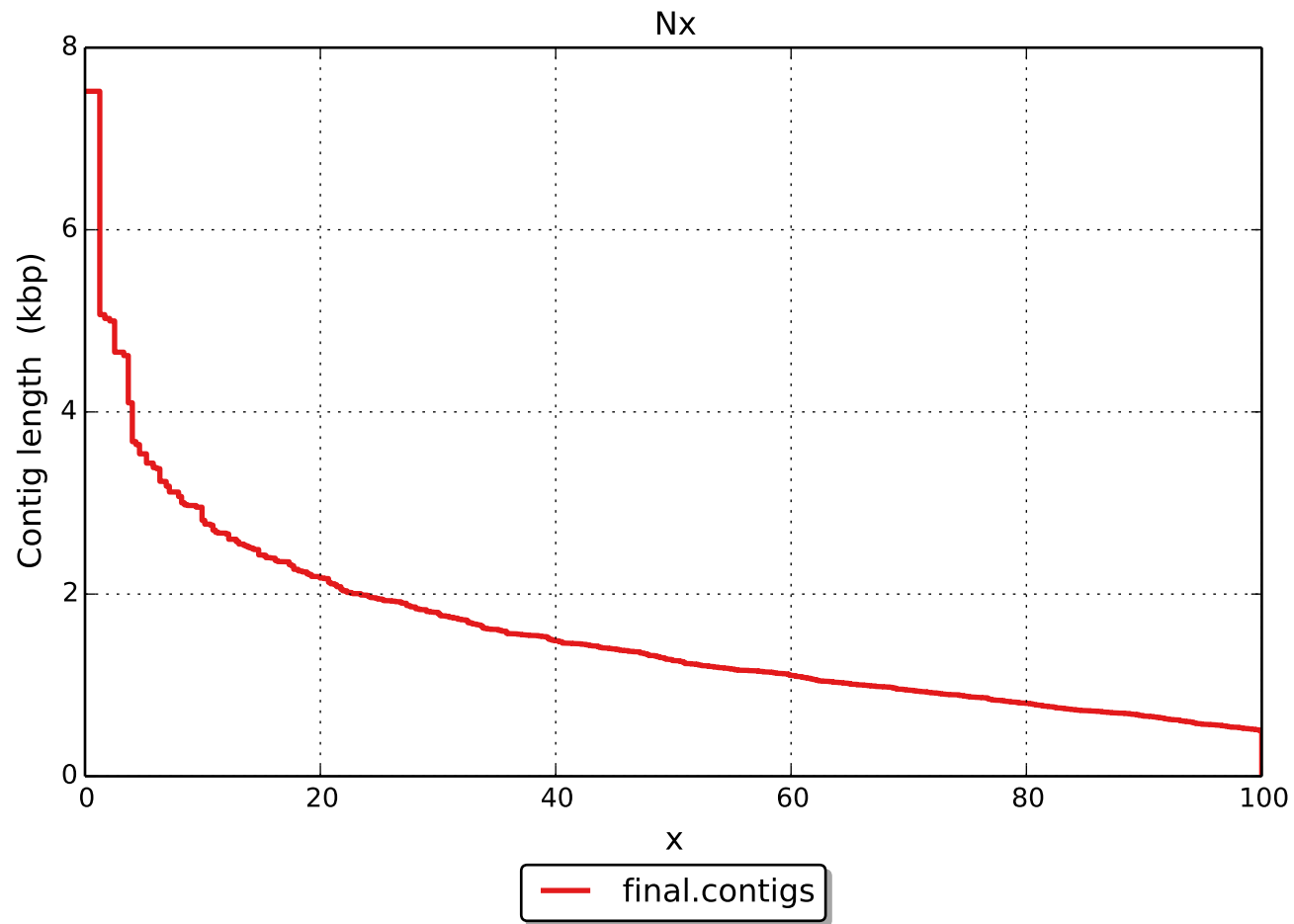
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

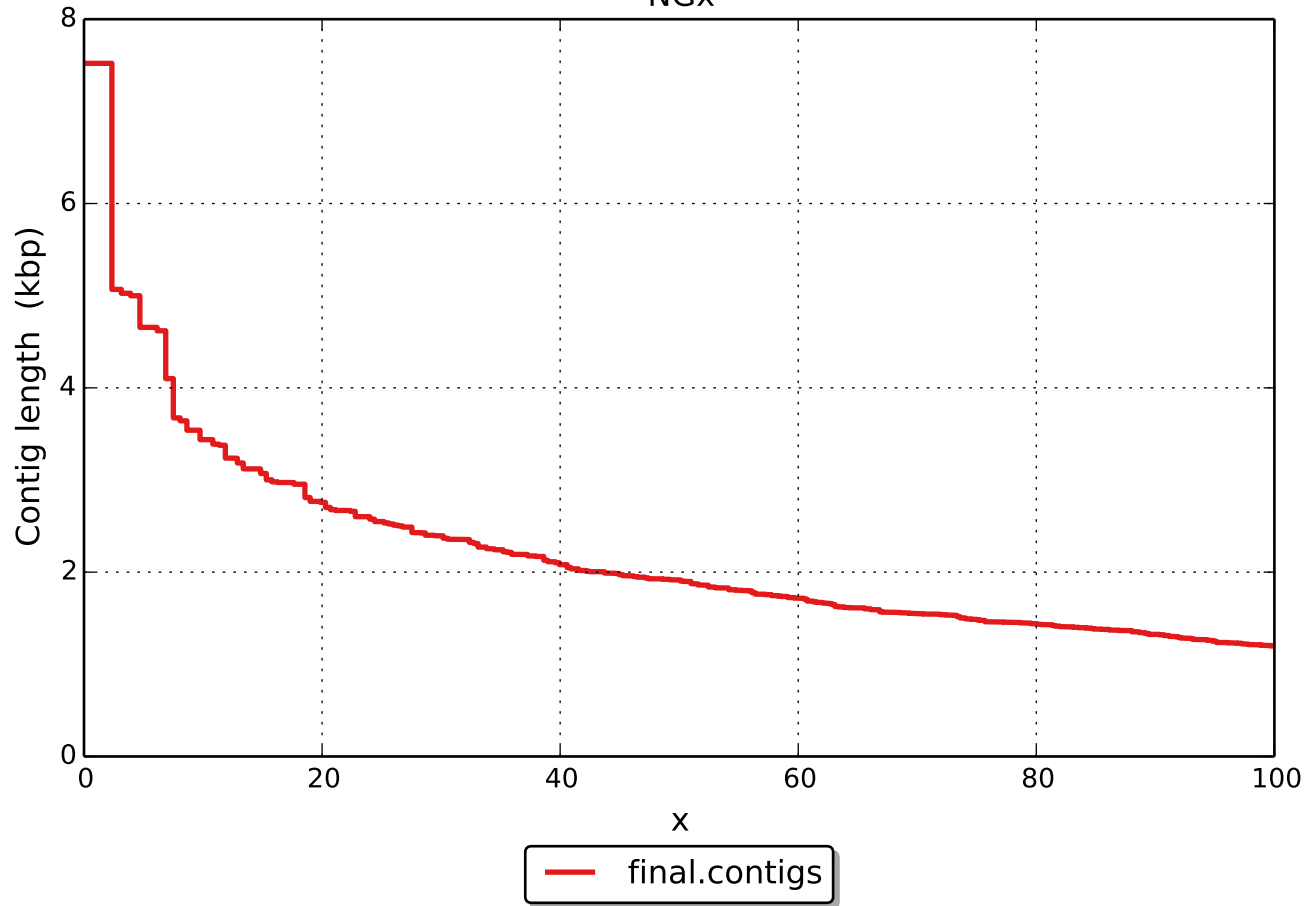


GC content

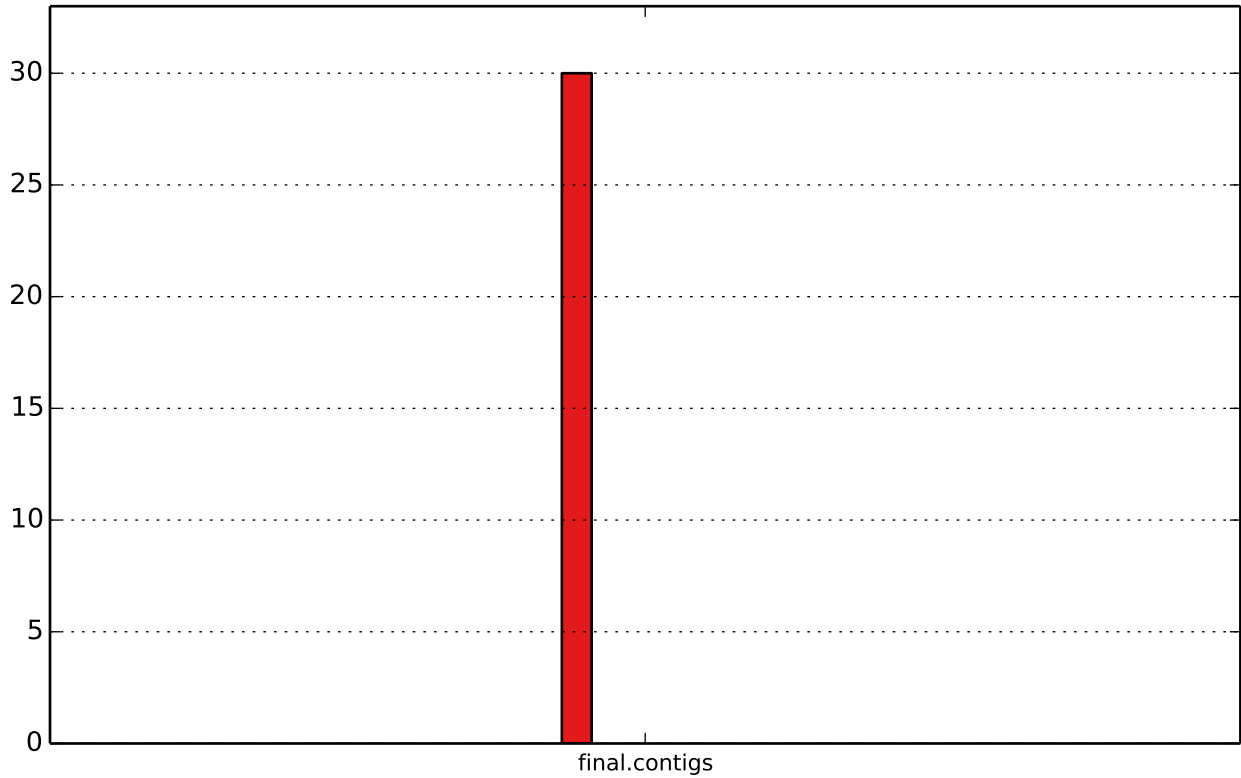




NGx



Misassemblies



 # relocations

Cumulative length (aligned contigs)

