

Report

	final.contigs
# contigs (≥ 0 bp)	3970
# contigs (≥ 1000 bp)	1122
Total length (≥ 0 bp)	3659589
Total length (≥ 1000 bp)	1687496
# contigs	3970
Largest contig	5163
Total length	3659589
Reference length	5478683
GC (%)	50.46
Reference GC (%)	50.50
N50	946
NG50	687
N75	687
L50	1269
LG50	2406
L75	2414
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	63.873
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	202.09
# indels per 100 kbp	0.14
Largest alignment	5163
NA50	946
NGA50	687
NA75	687
LA50	1269
LGA50	2406
LA75	2414

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

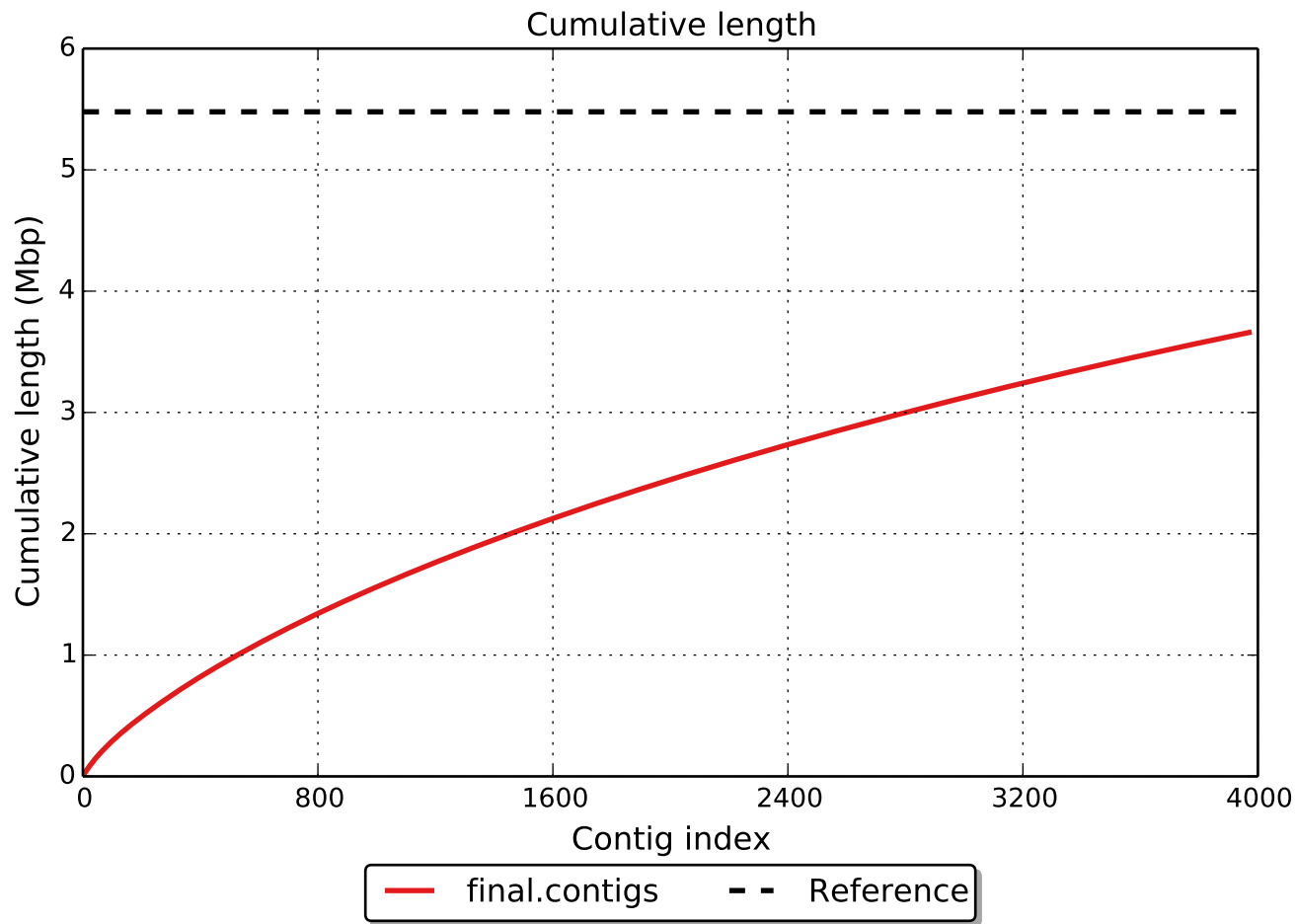
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	7072
# indels	5
# short indels	4
# long indels	1
Indels length	10

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).

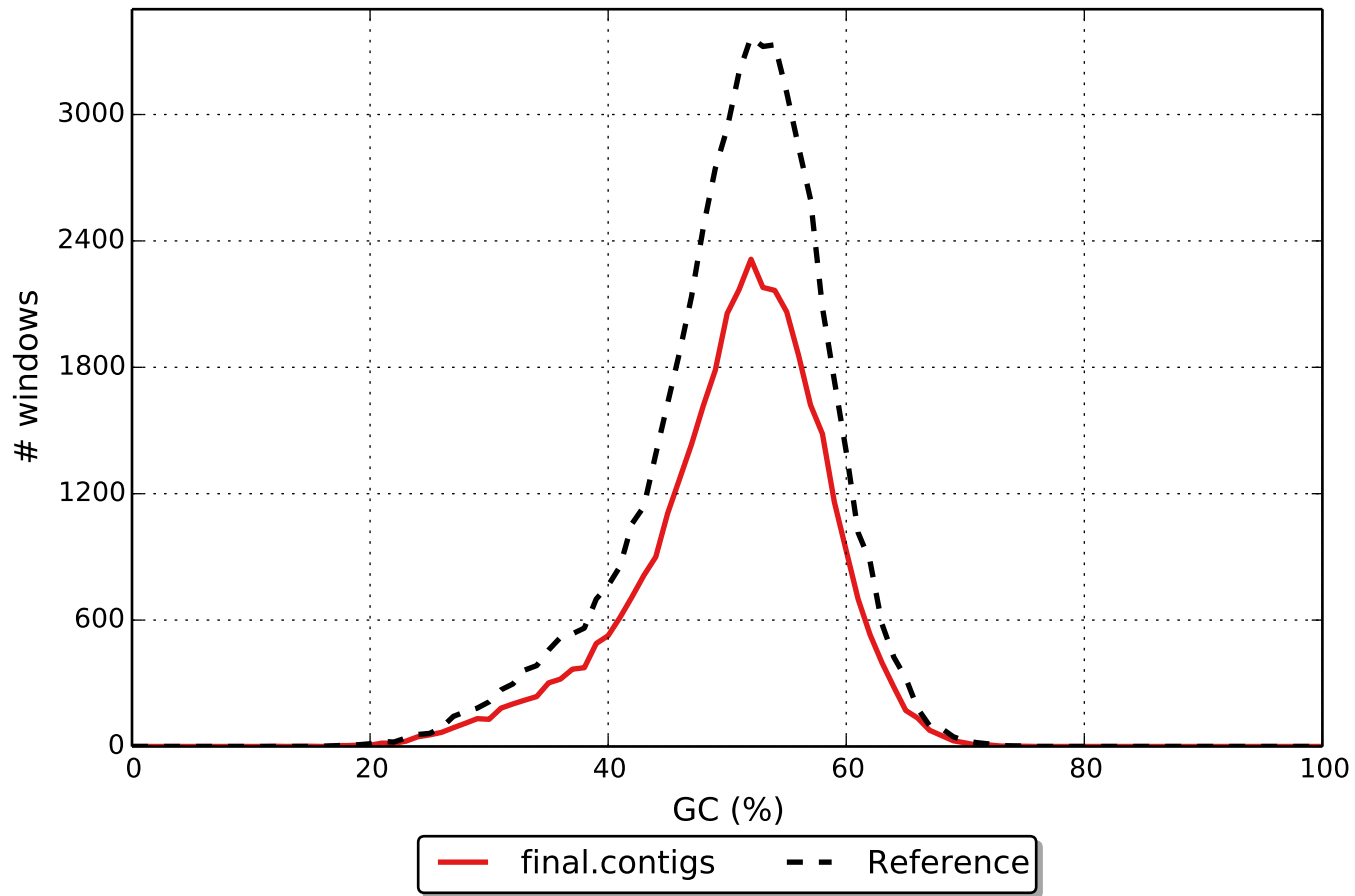
Unaligned report

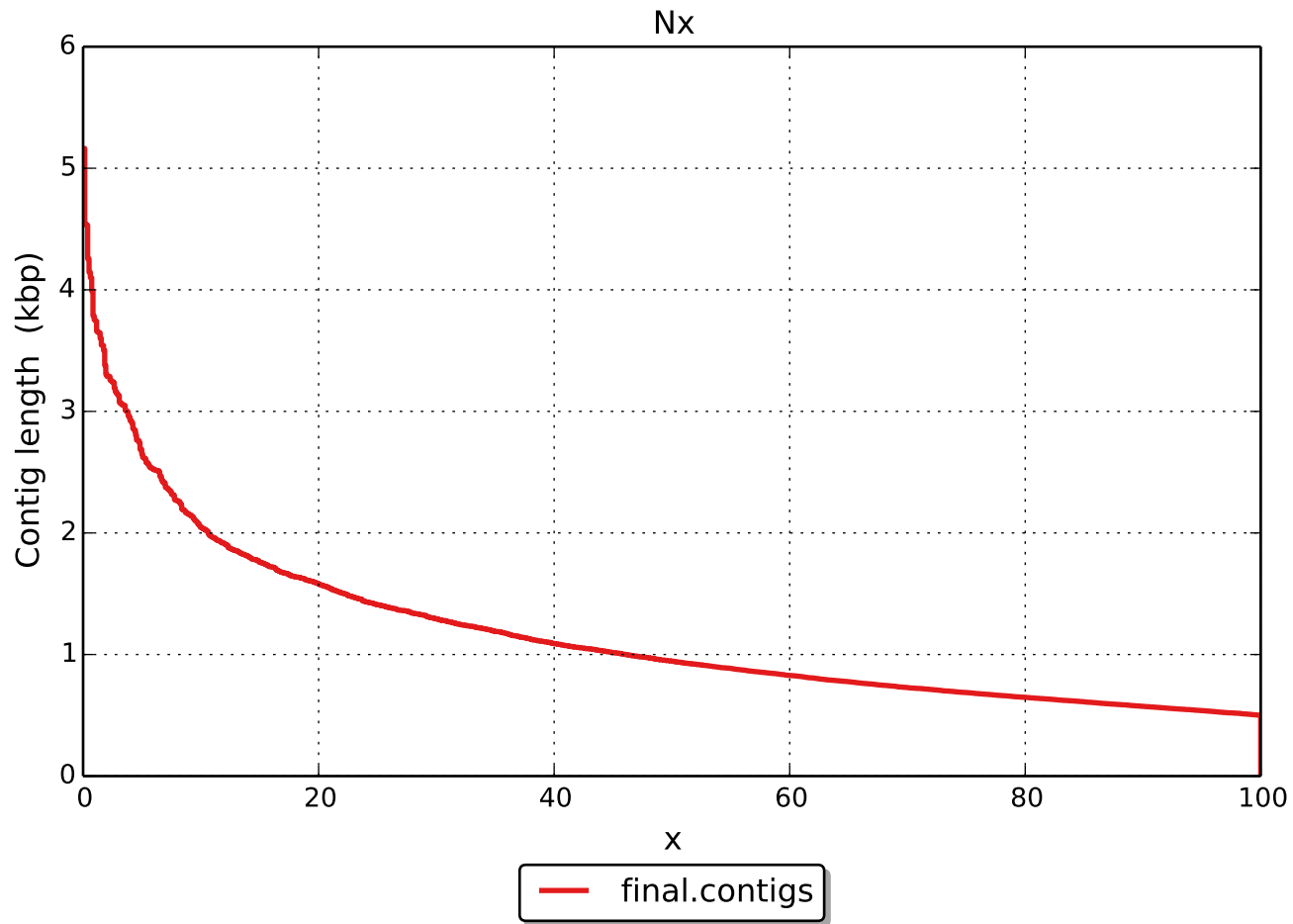
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

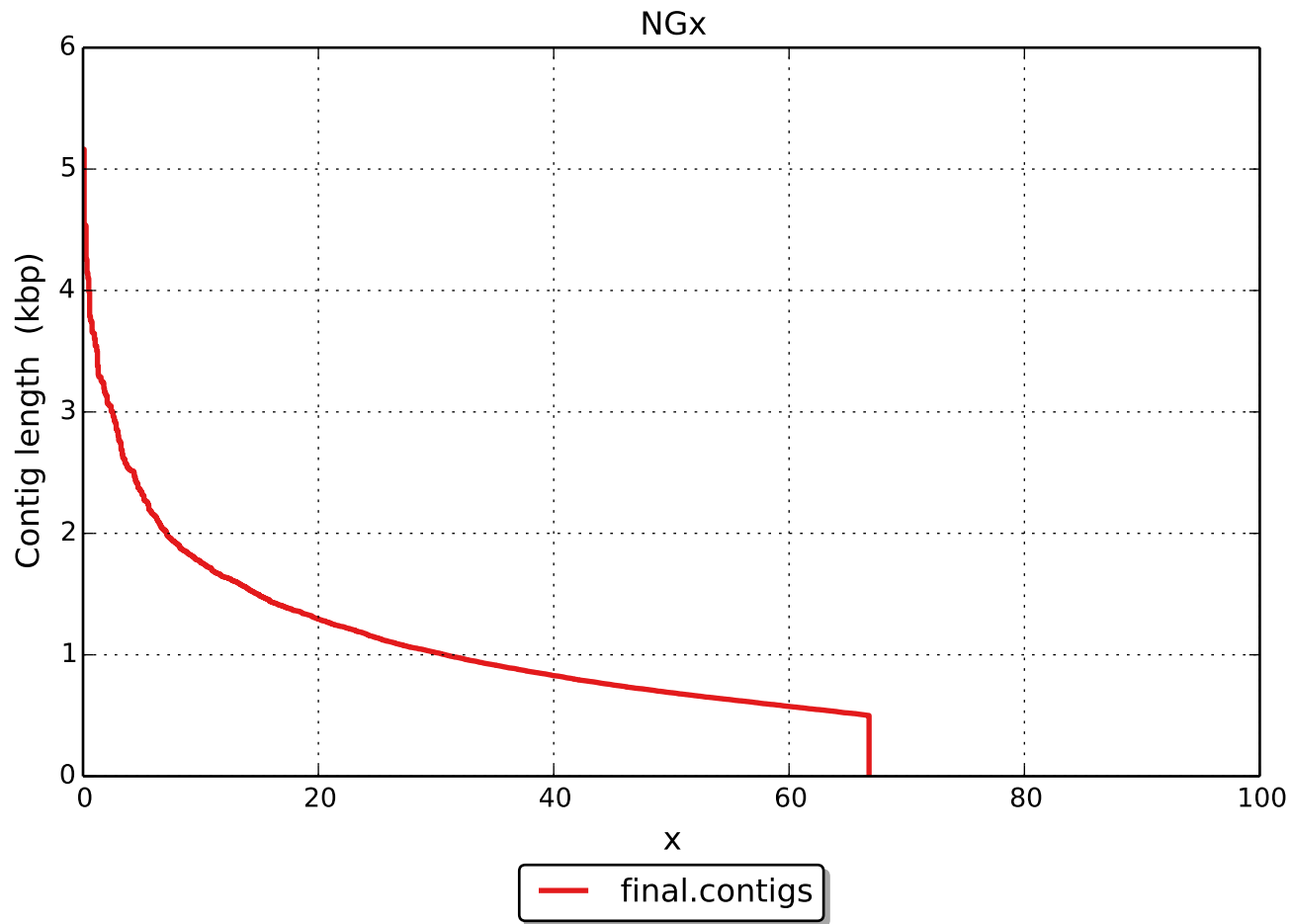
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



