

Report

	final.contigs
# contigs (>= 0 bp)	4010
# contigs (>= 1000 bp)	2195
Total length (>= 0 bp)	5352510
Total length (>= 1000 bp)	4041347
# contigs	4010
Largest contig	7685
Total length	5352510
Reference length	5547323
GC (%)	50.48
Reference GC (%)	50.49
N50	1577
NG50	1522
N75	1011
NG75	951
L50	1102
LG50	1165
L75	2169
LG75	2318
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.255
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	46.13
# indels per 100 kbp	0.08
Largest alignment	7685
NA50	1577
NGA50	1522
NA75	1011
NGA75	951
LA50	1102
LGA50	1165
LA75	2169
LGA75	2318

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

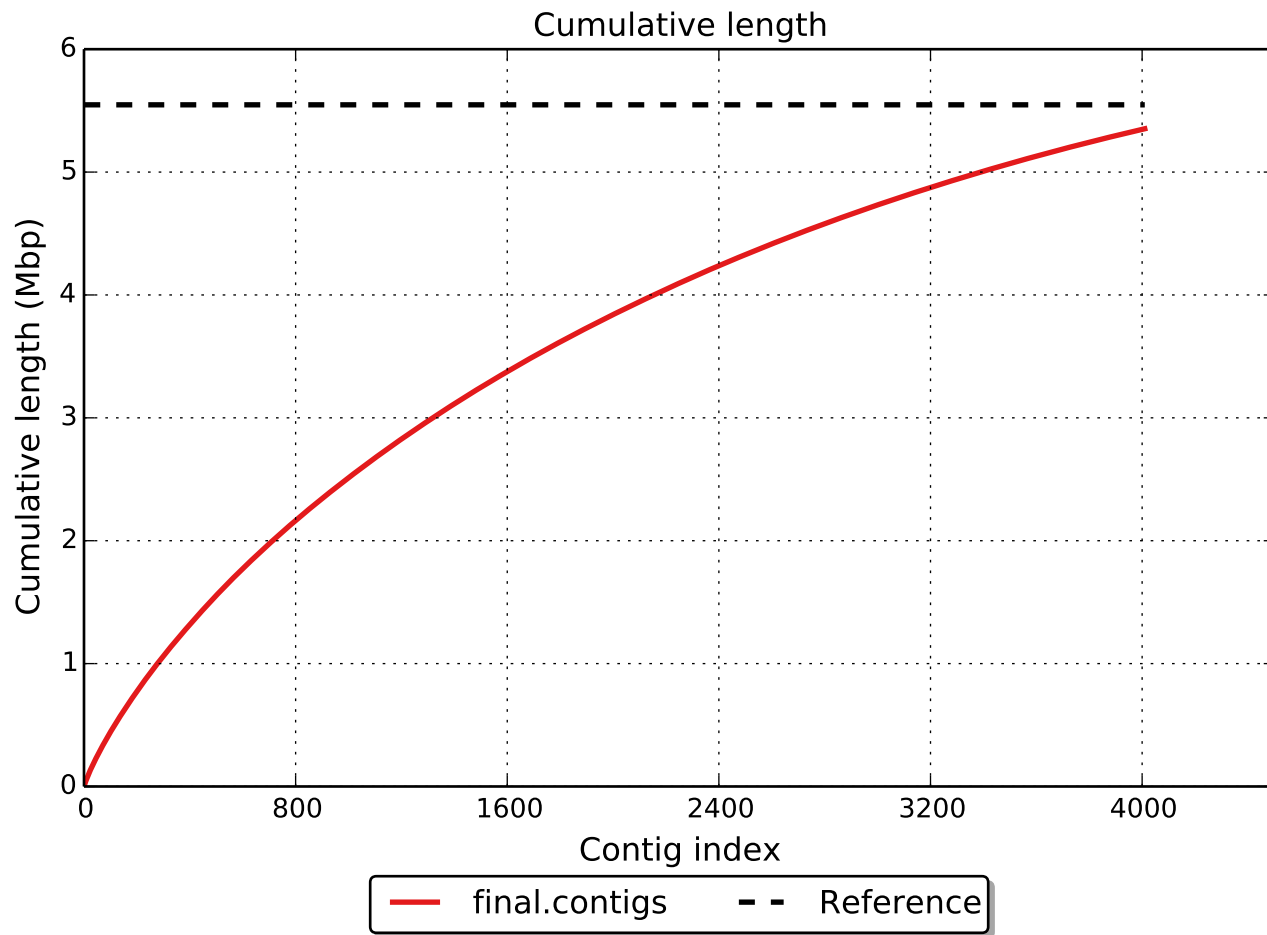
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	2361
# indels	4
# short indels	3
# long indels	1
Indels length	19

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).

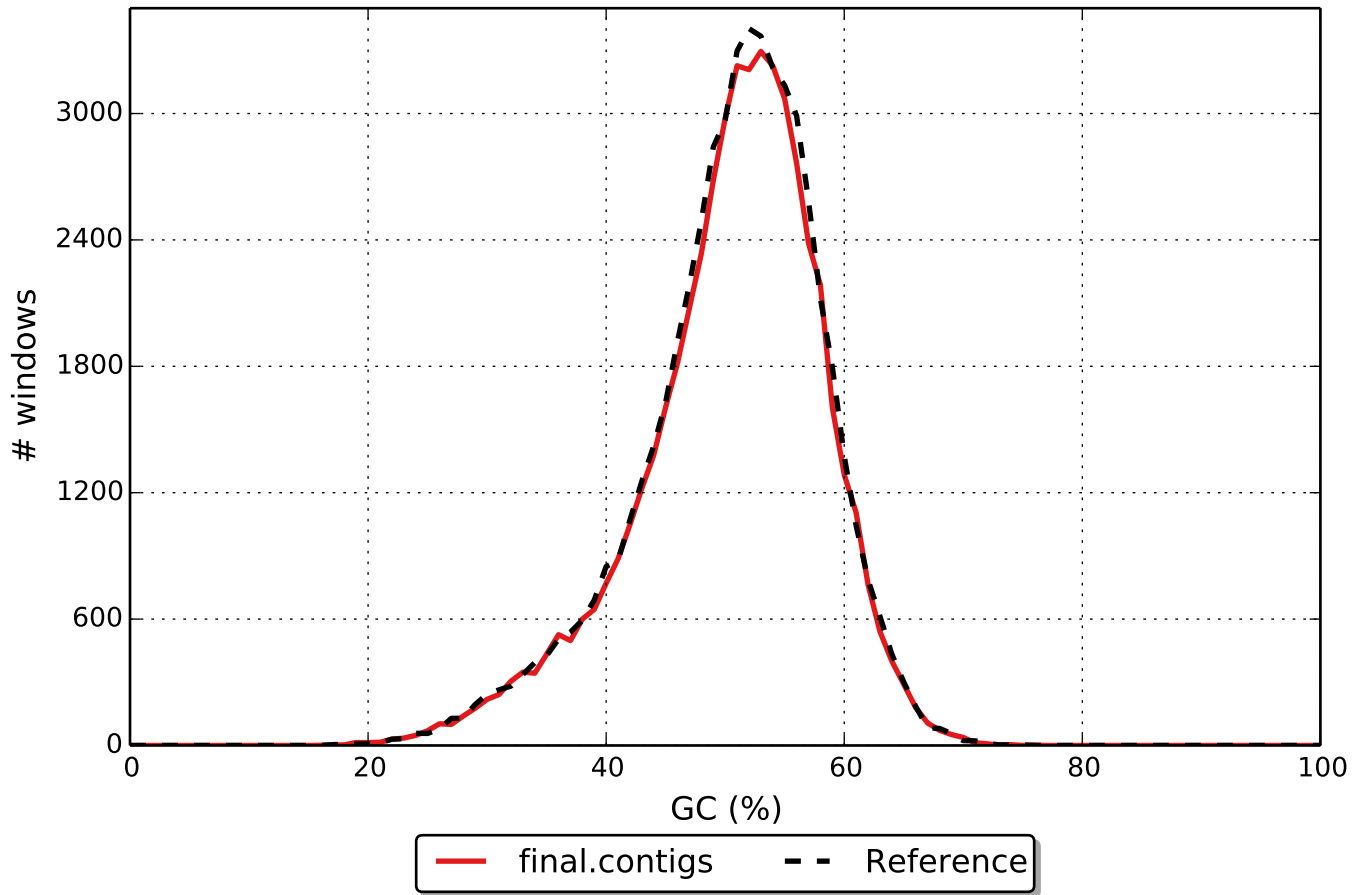
Unaligned report

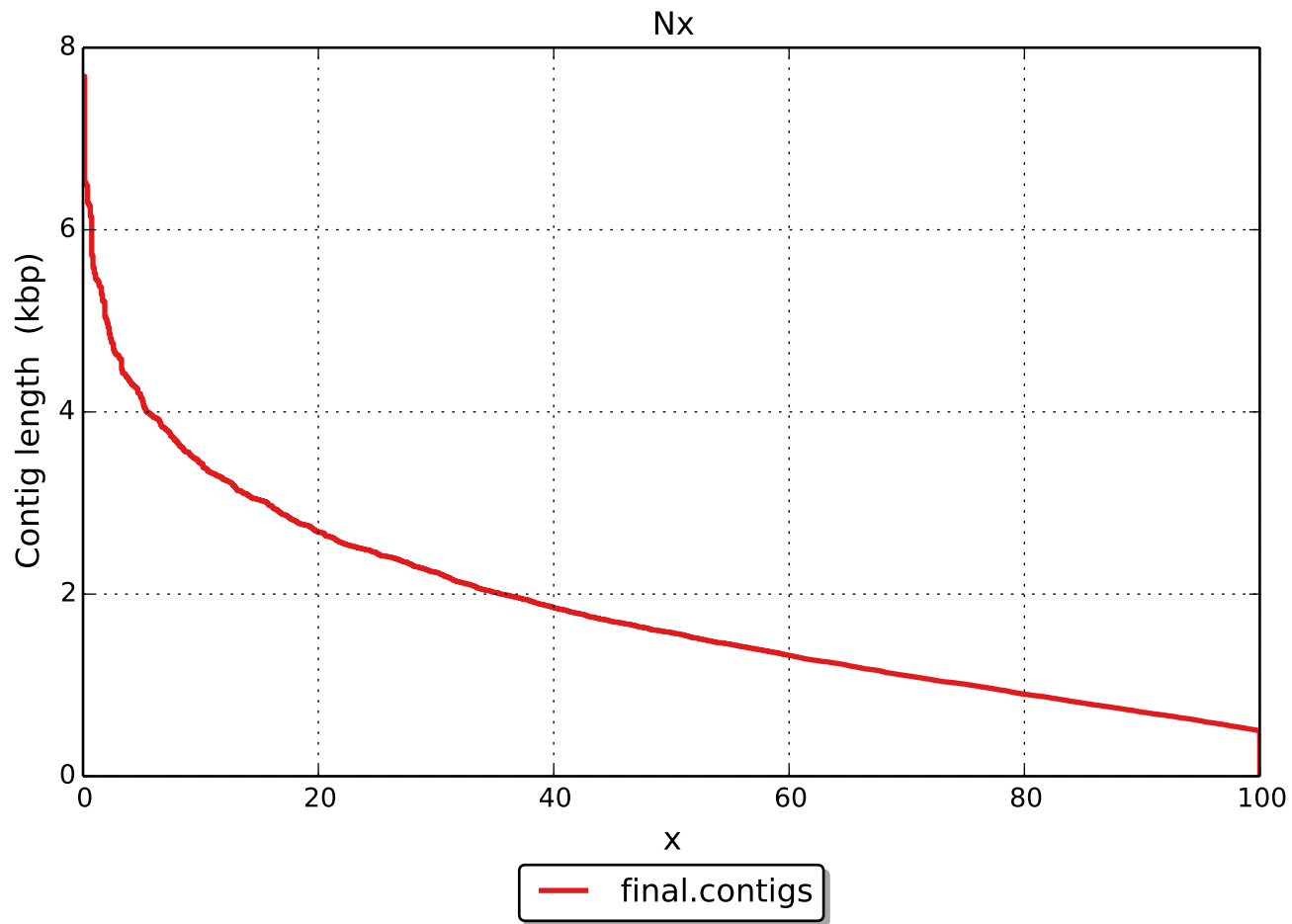
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

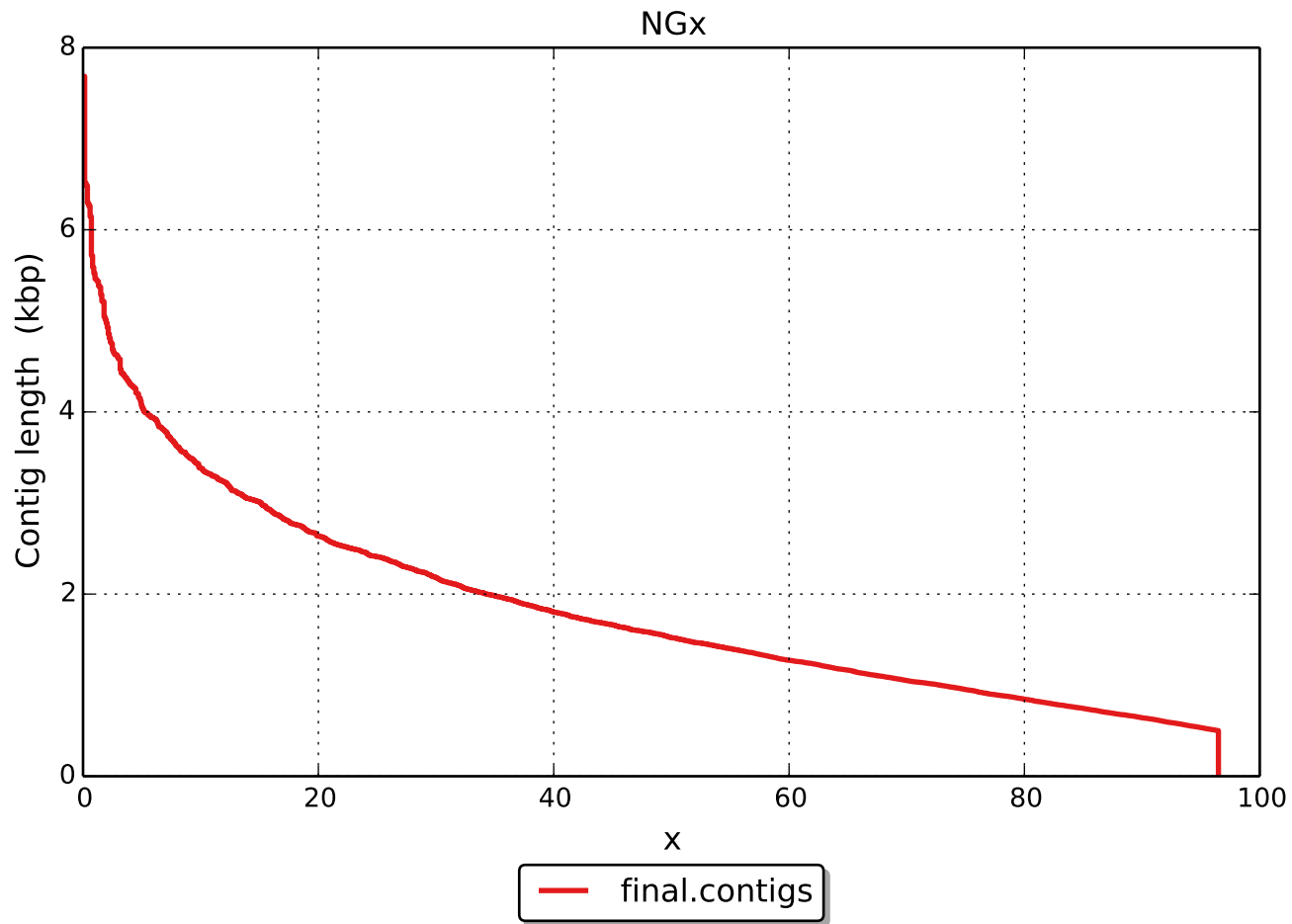
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



