

Report

	final.contigs
# contigs (>= 0 bp)	4065
# contigs (>= 1000 bp)	2219
Total length (>= 0 bp)	5424073
Total length (>= 1000 bp)	4092285
# contigs	4065
Largest contig	7685
Total length	5424073
Reference length	5547323
GC (%)	50.47
Reference GC (%)	50.49
N50	1576
NG50	1545
N75	1009
NG75	973
L50	1114
LG50	1153
L75	2195
LG75	2289
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	93.018
Duplication ratio	1.051
# N's per 100 kbp	0.00
# mismatches per 100 kbp	64.98
# indels per 100 kbp	0.08
Largest alignment	7685
NA50	1576
NGA50	1545
NA75	1009
NGA75	973
LA50	1114
LGA50	1153
LA75	2195
LGA75	2289

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

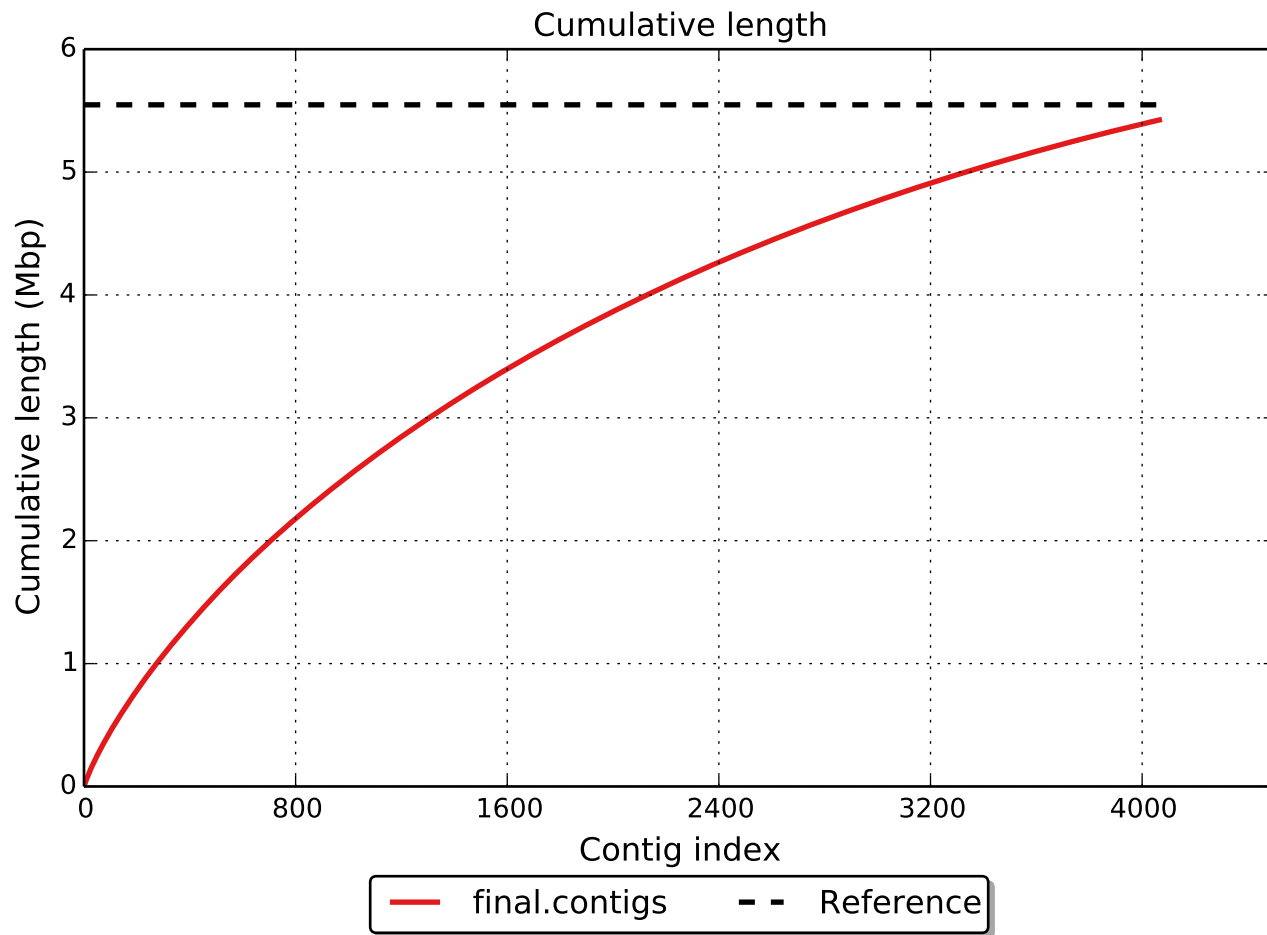
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	3353
# indels	4
# short indels	3
# long indels	1
Indels length	19

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).

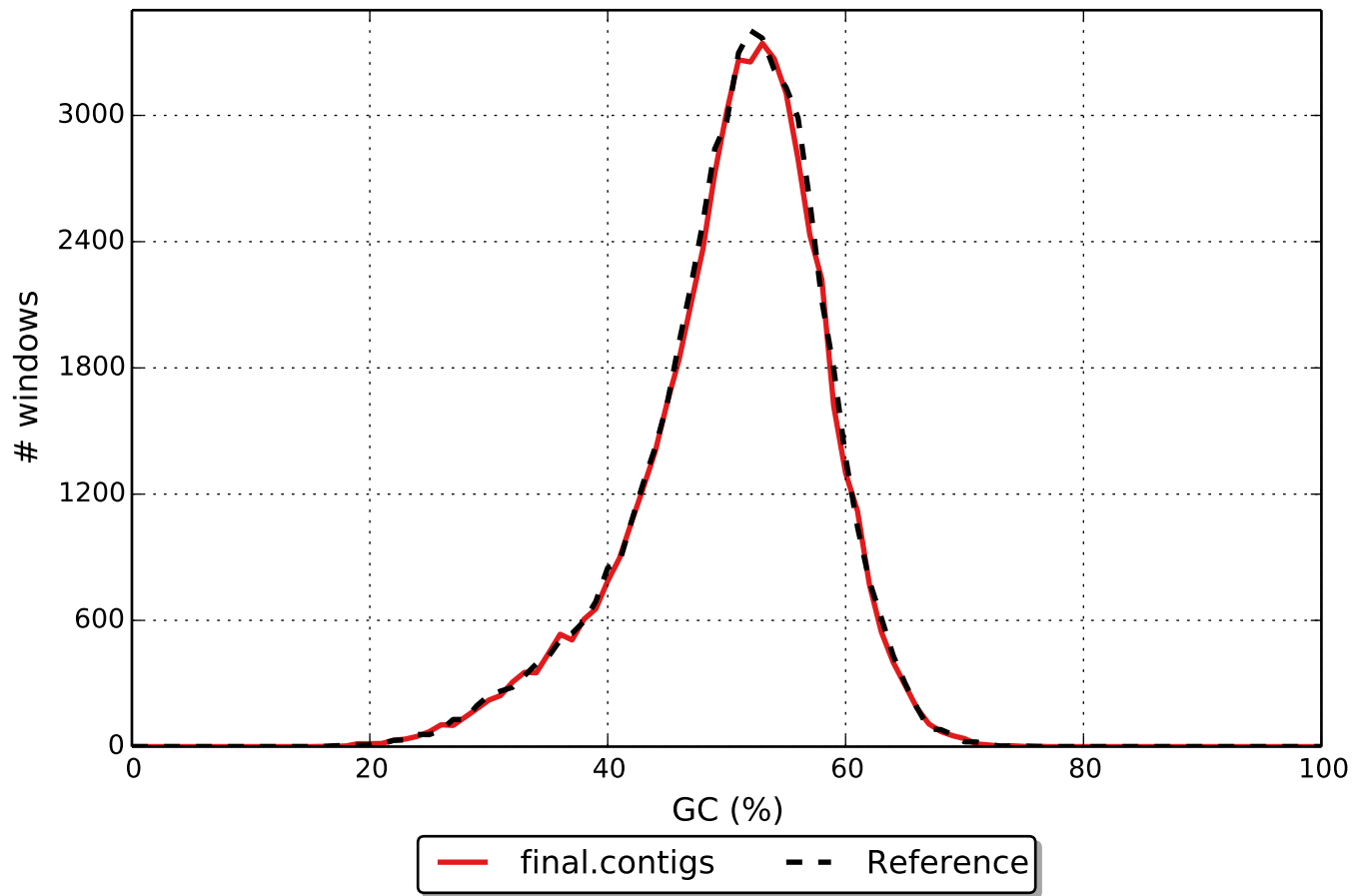
Unaligned report

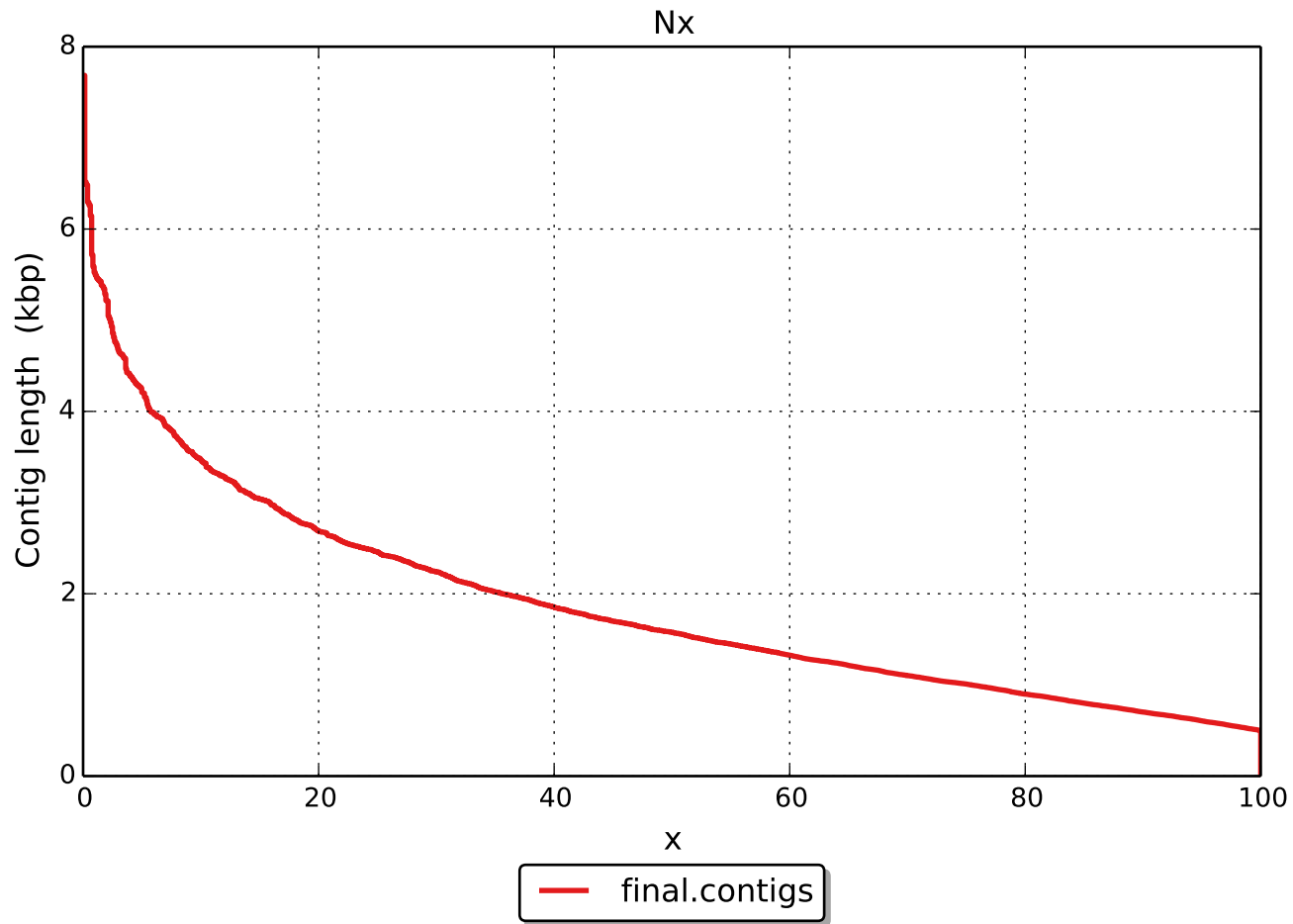
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

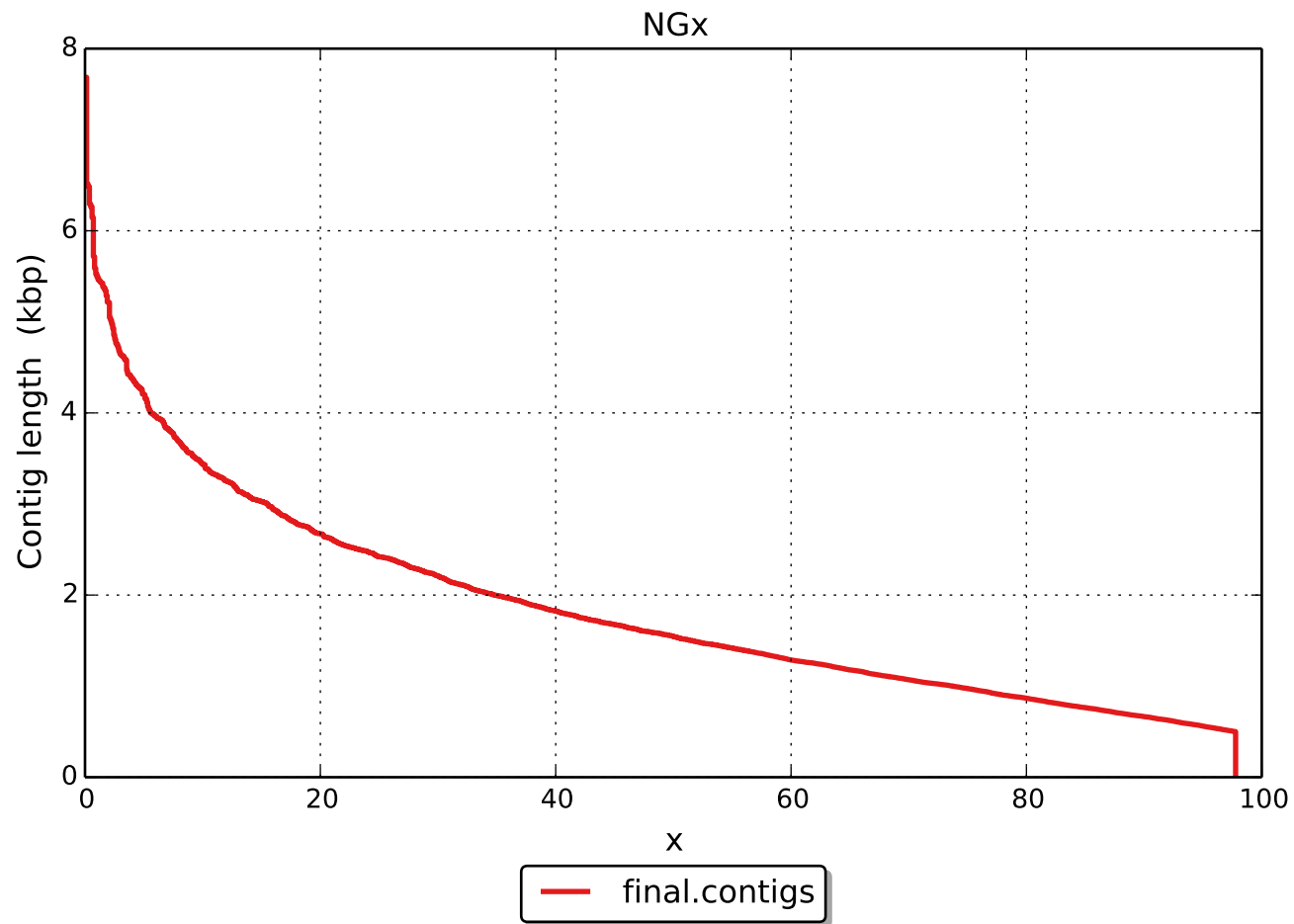
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content







Misassemblies



