

Report

	final.contigs
# contigs (≥ 0 bp)	4414
# contigs (≥ 1000 bp)	1188
Total length (≥ 0 bp)	3925507
Total length (≥ 1000 bp)	1667565
# contigs	4414
Largest contig	4257
Total length	3925507
Reference length	5547323
GC (%)	50.26
Reference GC (%)	50.48
N50	913
NG50	718
N75	683
L50	1496
LG50	2502
L75	2746
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	86
Genome fraction (%)	67.487
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	128.19
# indels per 100 kbp	0.16
Largest alignment	4257
NA50	913
NGA50	718
NA75	683
LA50	1496
LGA50	2502
LA75	2746

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

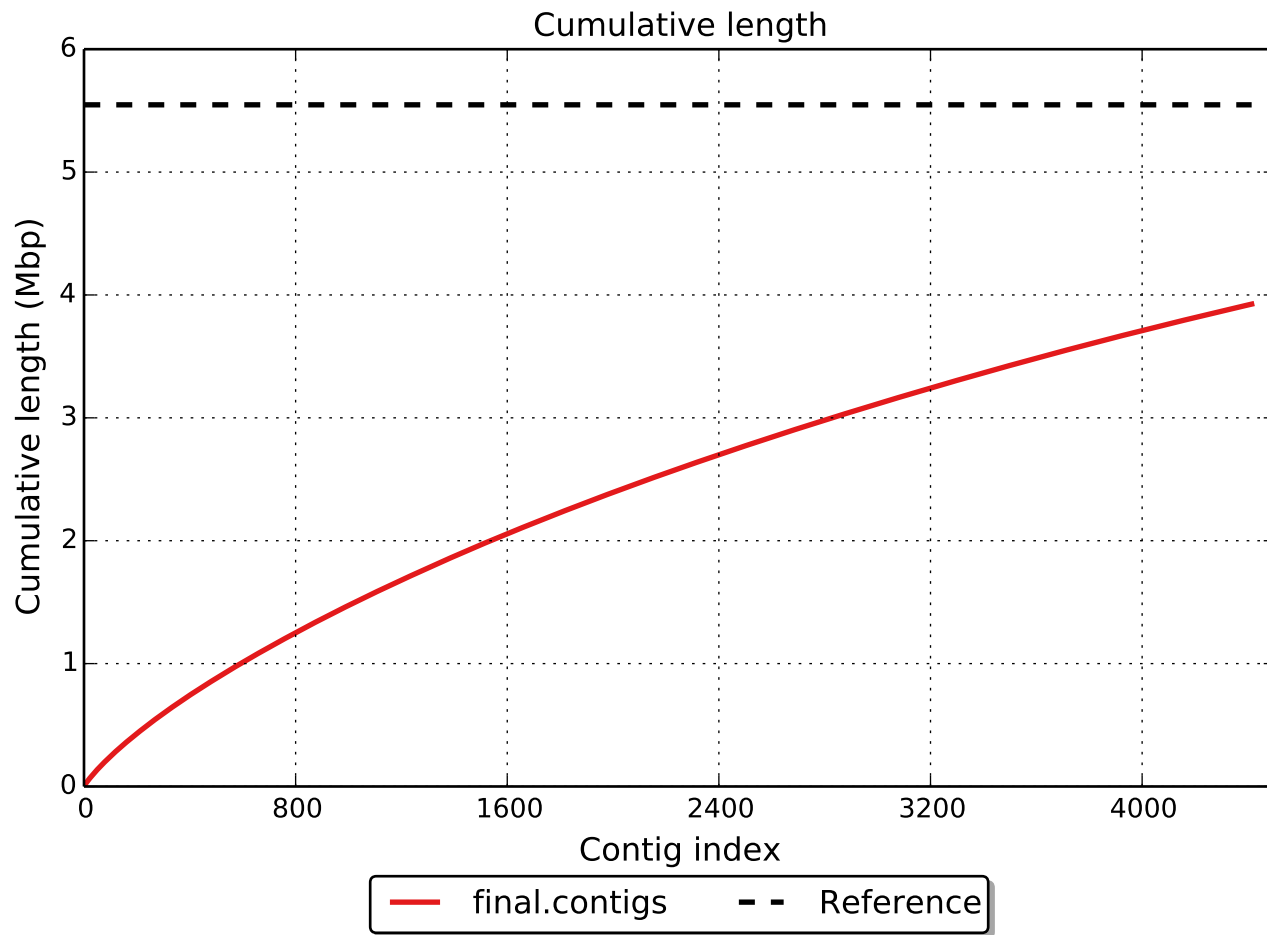
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	4799
# indels	6
# short indels	5
# long indels	1
Indels length	25

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).

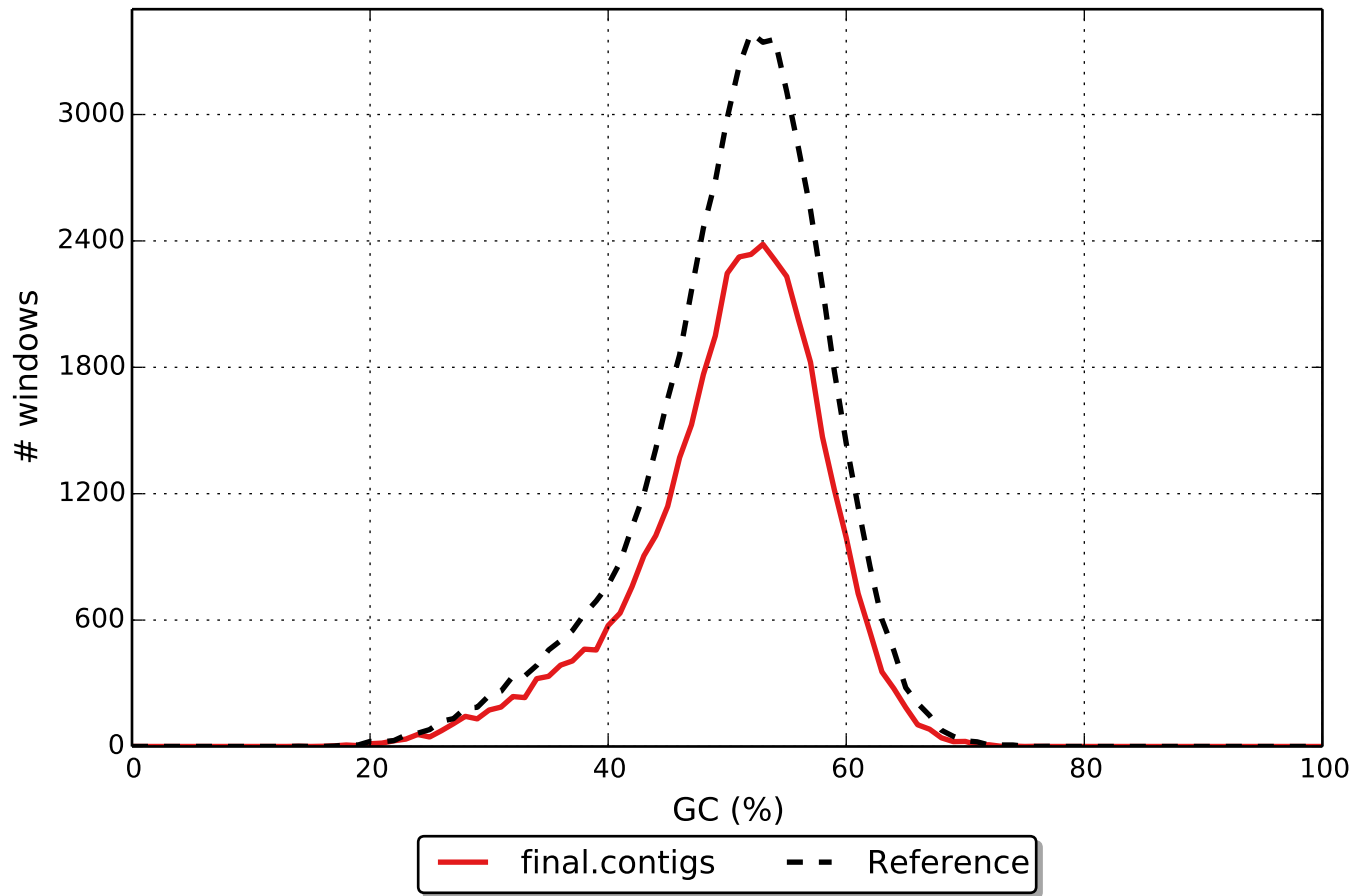
Unaligned report

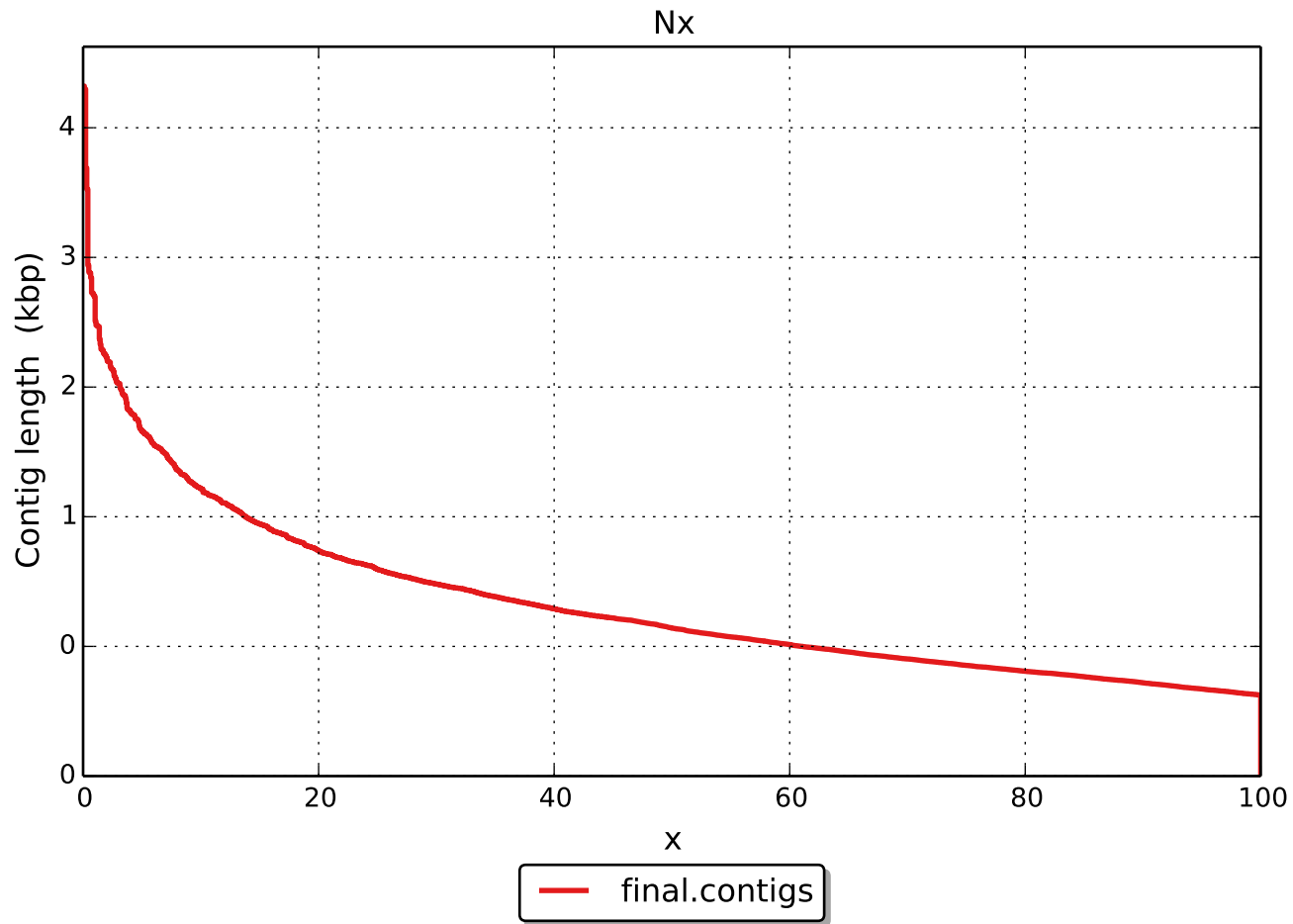
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	86
# N's	0

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).

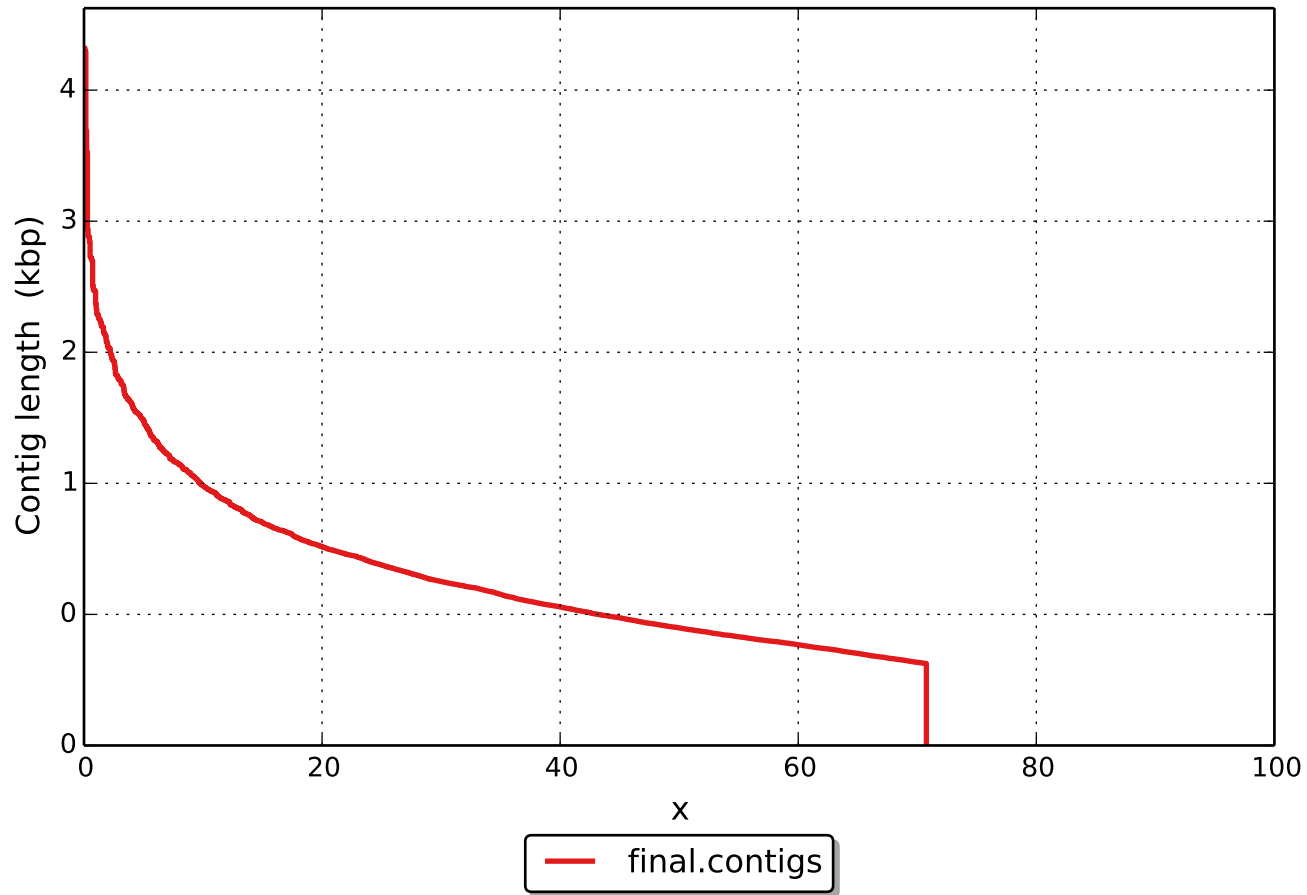


GC content



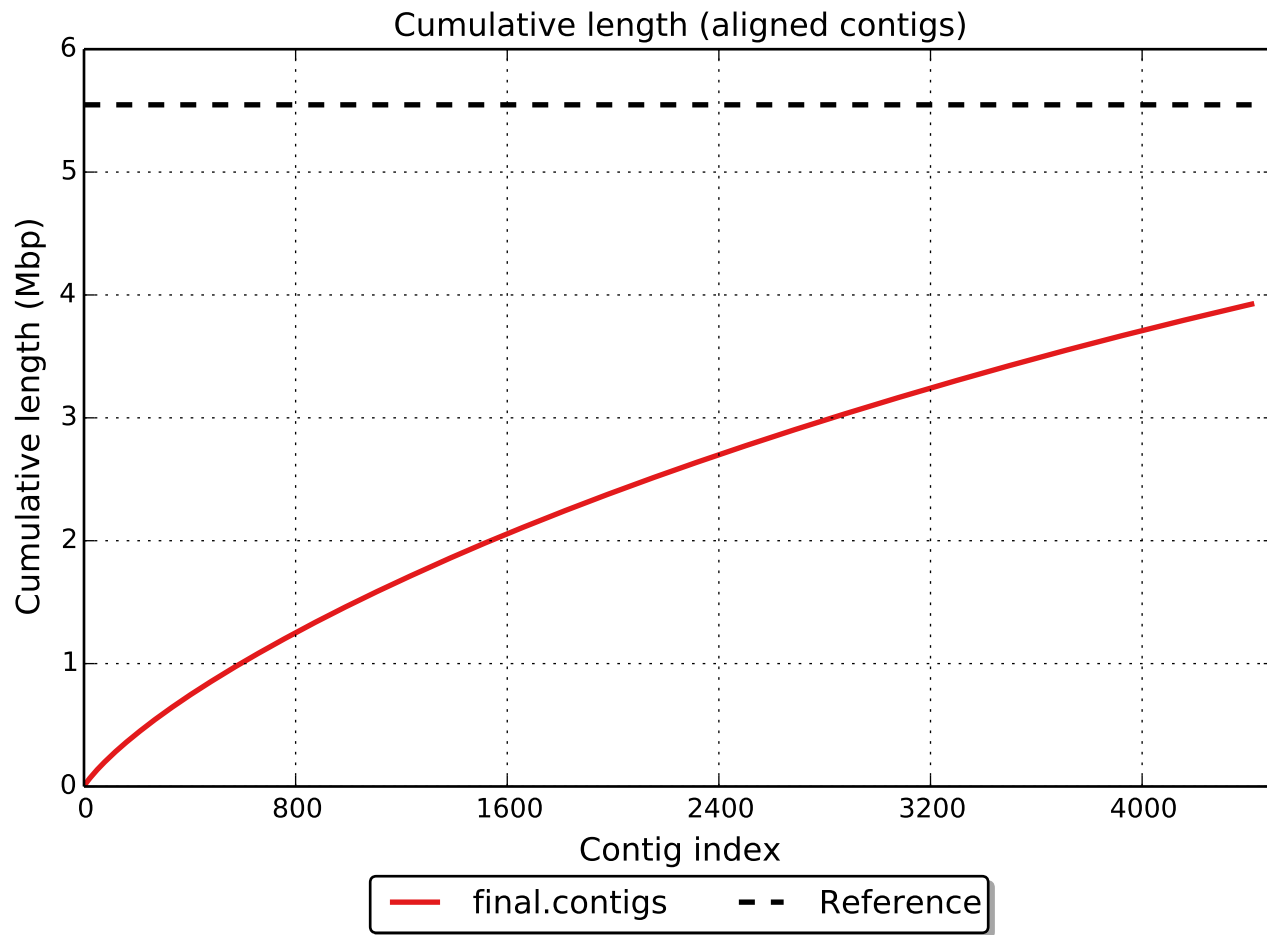


NGx

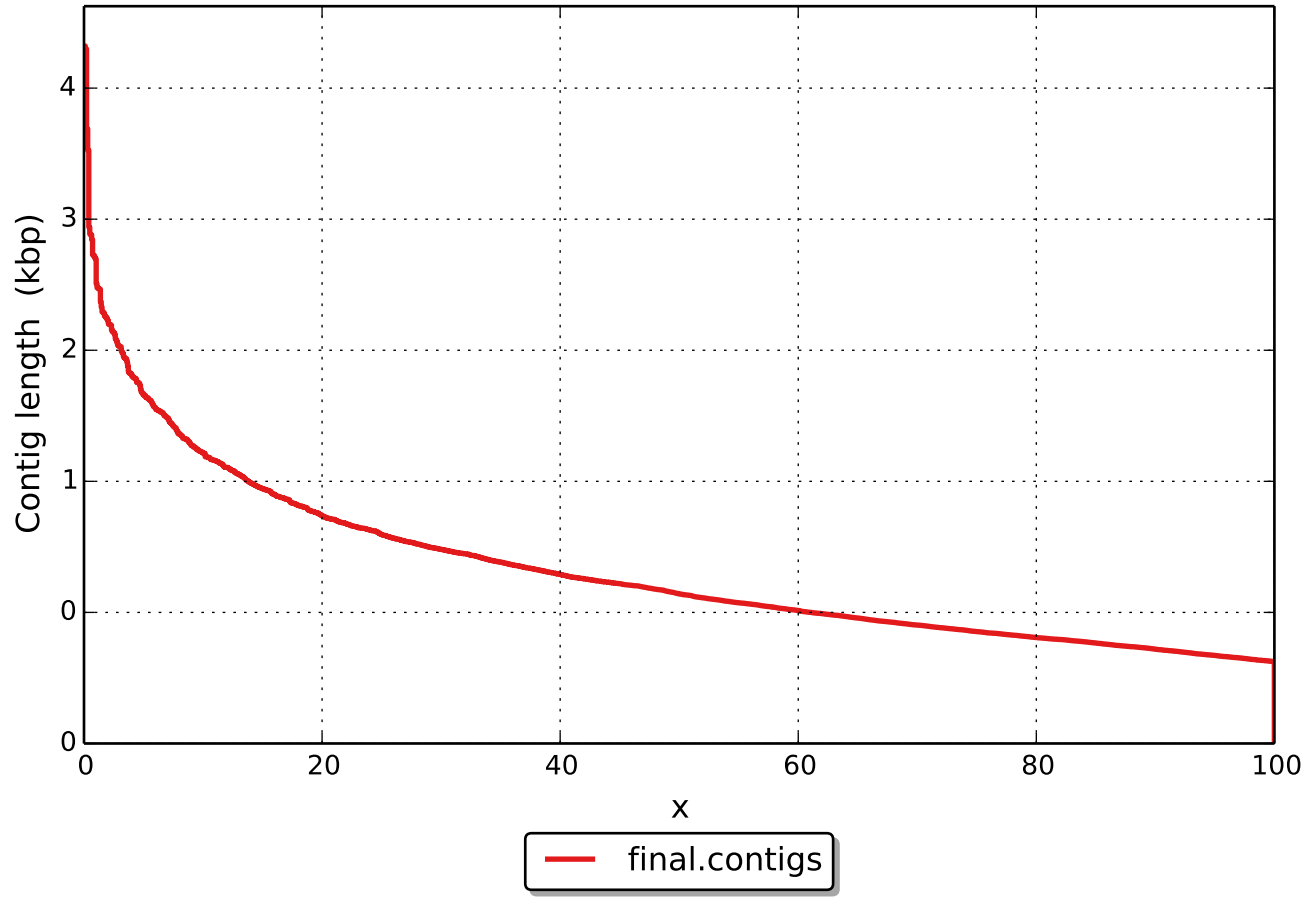


Misassemblies





NAx



NGAx

