

Report

	final.contigs
# contigs (≥ 0 bp)	4354
# contigs (≥ 1000 bp)	1832
Total length (≥ 0 bp)	4812783
Total length (≥ 1000 bp)	2999218
# contigs	4354
Largest contig	6941
Total length	4812783
Reference length	5478683
GC (%)	50.28
Reference GC (%)	50.49
N50	1230
NG50	1096
N75	827
NG75	691
L50	1297
LG50	1584
L75	2504
LG75	3164
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	83.432
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.31
# indels per 100 kbp	0.15
Largest alignment	6941
NA50	1230
NGA50	1096
NA75	827
NGA75	691
LA50	1297
LGA50	1584
LA75	2504
LGA75	3164

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

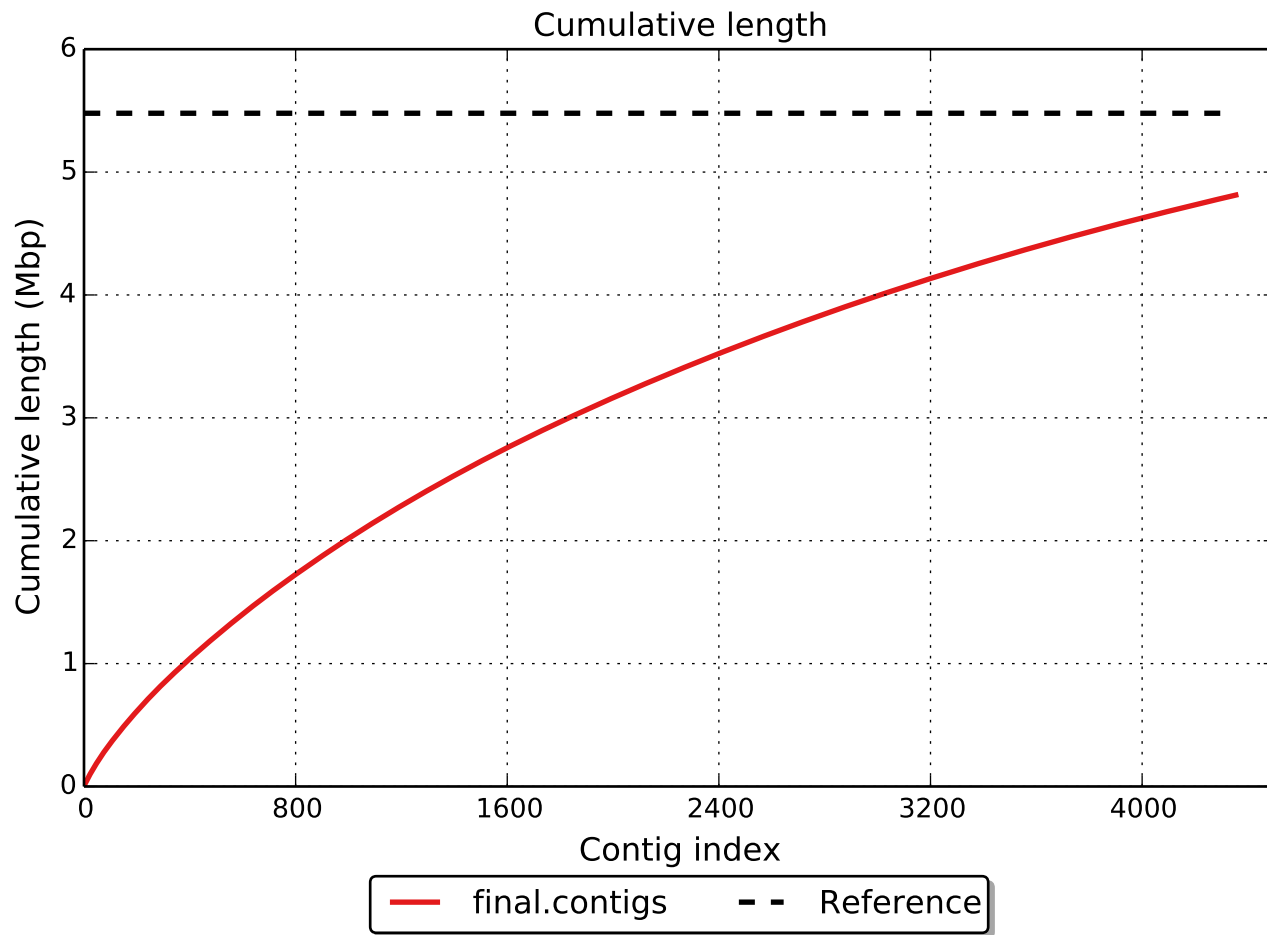
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3945
# indels	7
# short indels	4
# long indels	3
Indels length	52

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).

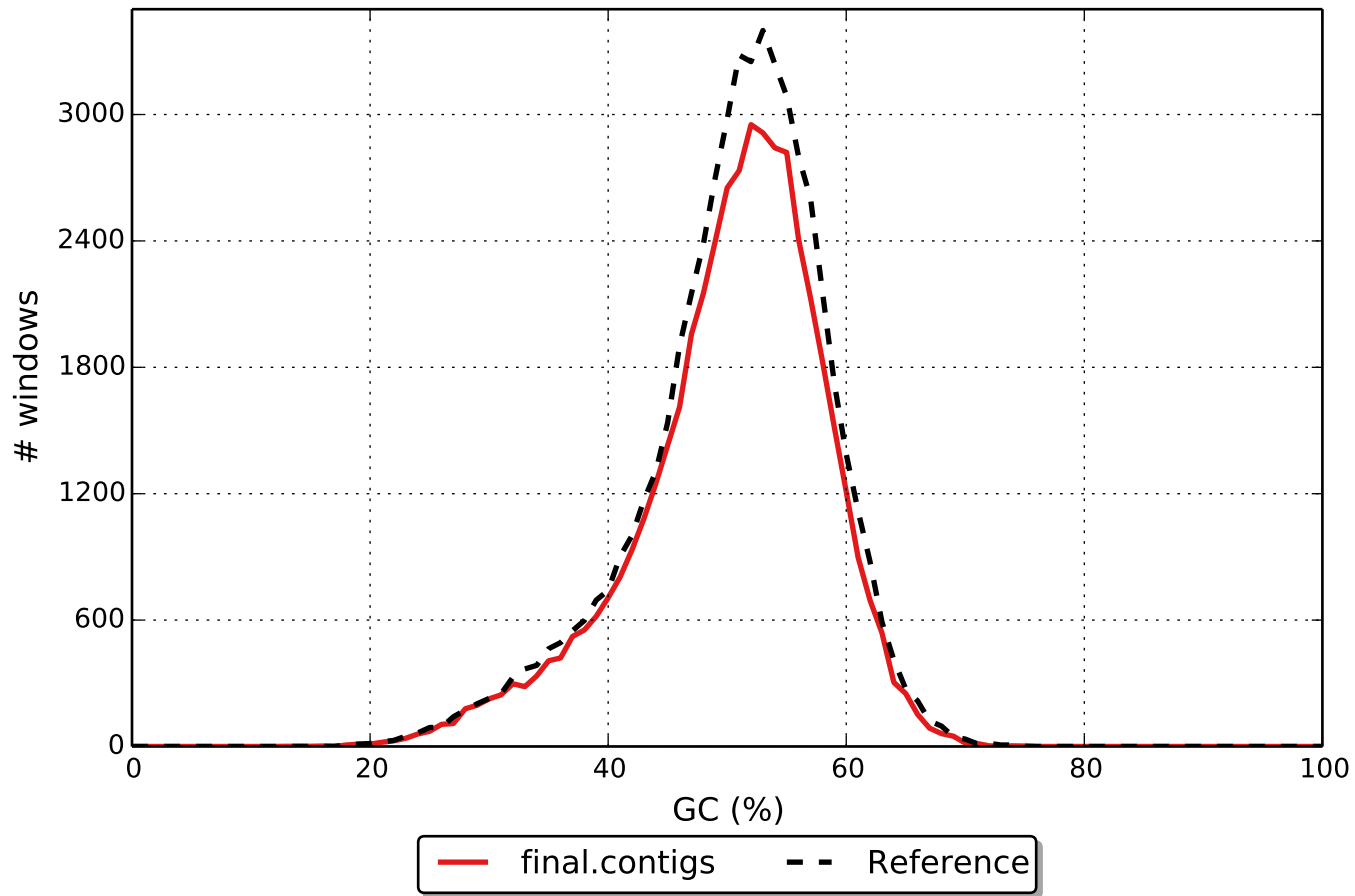
Unaligned report

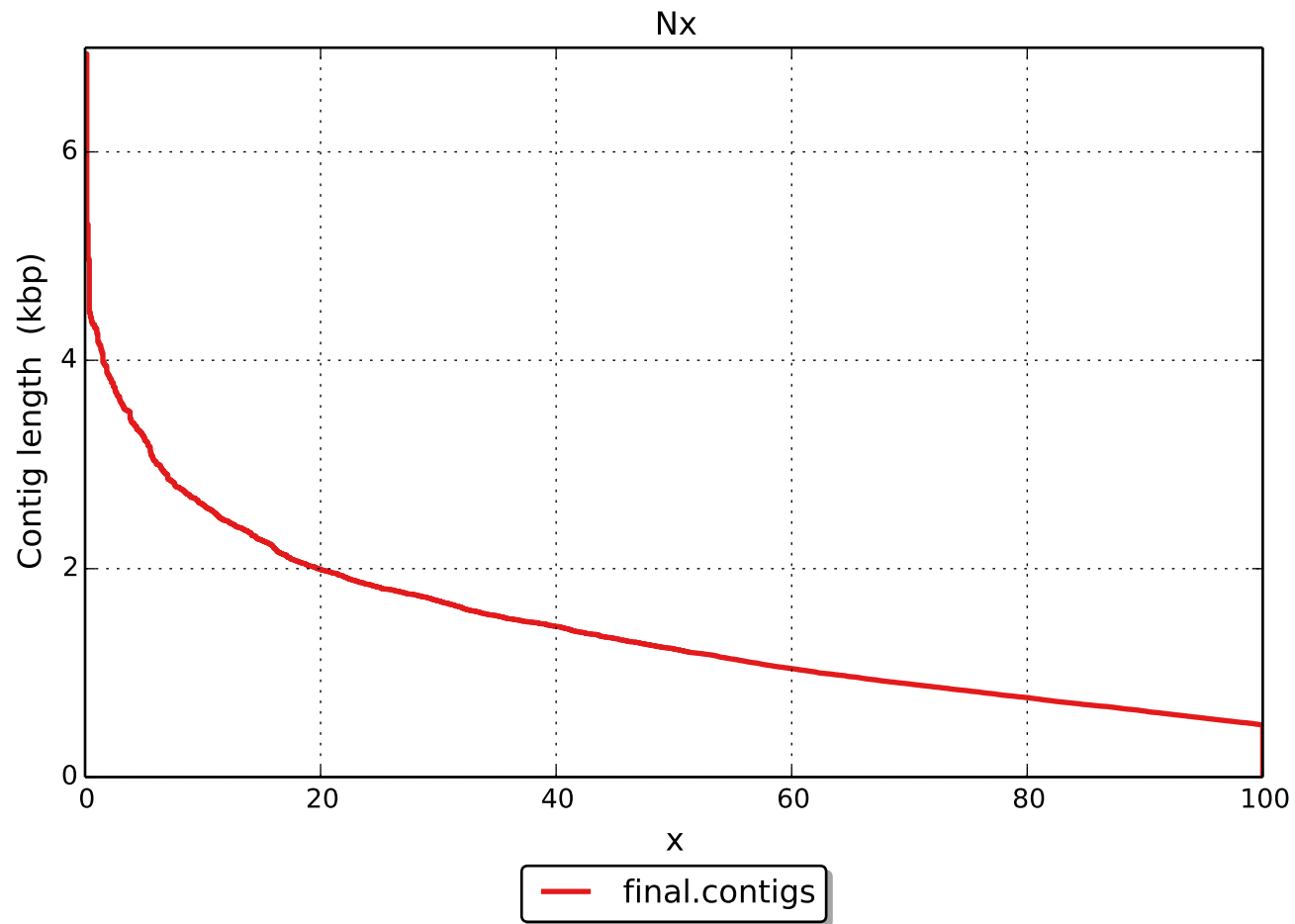
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

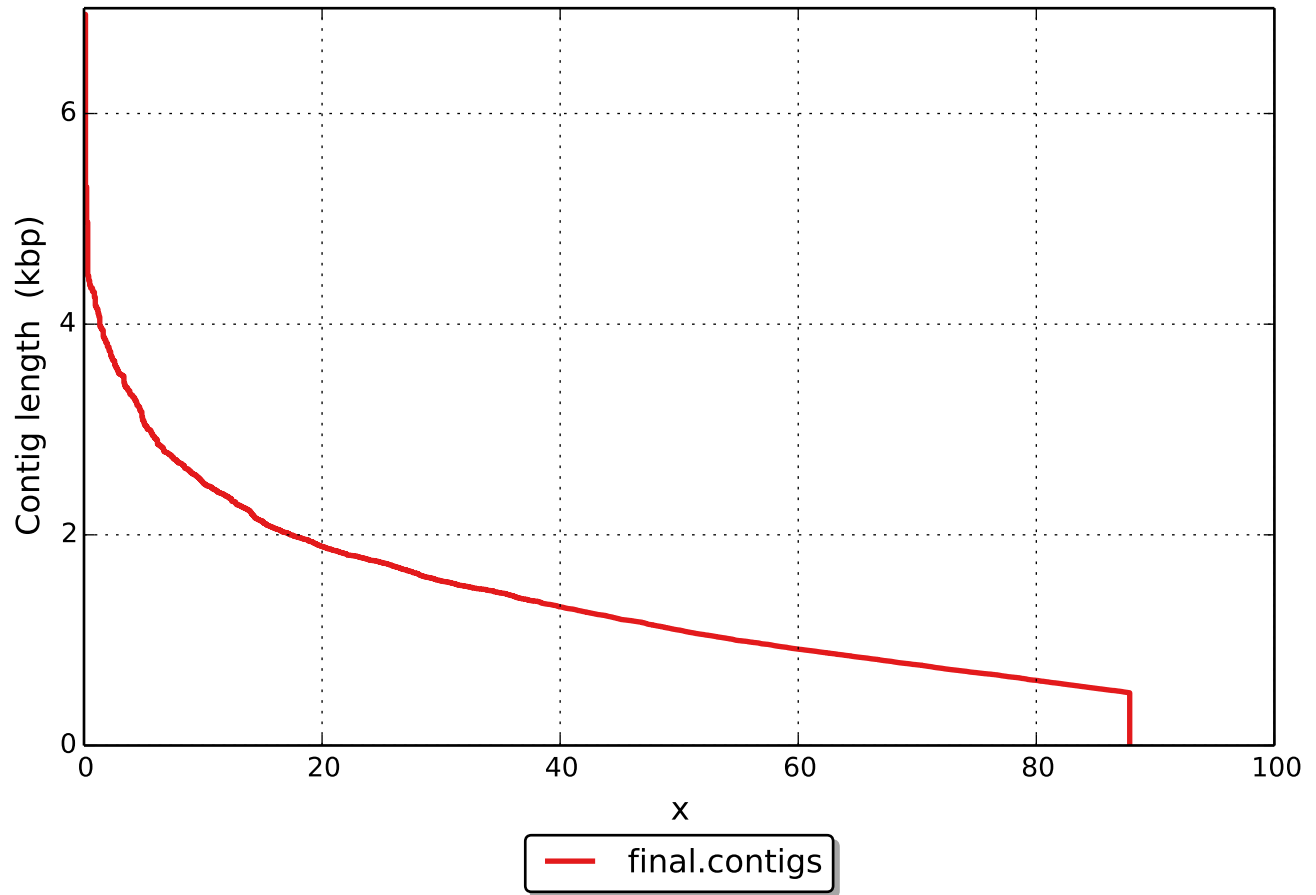


GC content



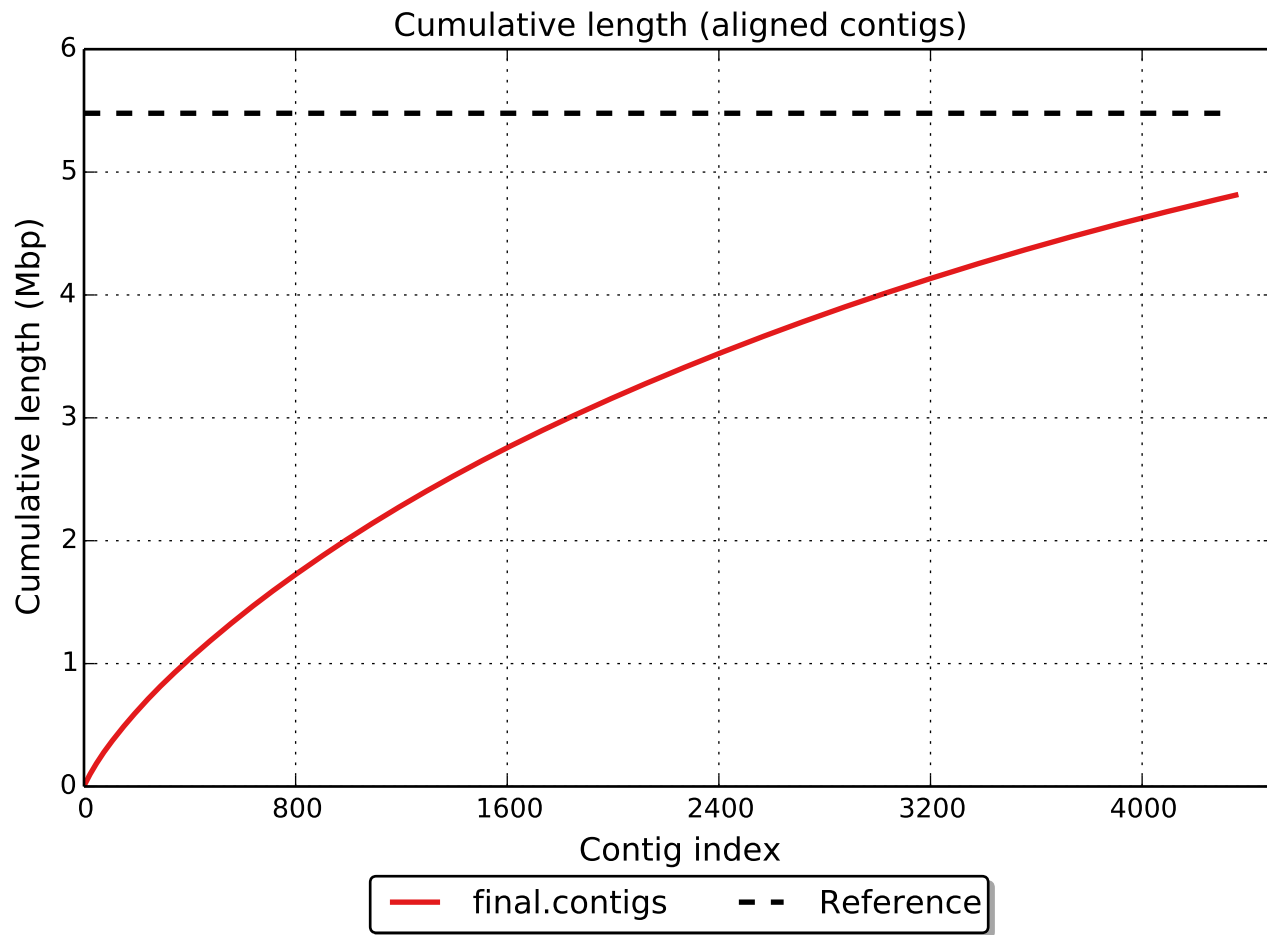


NGx

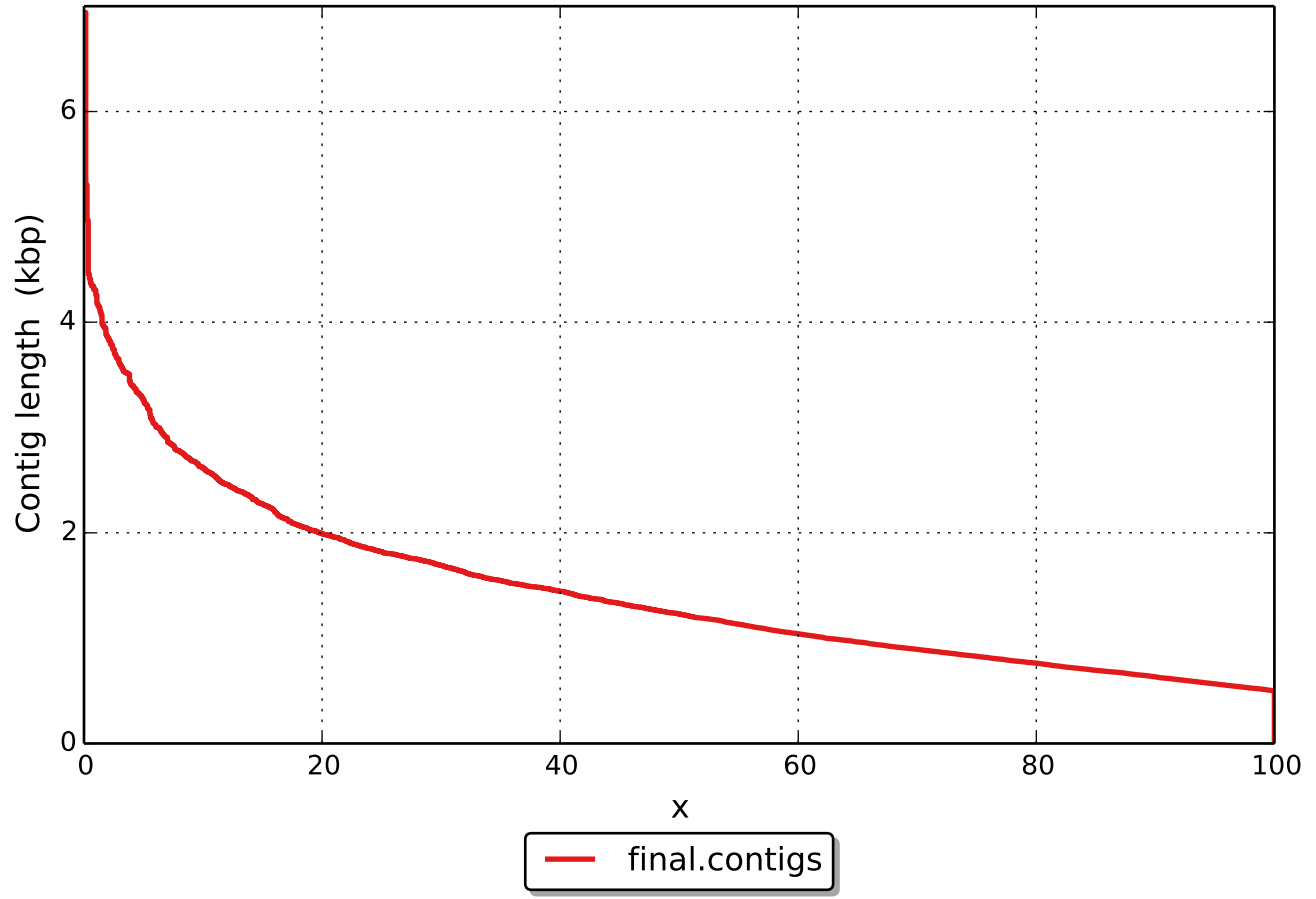


Misassemblies





NAx



NGAx

