

Report

	final.contigs
# contigs (>= 0 bp)	83
# contigs (>= 1000 bp)	81
Total length (>= 0 bp)	1289930
Total length (>= 1000 bp)	1288922
# contigs	83
Largest contig	60549
Total length	1289930
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	23452
NG50	43302
N75	14400
NG75	33068
L50	17
LG50	7
L75	34
LG75	11
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	39 + 2 part
Unaligned length	643905
Genome fraction (%)	99.976
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.96
# indels per 100 kbp	0.00
Largest alignment	60549
NA50	504
NGA50	23452
NGA75	12992
LA50	42
LGA50	7
LGA75	16

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	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	19
# indels	0
# short indels	0
# long indels	0
Indels length	0

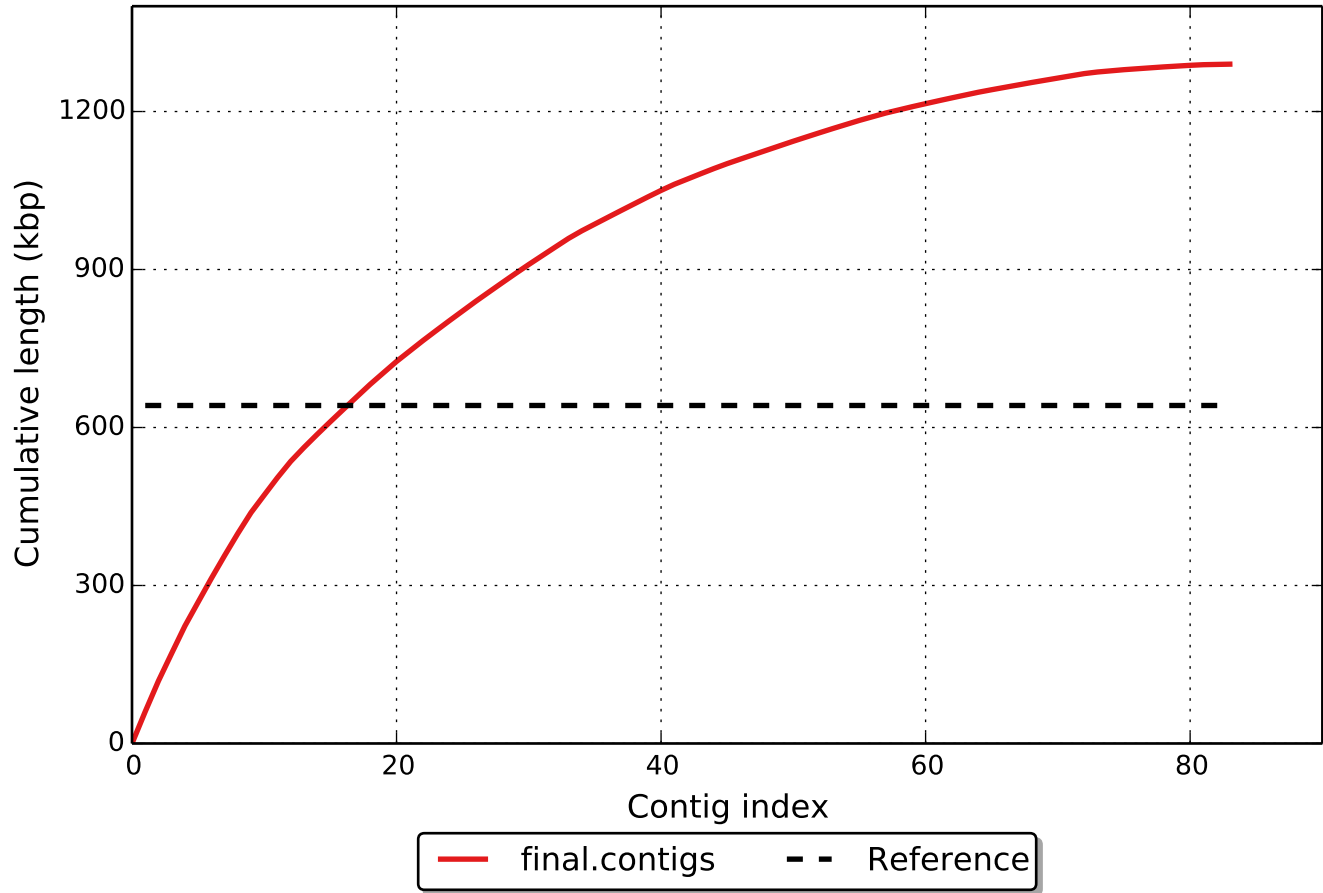
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

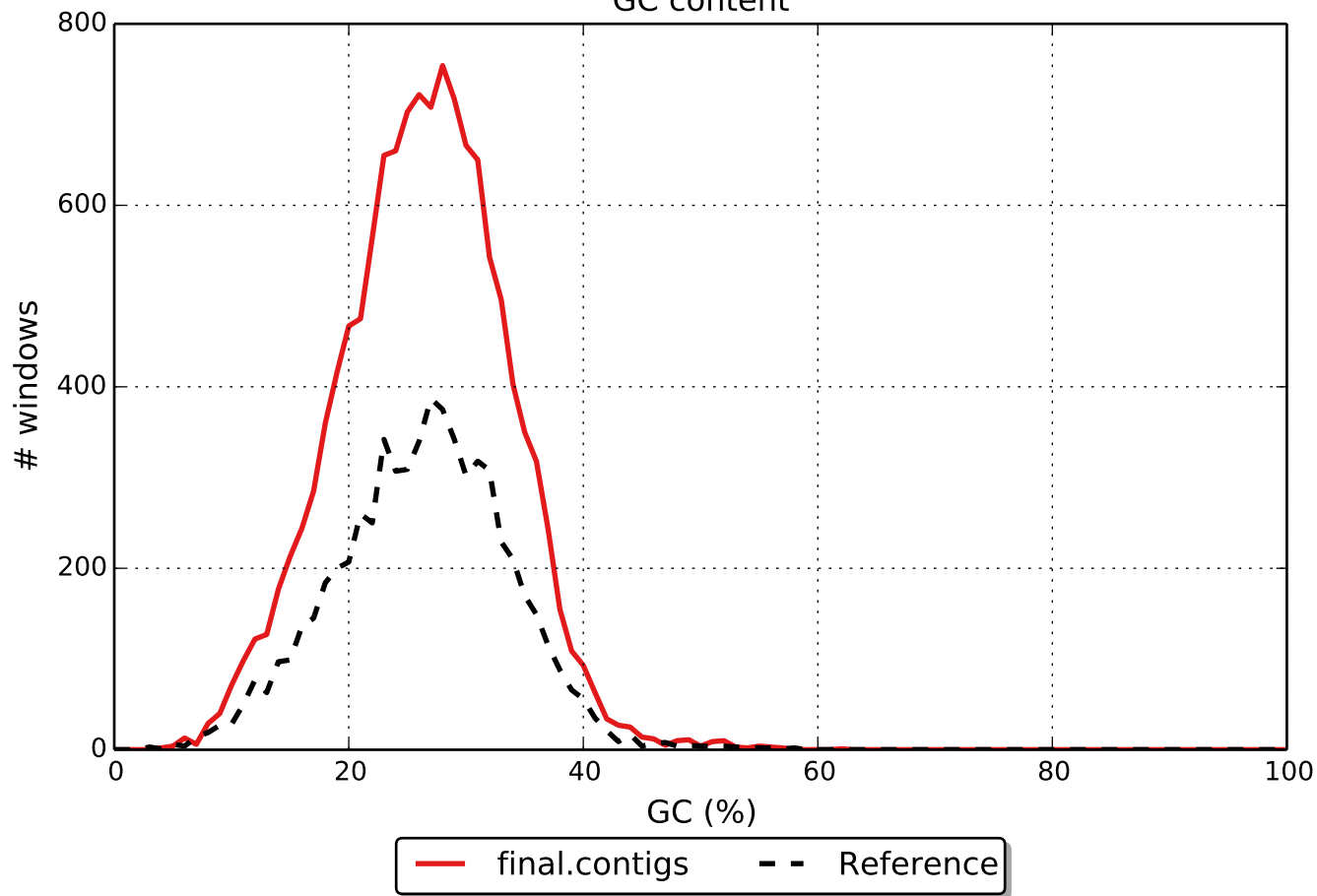
	final.contigs
# fully unaligned contigs	39
Fully unaligned length	602115
# partially unaligned contigs	2
# with misassembly	1
# both parts are significant	1
Partially unaligned length	41790
# N's	0

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).

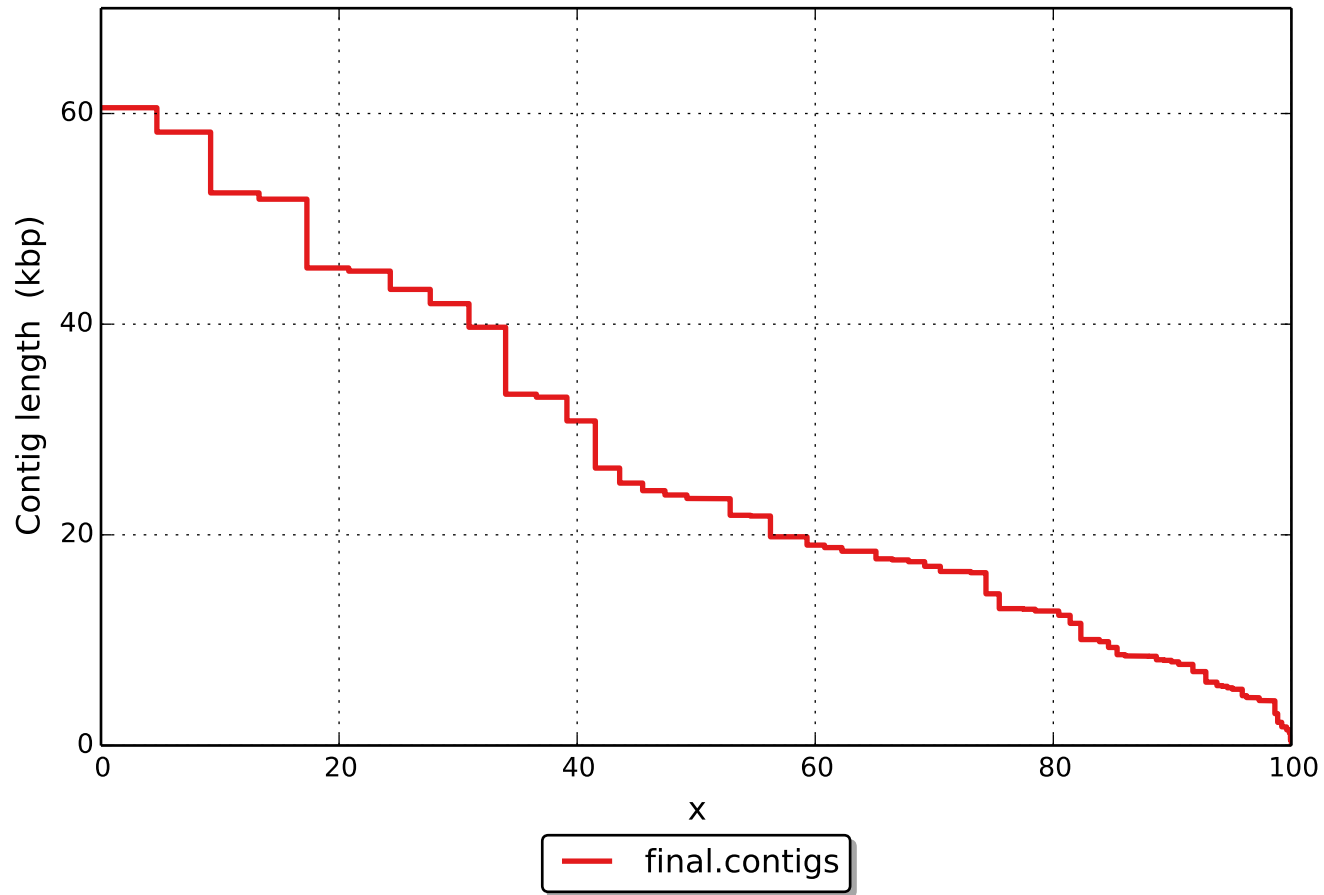
Cumulative length



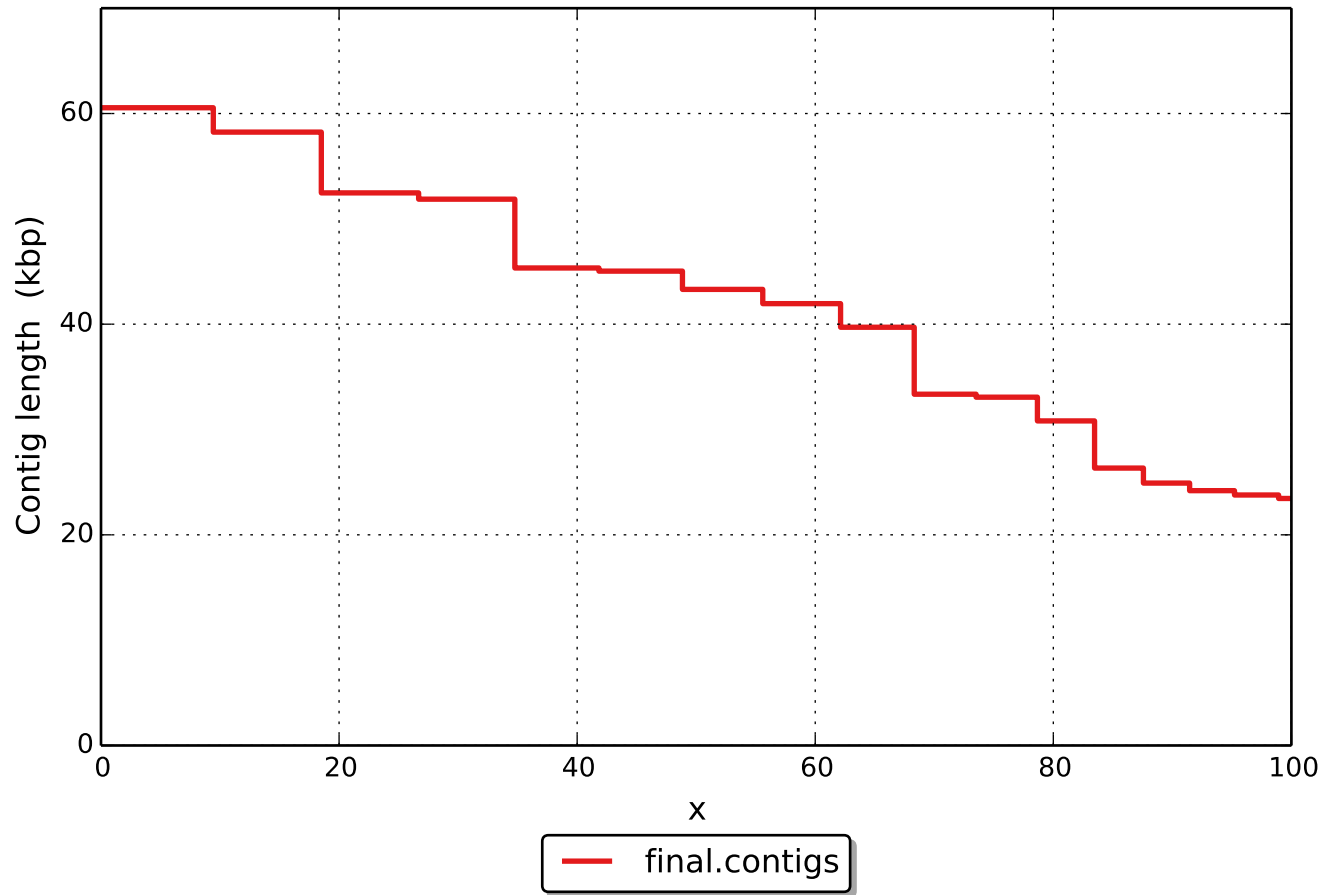
GC content



Nx

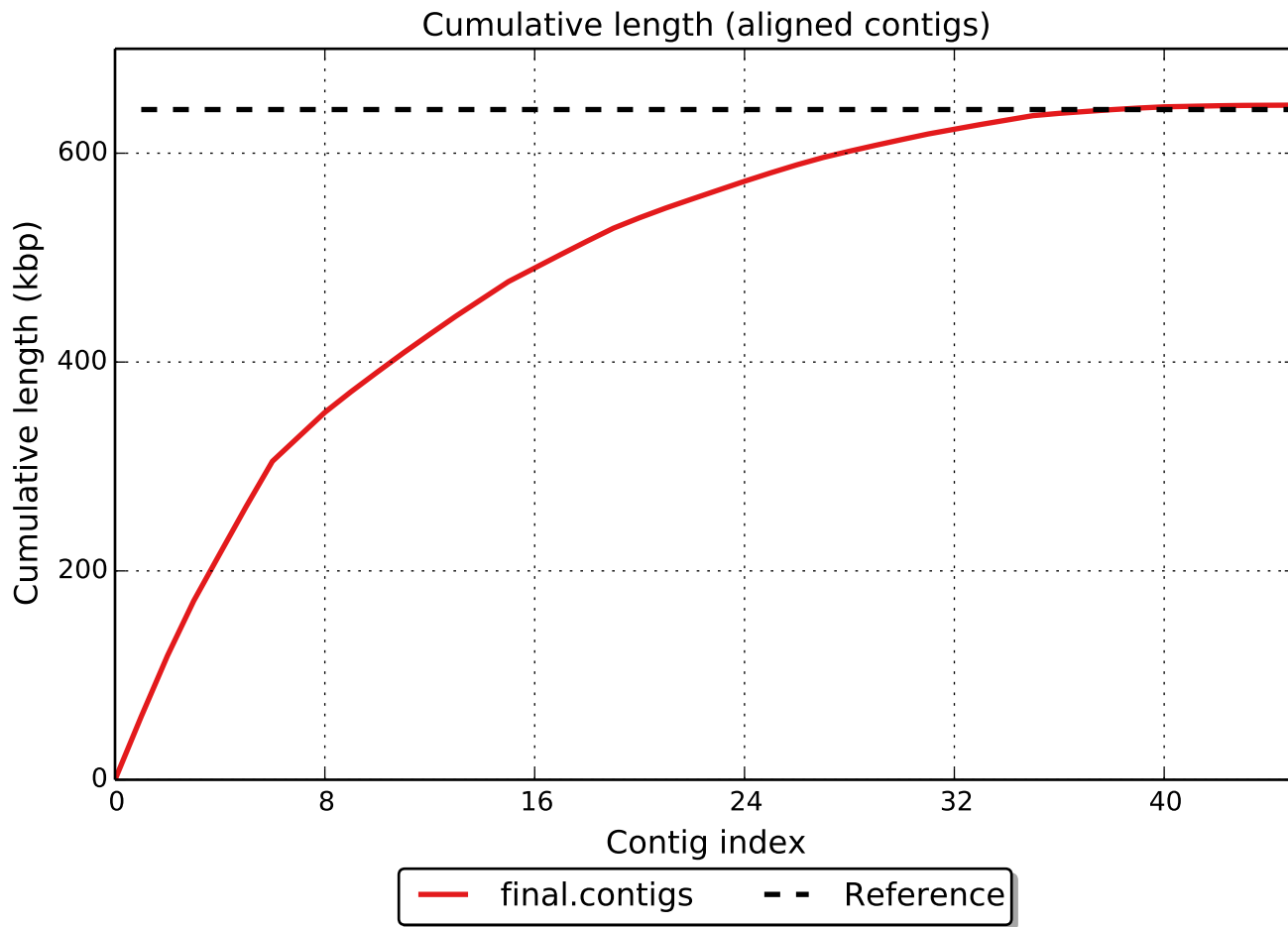


NGx

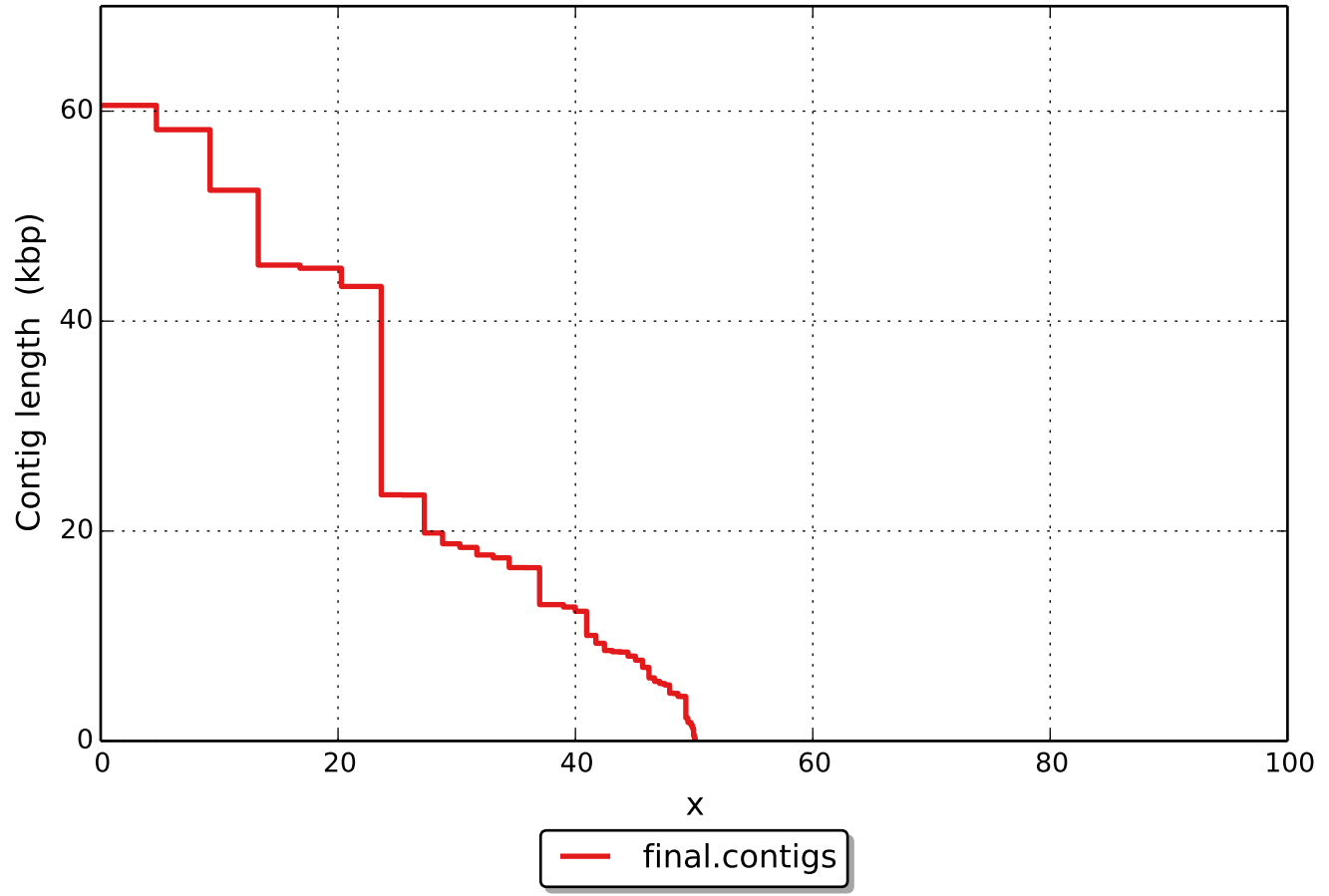


Misassemblies





NAx



NGAx

