

Report

	final.contigs
# contigs (≥ 0 bp)	12625
# contigs (≥ 1000 bp)	3765
Total length (≥ 0 bp)	11095585
Total length (≥ 1000 bp)	6152814
# contigs	8675
Largest contig	6941
Total length	9694430
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	1239
NG50	1118
N75	839
NG75	708
L50	2591
LG50	3128
L75	4983
LG75	6211
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.677
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	52.23
# indels per 100 kbp	0.09
Largest alignment	6941
NA50	1239
NGA50	1118
NA75	839
NGA75	708
LA50	2591
LGA50	3128
LA75	4983
LGA75	6211

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

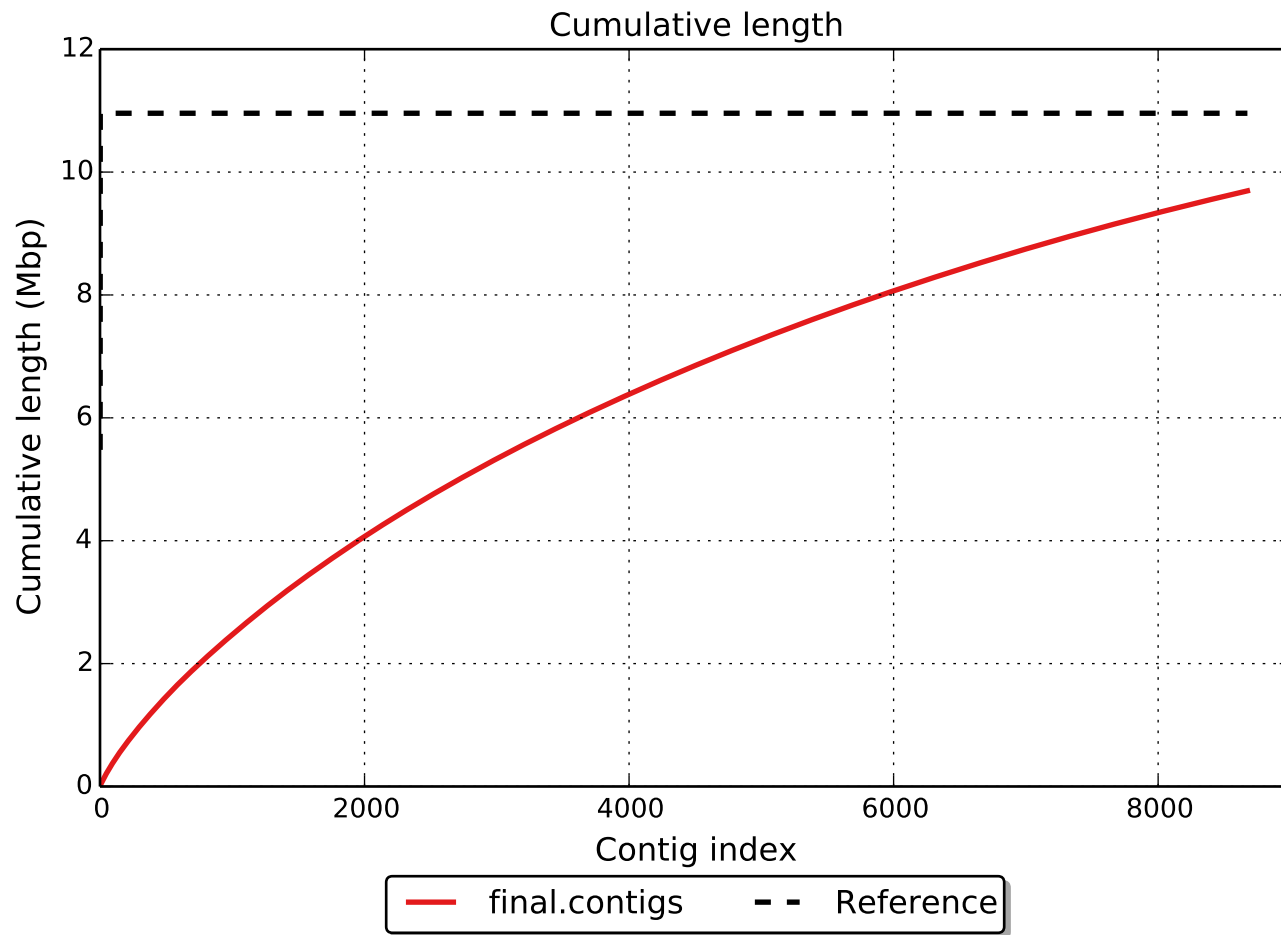
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	4846
# indels	8
# short indels	4
# long indels	4
Indels length	76

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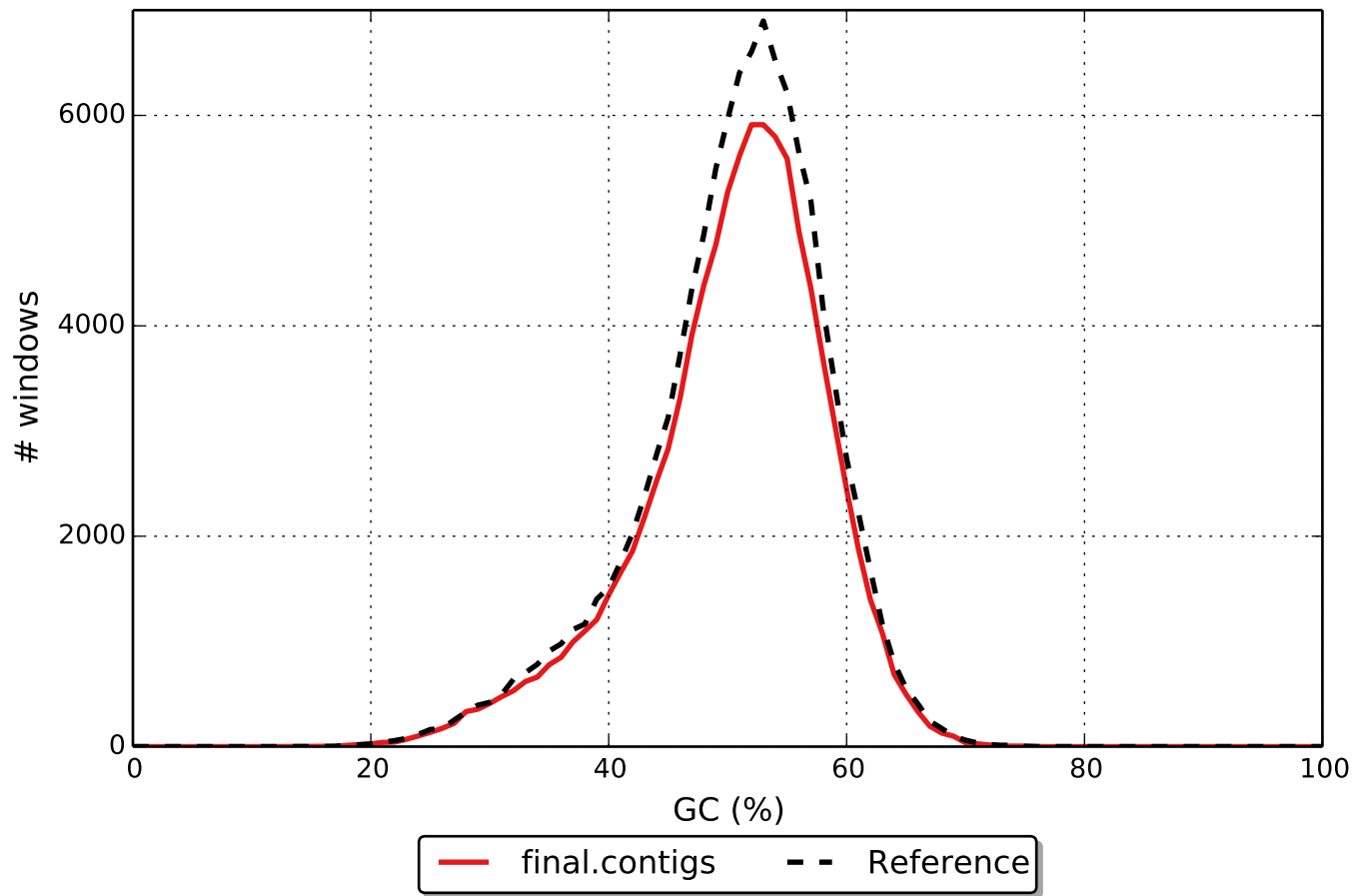
Unaligned report

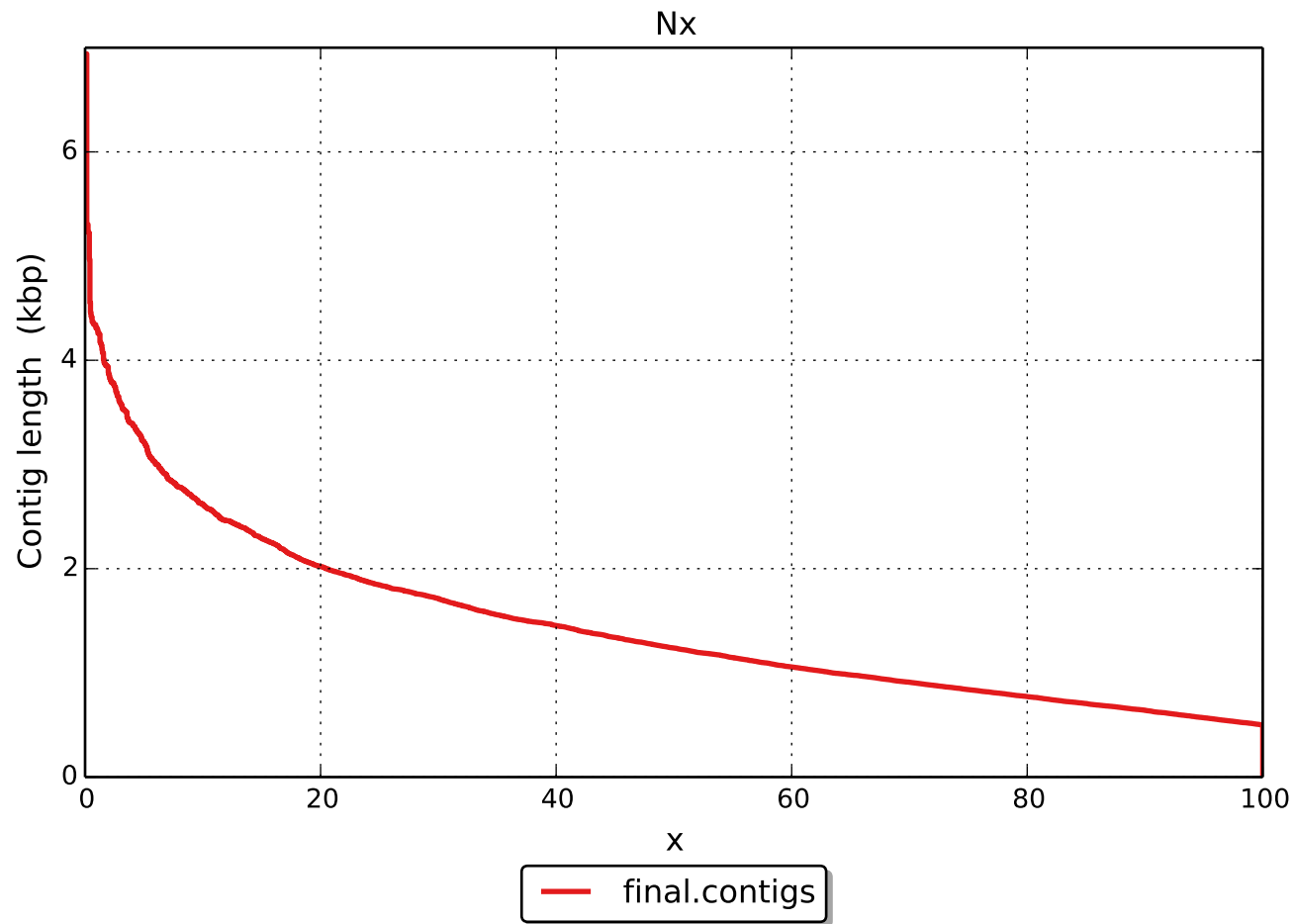
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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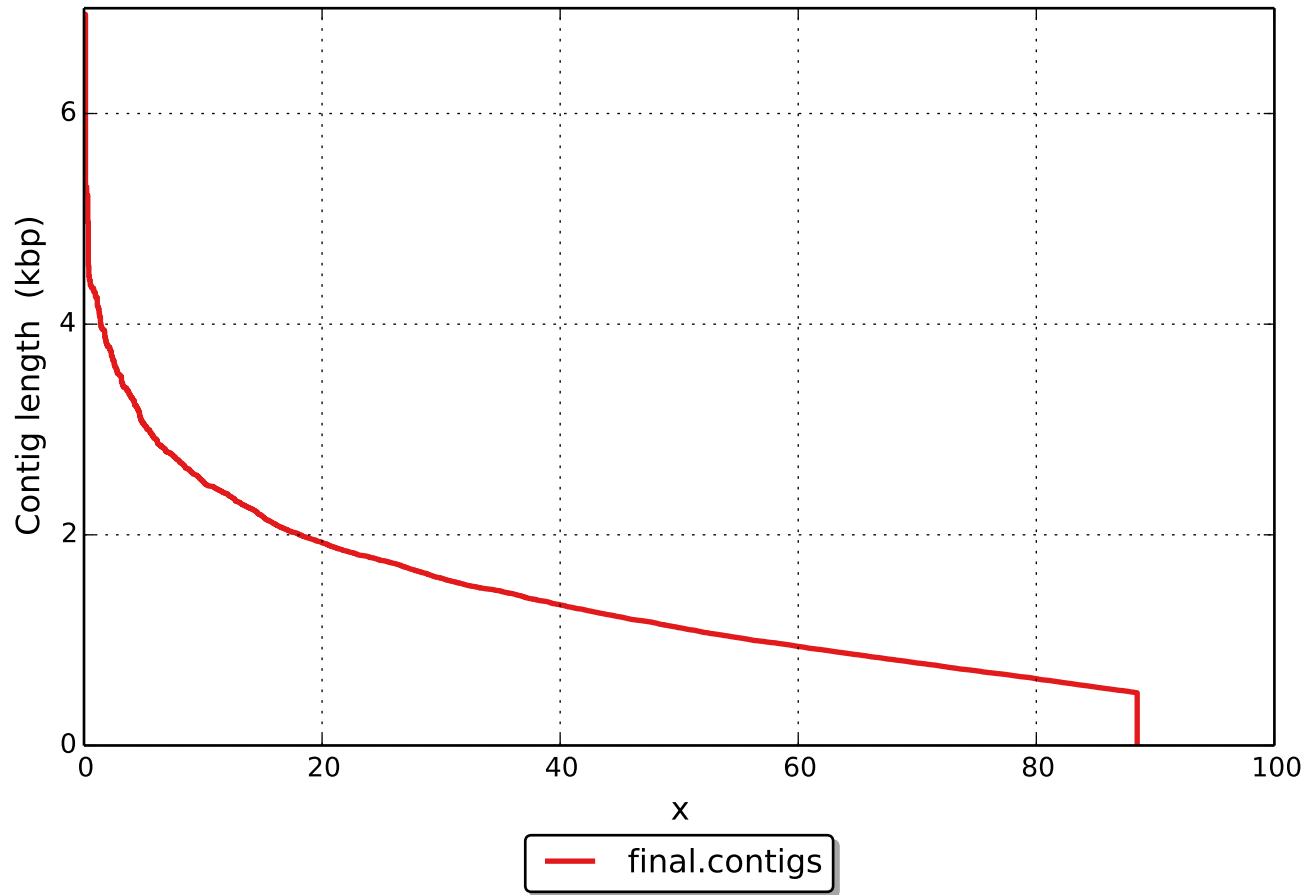


GC content



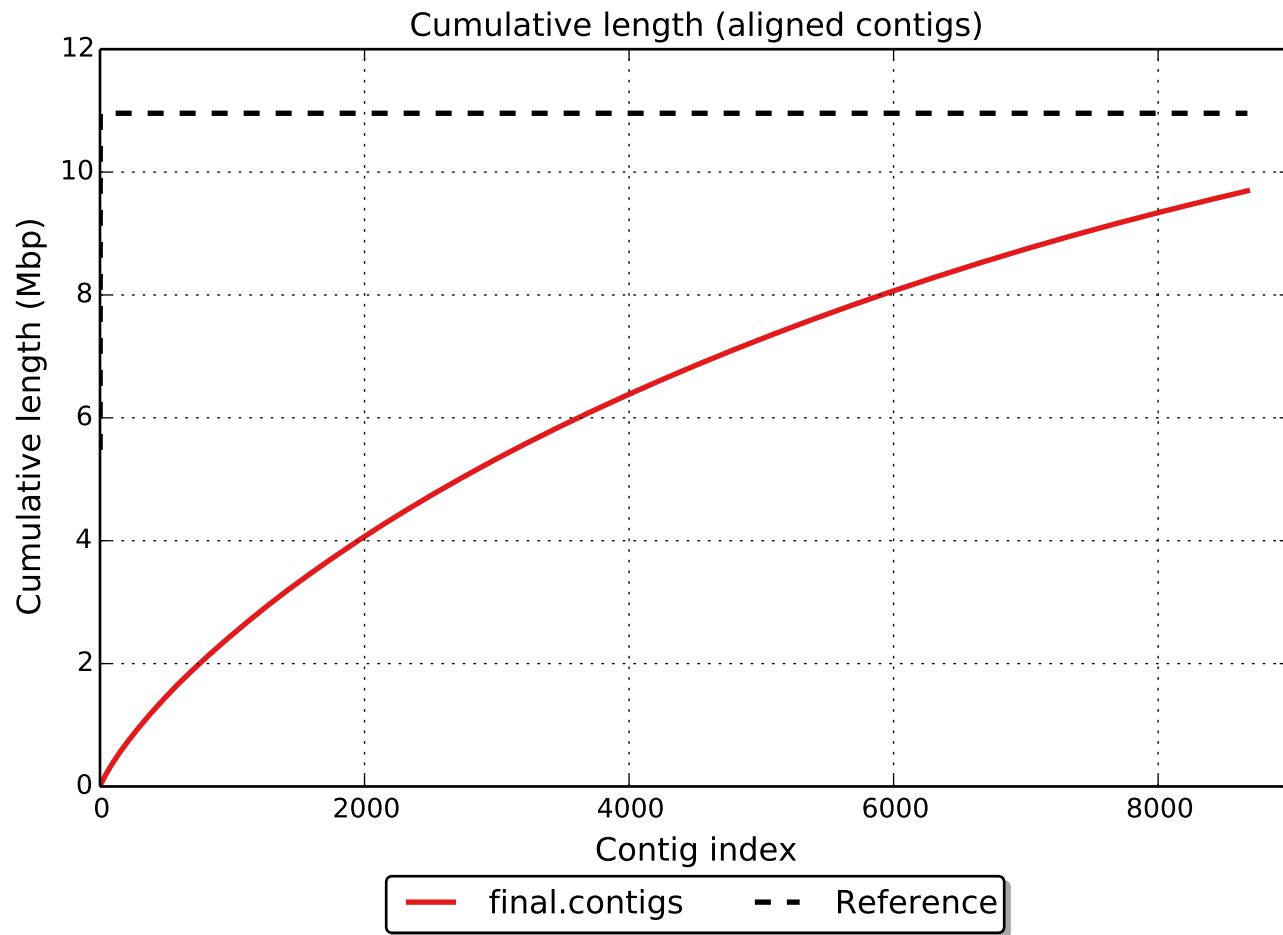


NGx

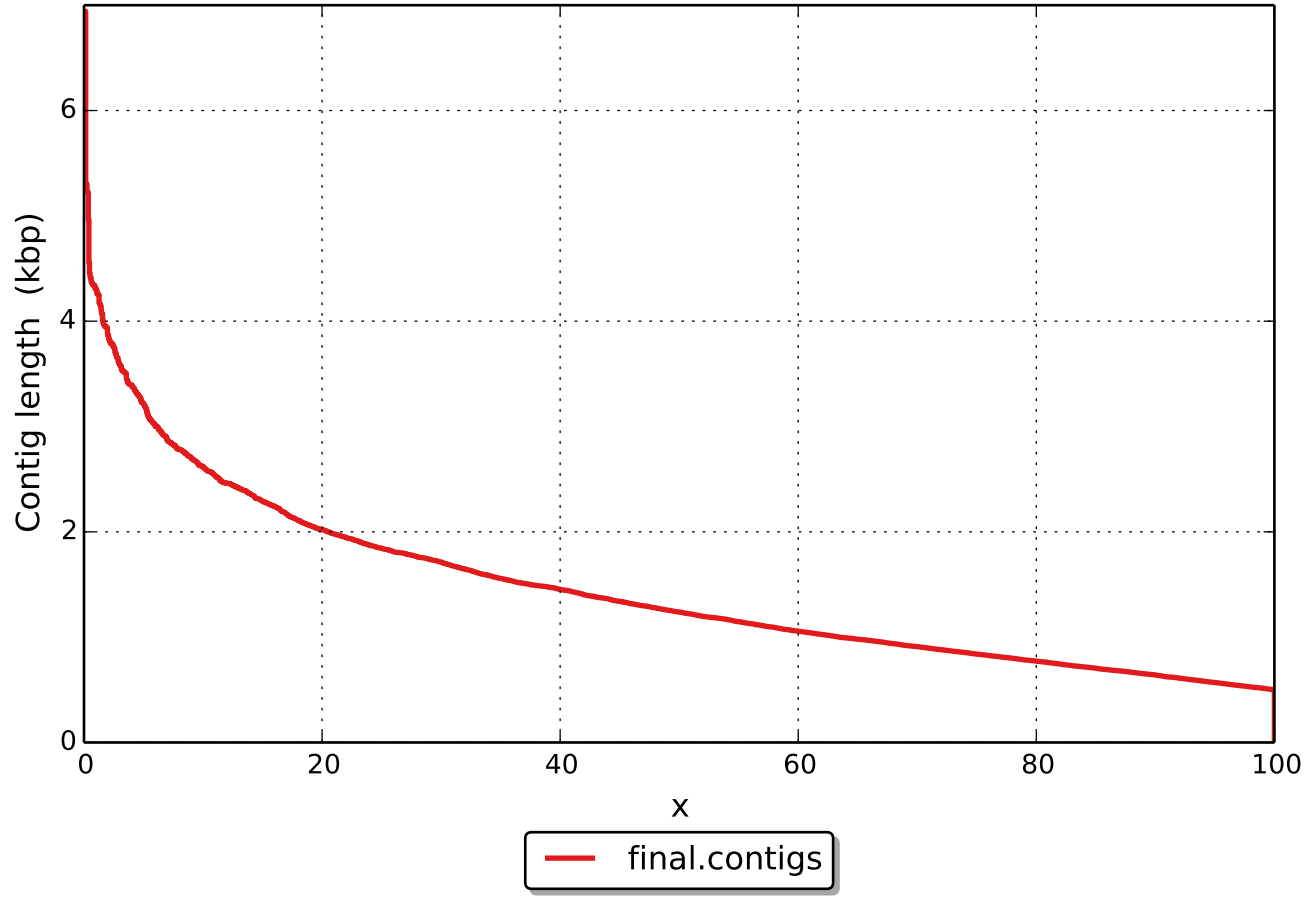


Misassemblies





NAx



NGAx

