

Report

	final.contigs
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	2660
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	108
Largest contig	1482
Total length	65612
Reference length	4641652
GC (%)	51.61
Reference GC (%)	50.79
N50	585
N75	533
L50	47
L75	77
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1482
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	10
Genome fraction (%)	1.405
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1947.17
# indels per 100 kbp	16.87
Largest alignment	1412
NA50	584
NGA50	-
NA75	533
LA50	47
LA75	77

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	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1482
# local misassemblies	0
# mismatches	1270
# indels	11
# short indels	11
# long indels	0
Indels length	14

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	10
# 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).

Report

	final.contigs
# contigs (≥ 0 bp)	728
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	300830
Total length (≥ 1000 bp)	2660
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	108
Largest contig	1482
Total length	65612
Reference length	4641652
N50	585
N75	533
L50	47
L75	77
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1482
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	10
Genome fraction (%)	1.405
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1947.17
# indels per 100 kbp	16.87
Largest alignment	1412
NA50	584
NA75	533
LA50	47
LA75	77

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Misassemblies report

	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1482
# local misassemblies	0
# mismatches	1270
# indels	11
# short indels	11
# long indels	0
Indels length	14

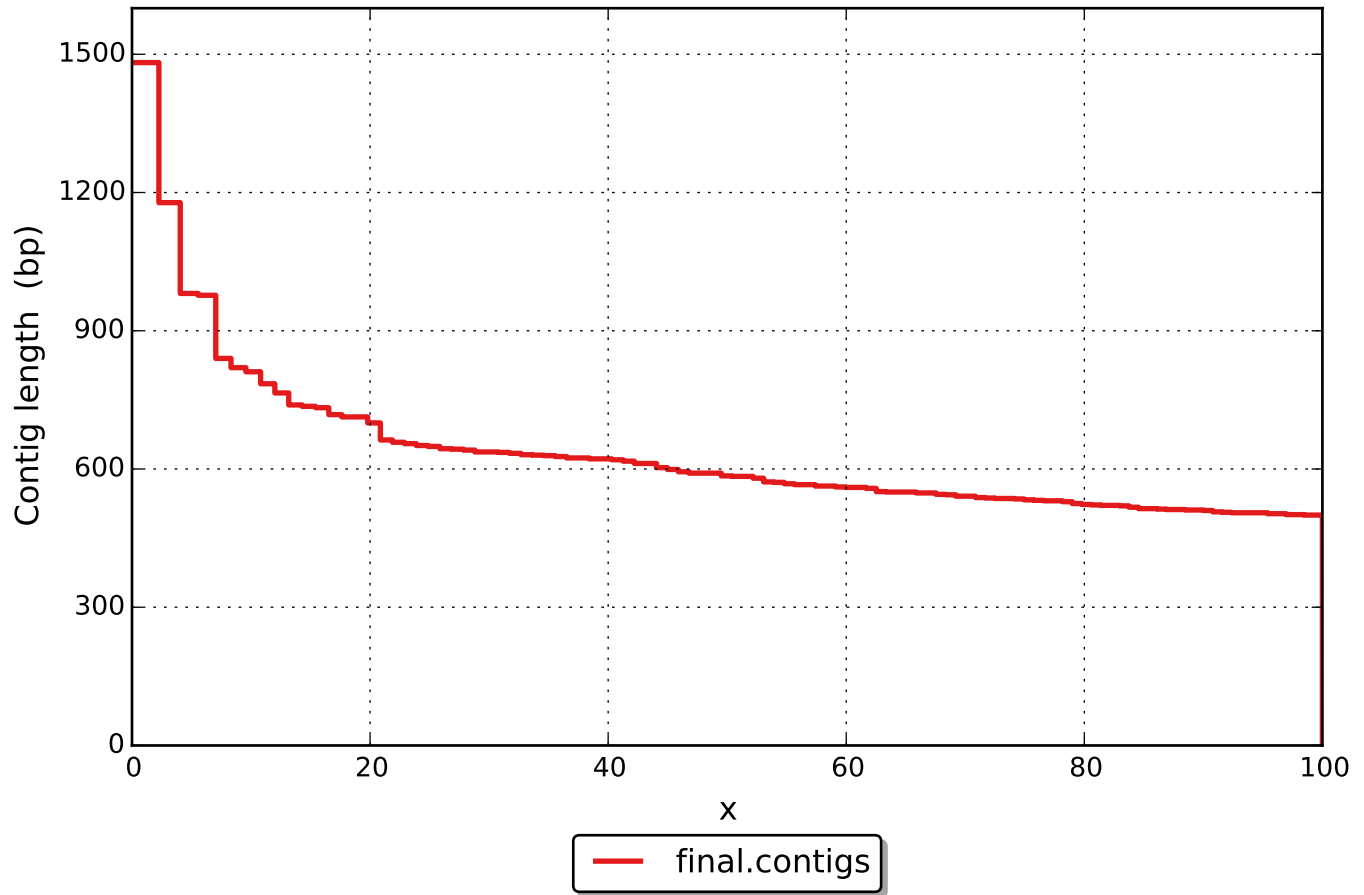
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

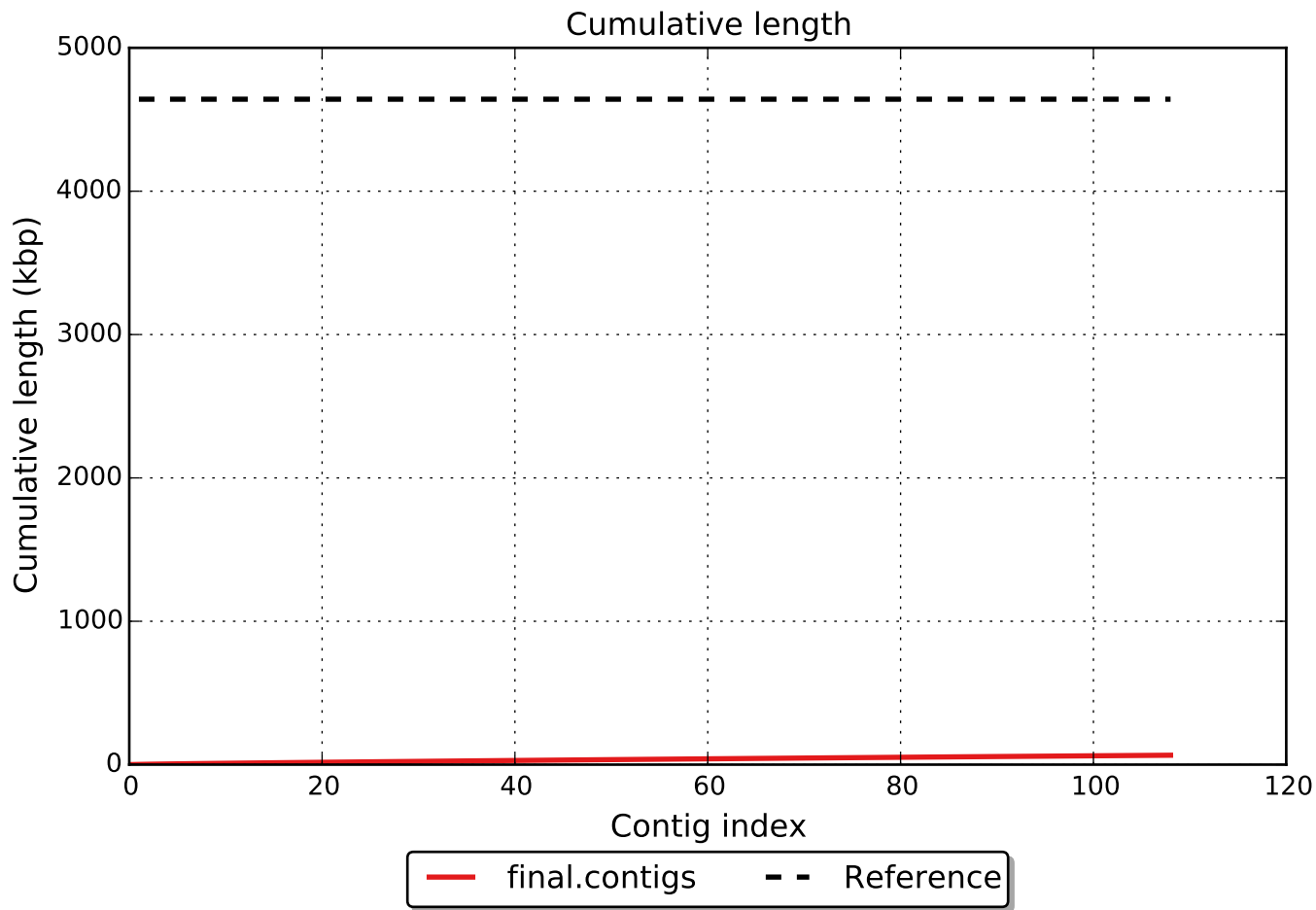
Unaligned report

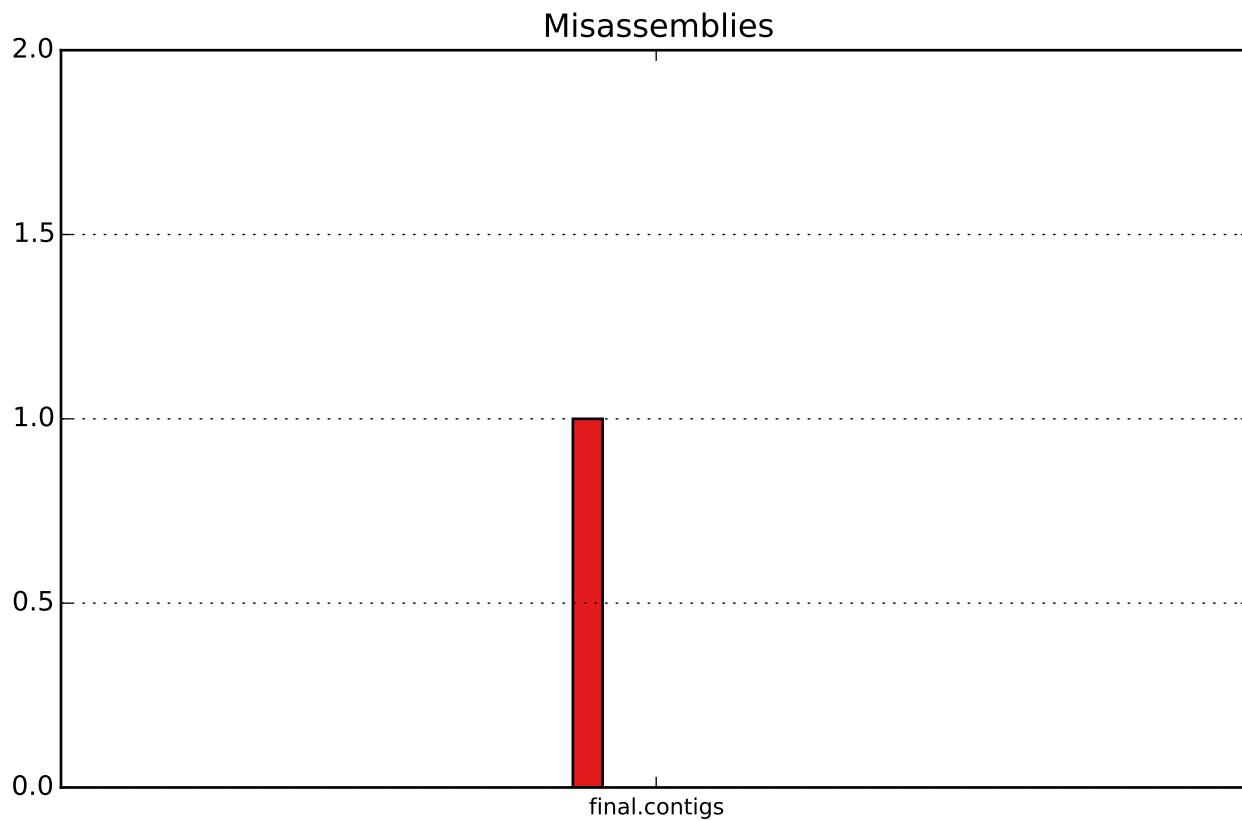
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	10
# N's	0

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).

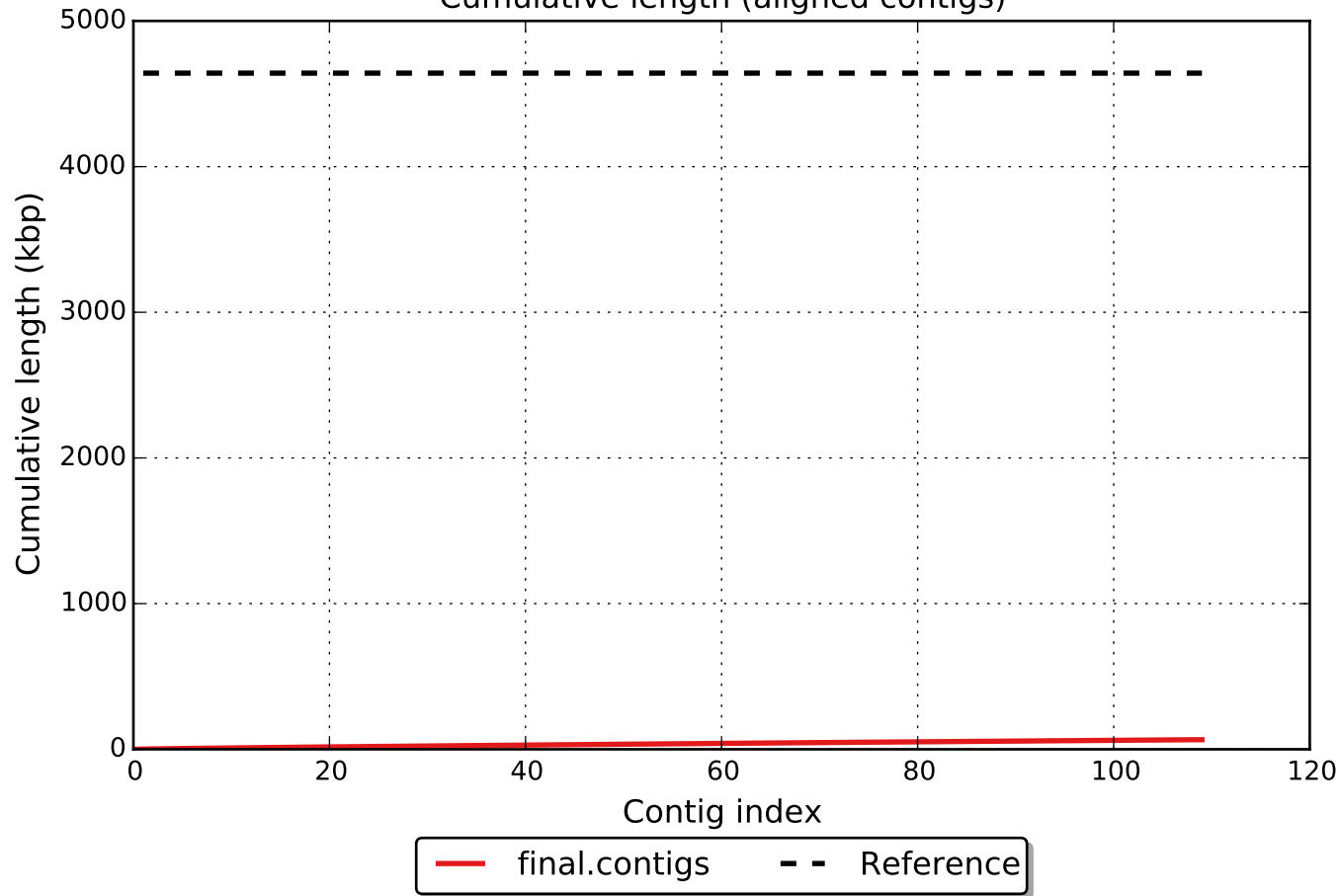
Nx



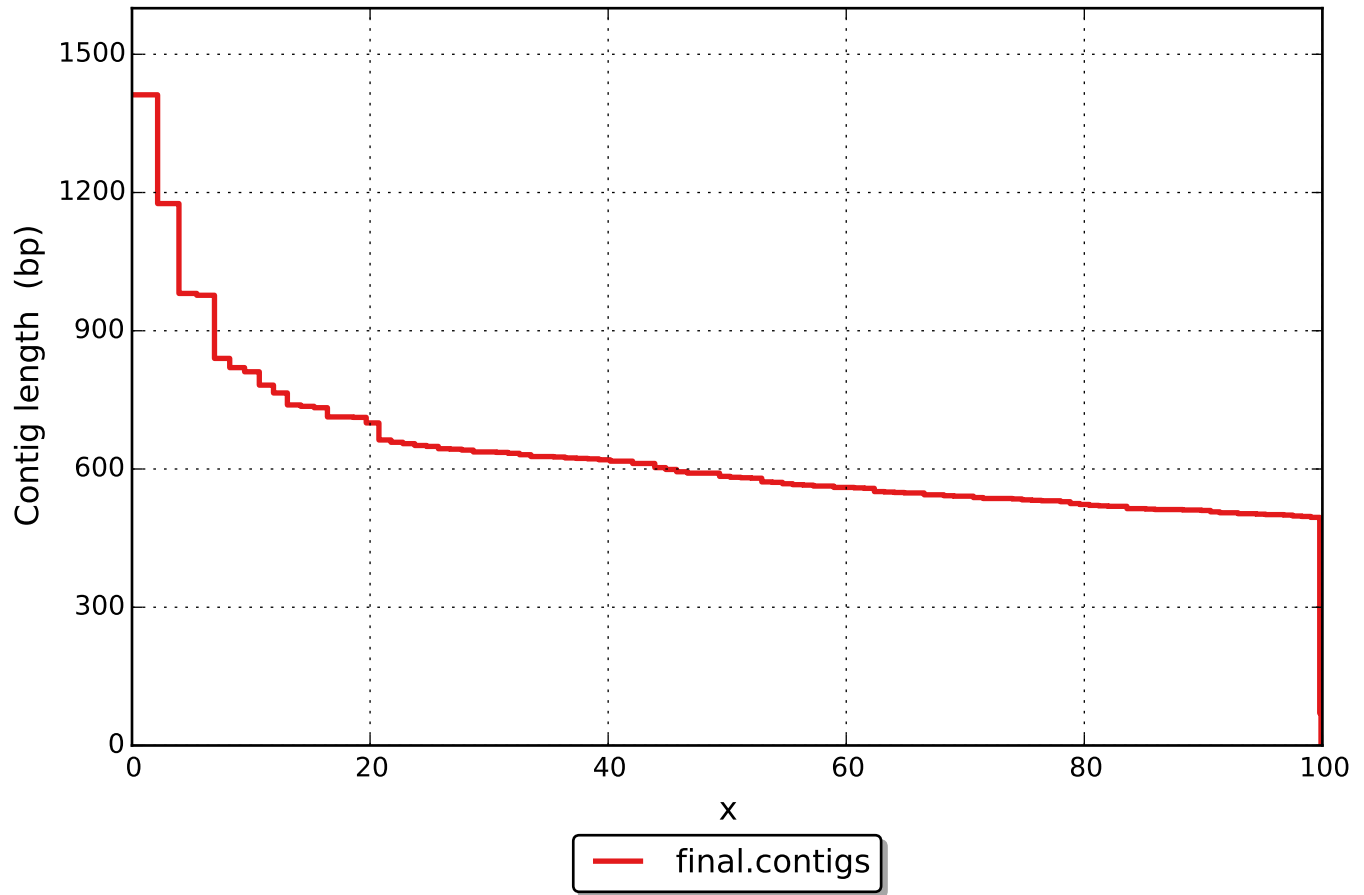




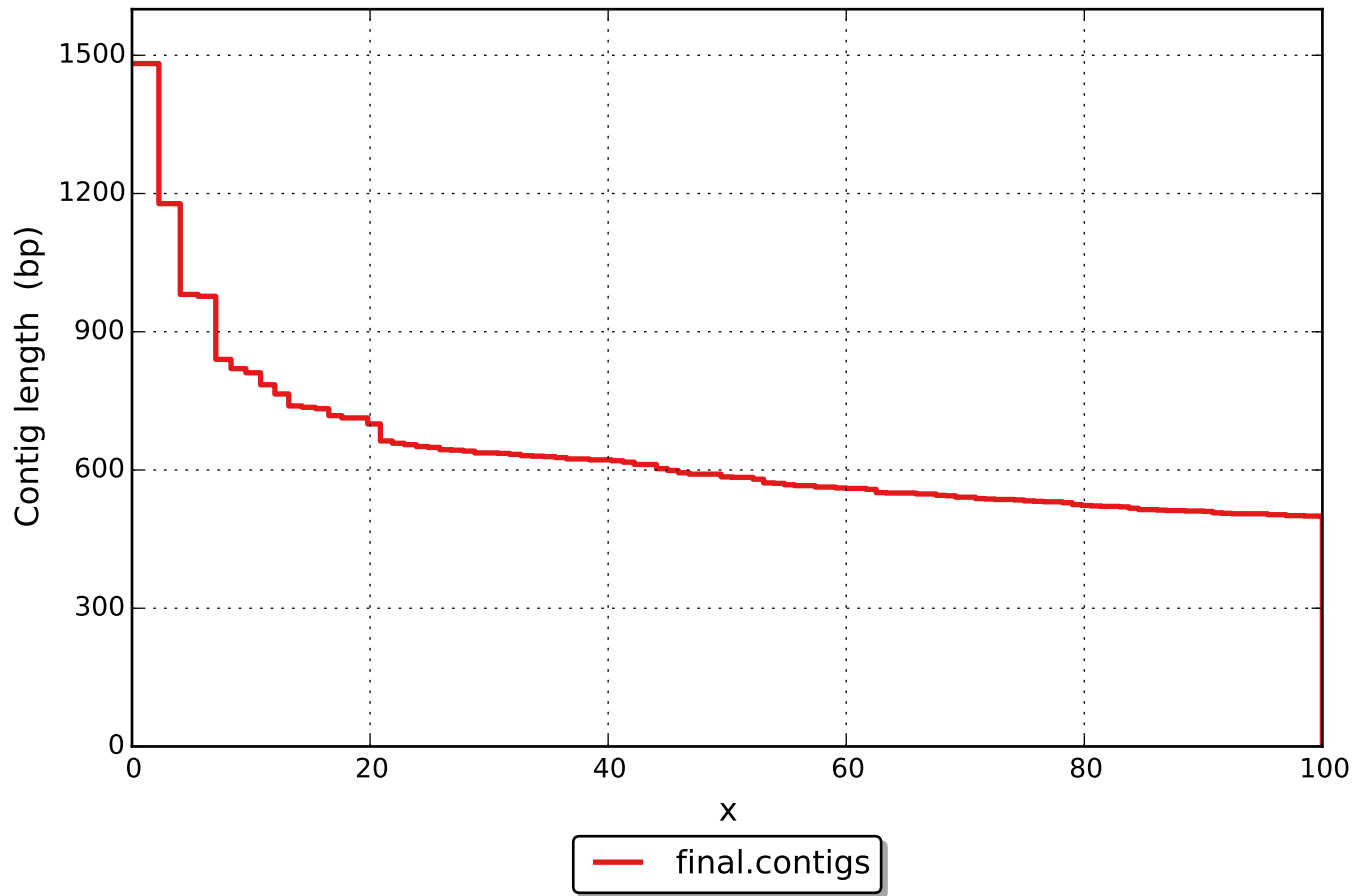
Cumulative length (aligned contigs)



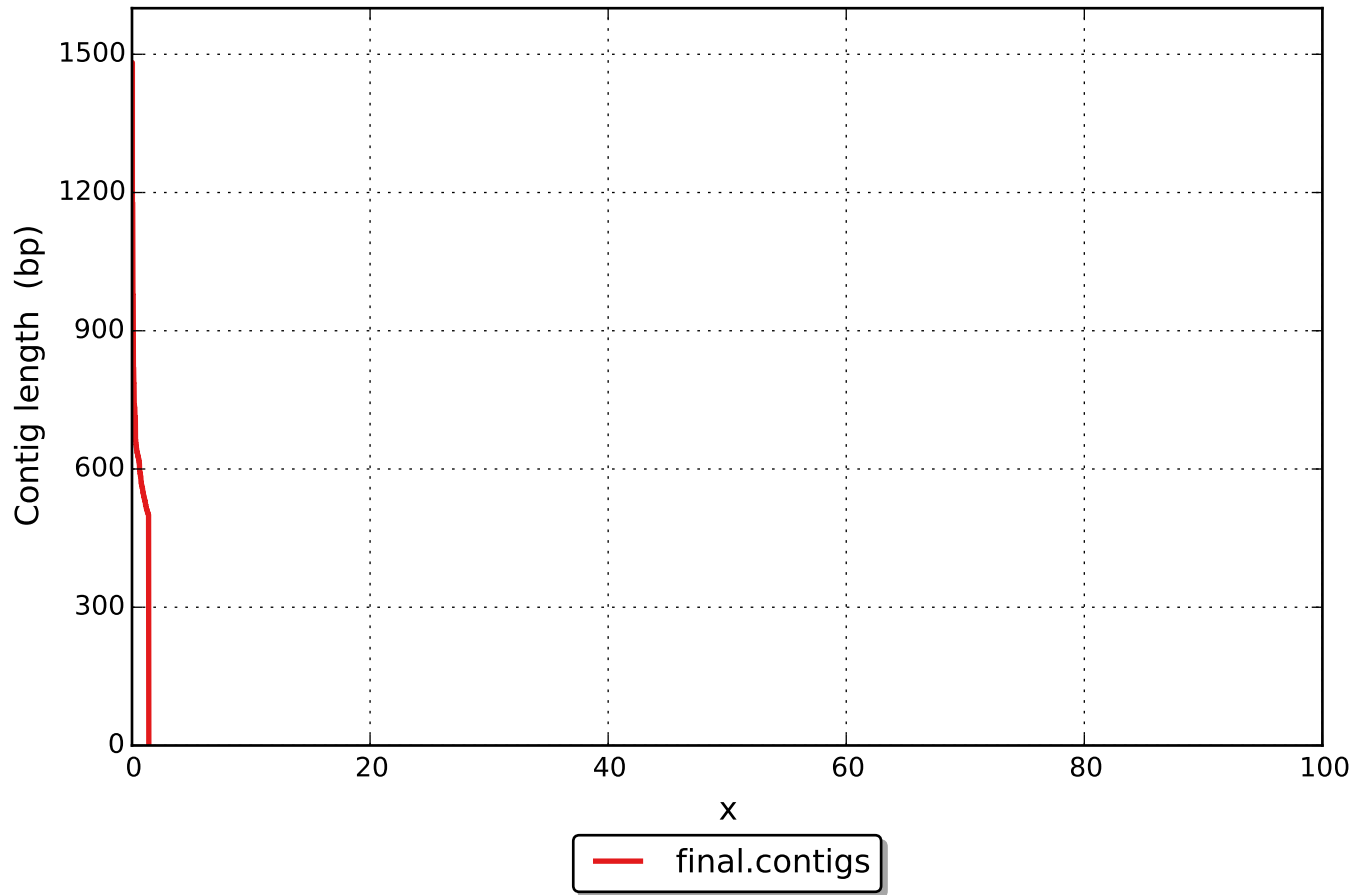
NAx

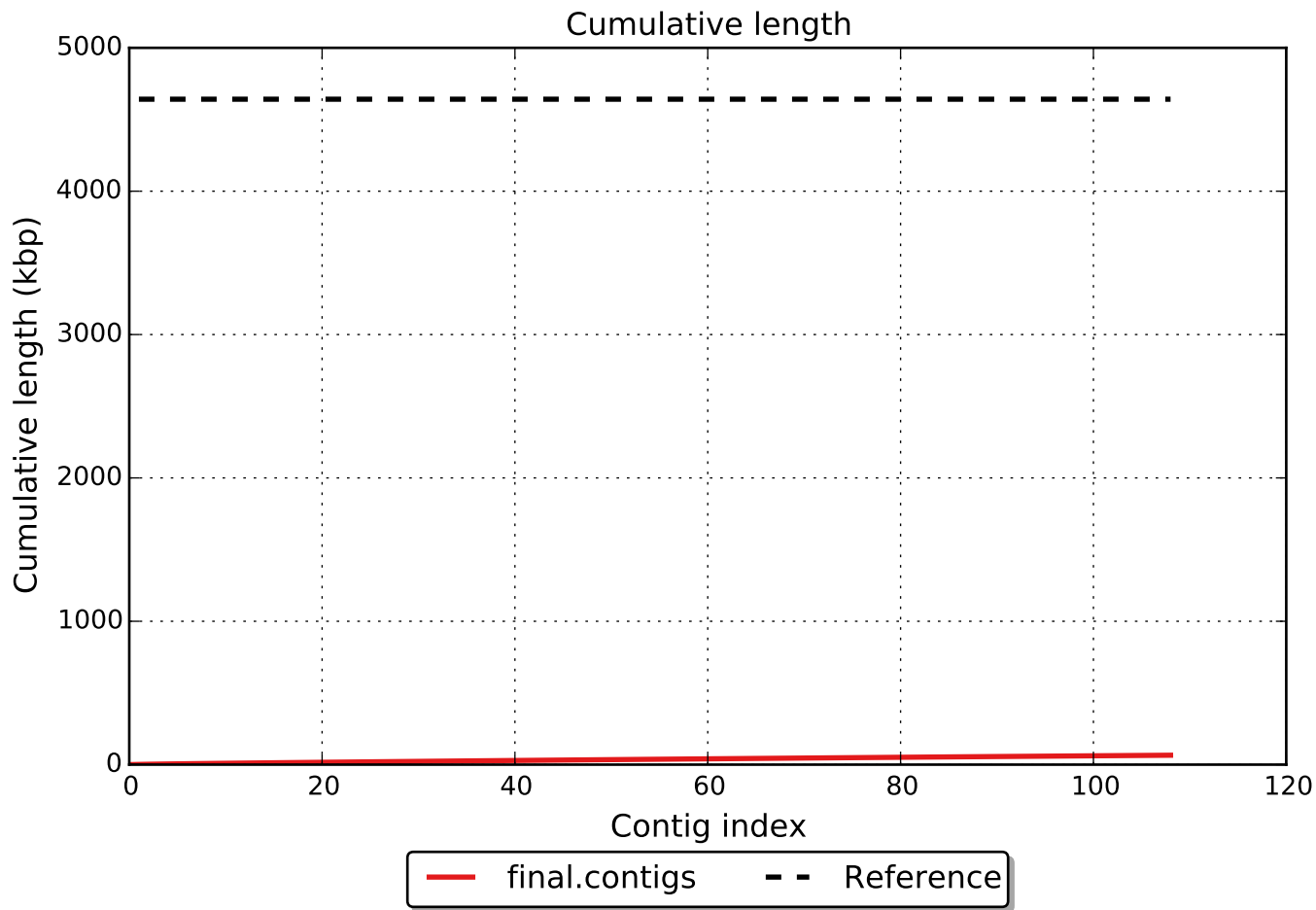


Nx

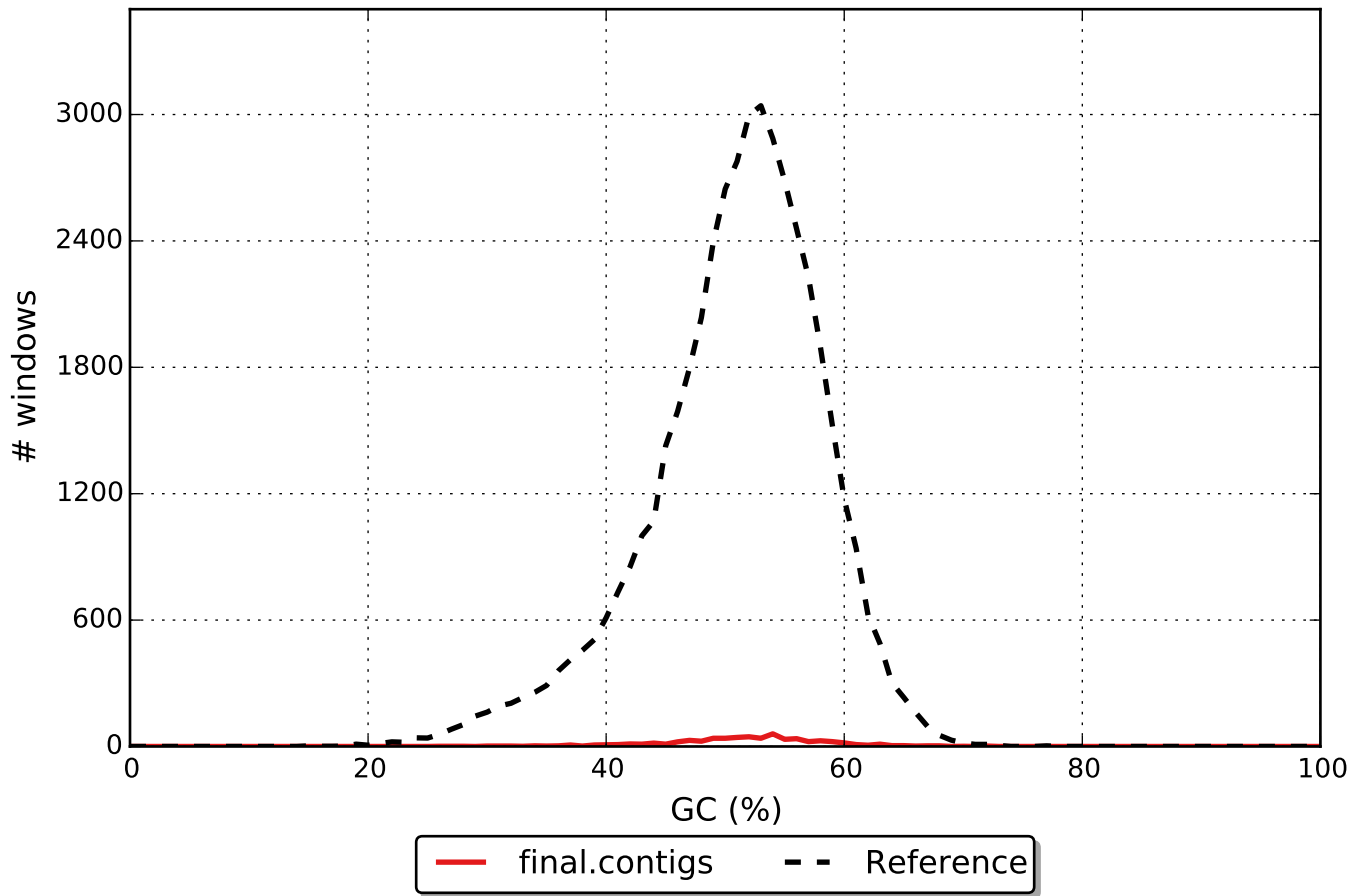


NGx



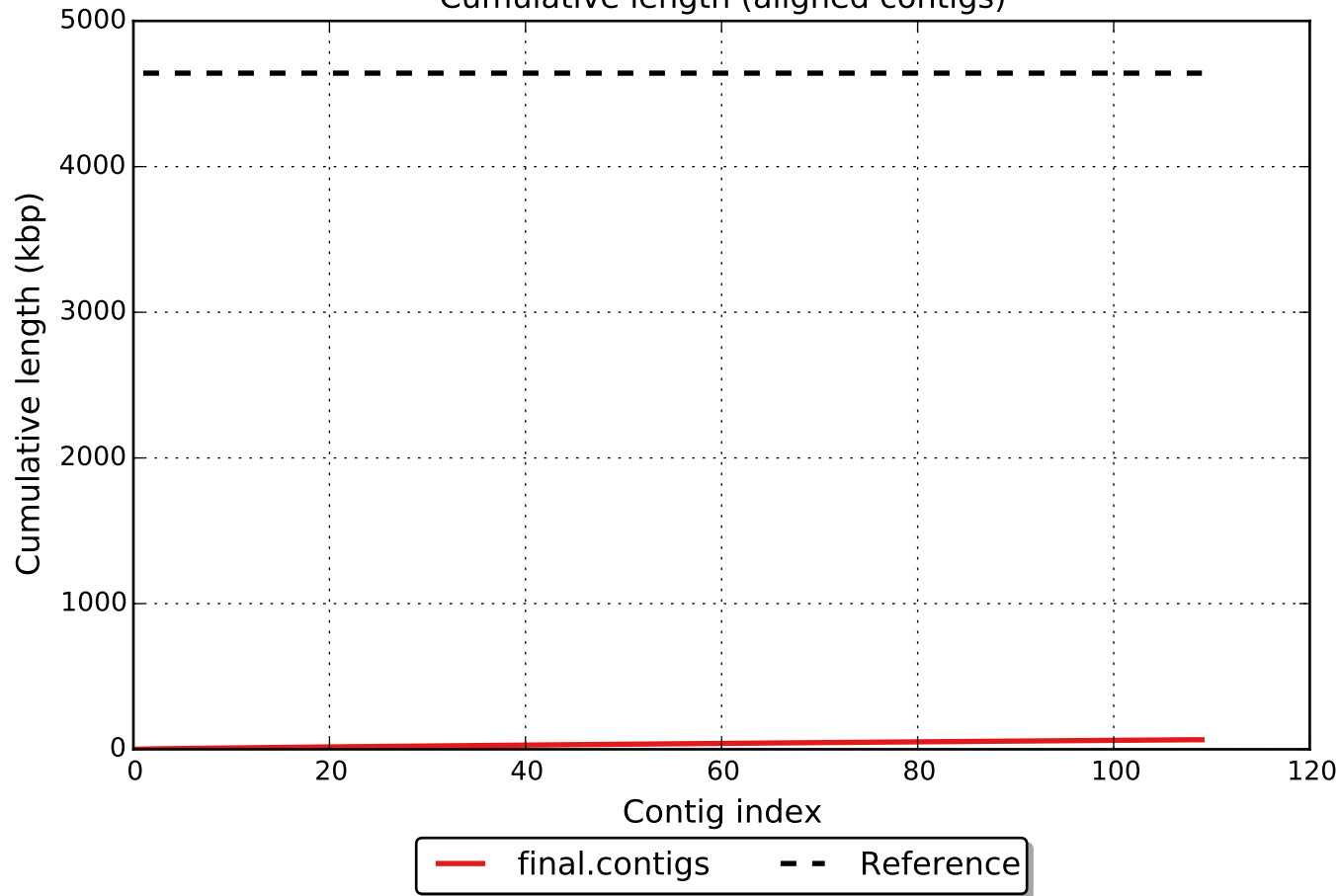


GC content

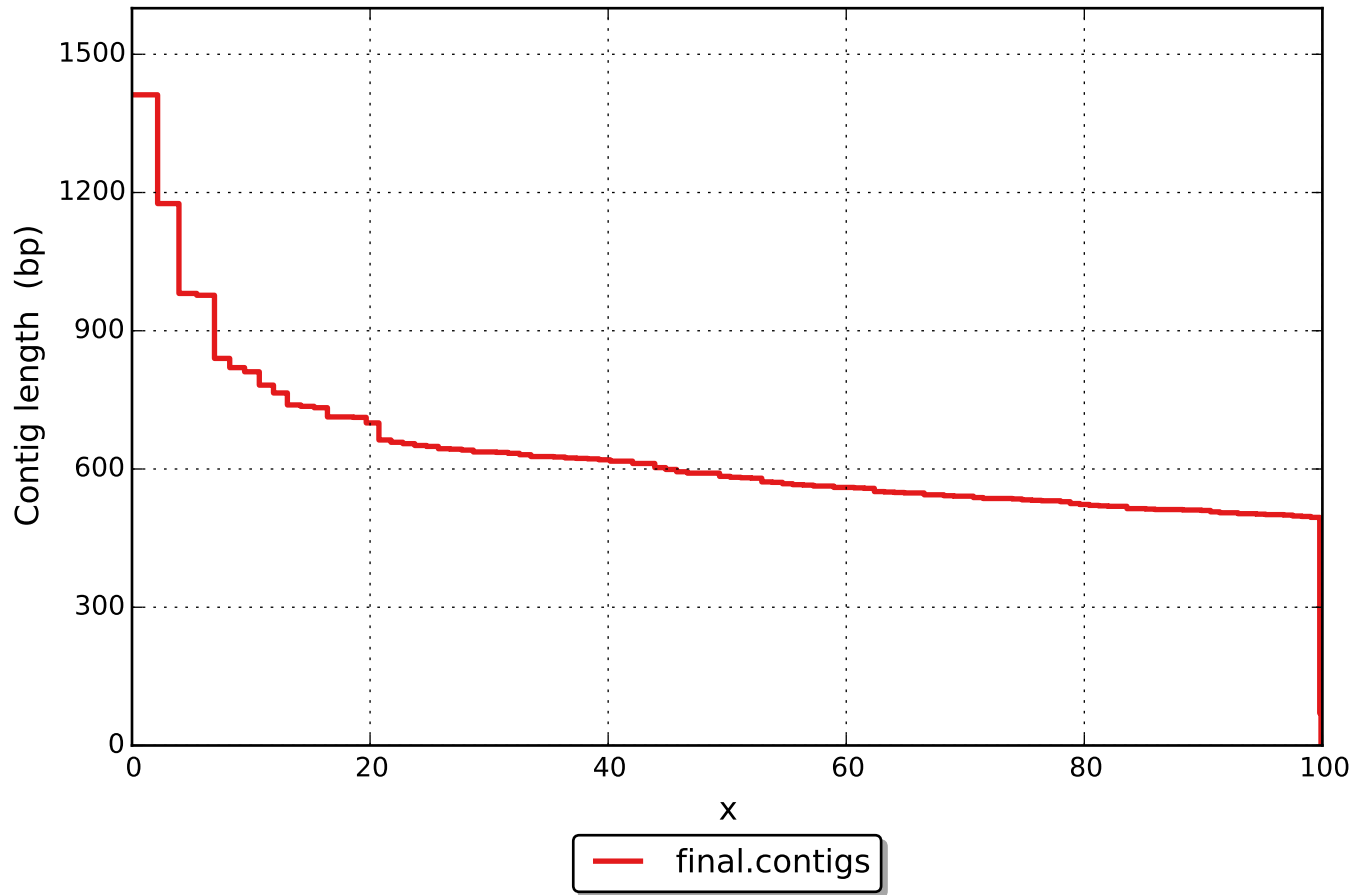




Cumulative length (aligned contigs)



NAx



NGAx

