

Report

	final.contigs
# contigs (≥ 0 bp)	466
# contigs (≥ 1000 bp)	344
Total length (≥ 0 bp)	1312972
Total length (≥ 1000 bp)	1239024
# contigs	425
Largest contig	13166
Total length	1297290
Reference length	1283598
GC (%)	26.29
Reference GC (%)	26.30
N50	4334
NG50	4342
N75	2499
NG75	2602
L50	98
LG50	96
L75	192
LG75	188
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6898
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.154
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.13
# indels per 100 kbp	0.00
Largest alignment	13166
NA50	4334
NGA50	4342
NA75	2478
NGA75	2557
LA50	98
LGA50	96
LA75	193
LGA75	189

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	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	6898
# local misassemblies	0
# mismatches	367
# indels	0
# short indels	0
# long indels	0
Indels length	0

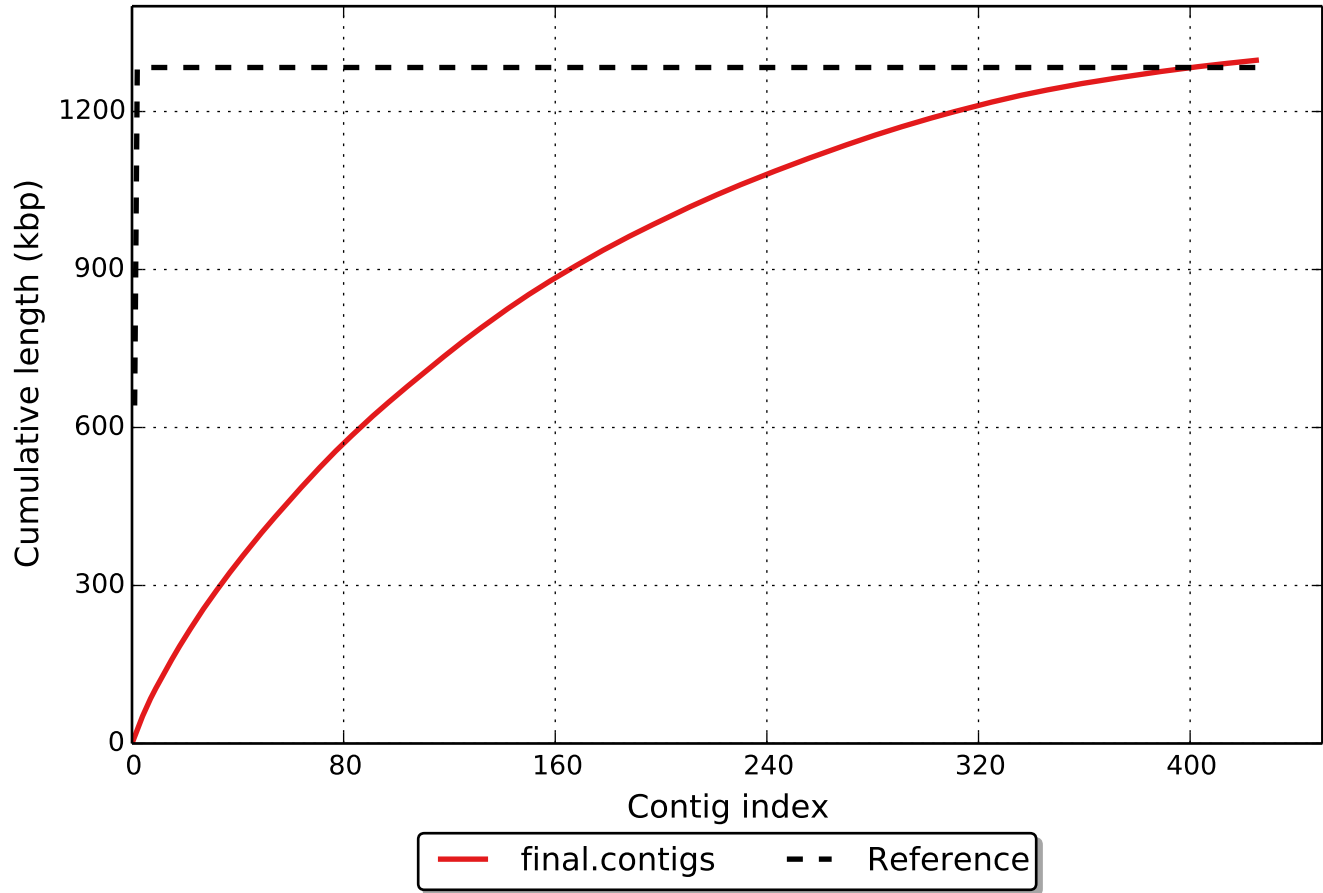
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

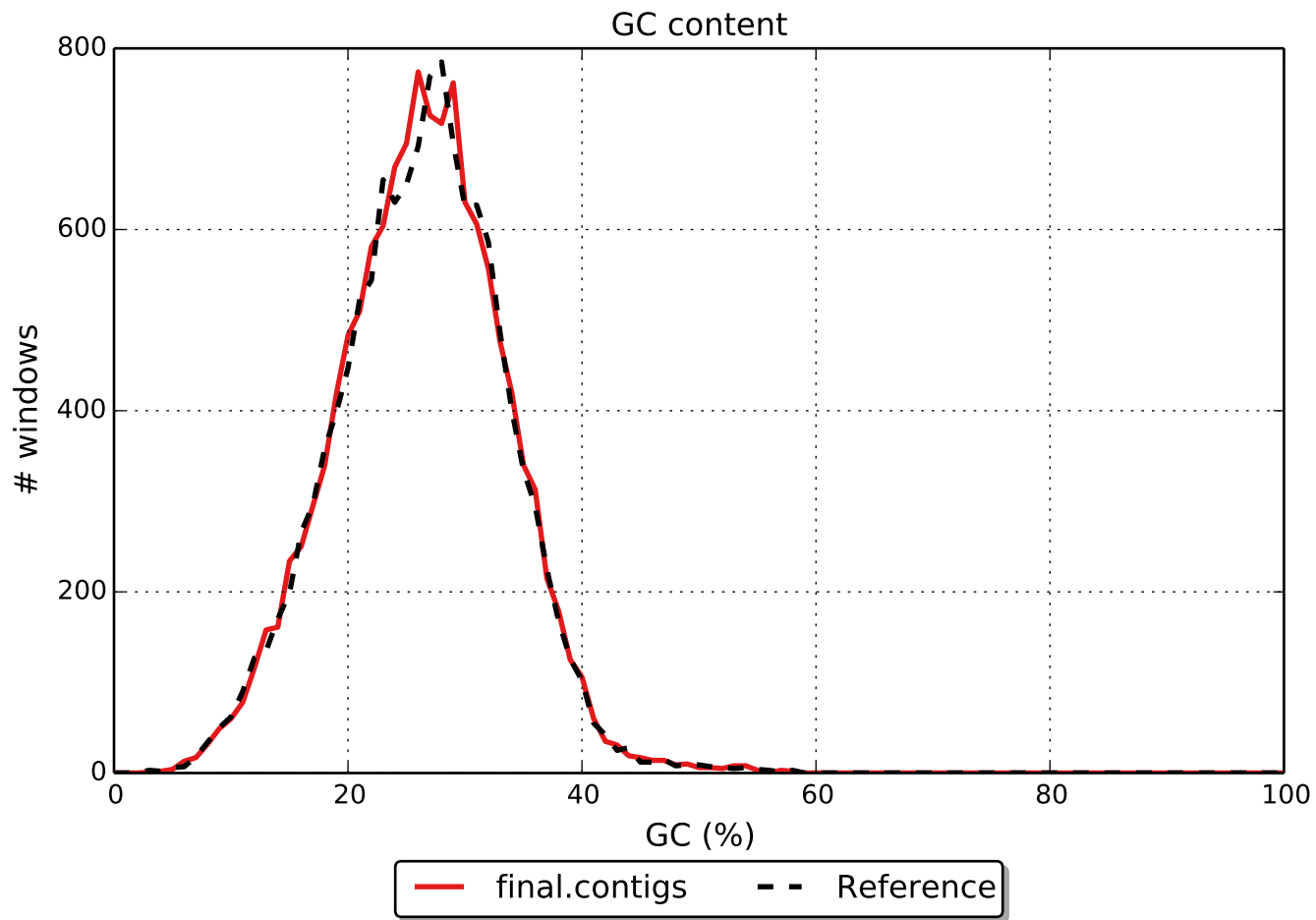
Unaligned report

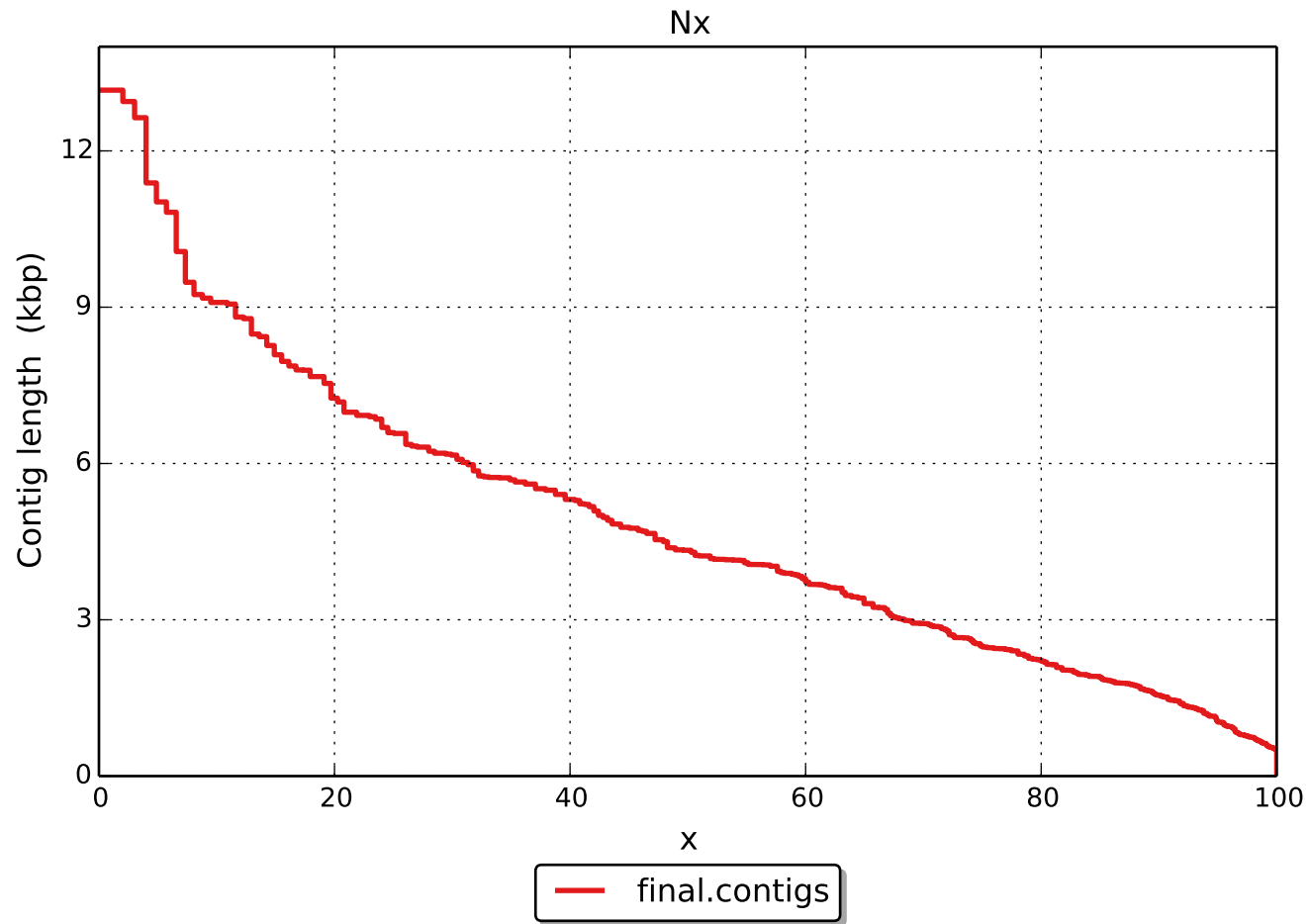
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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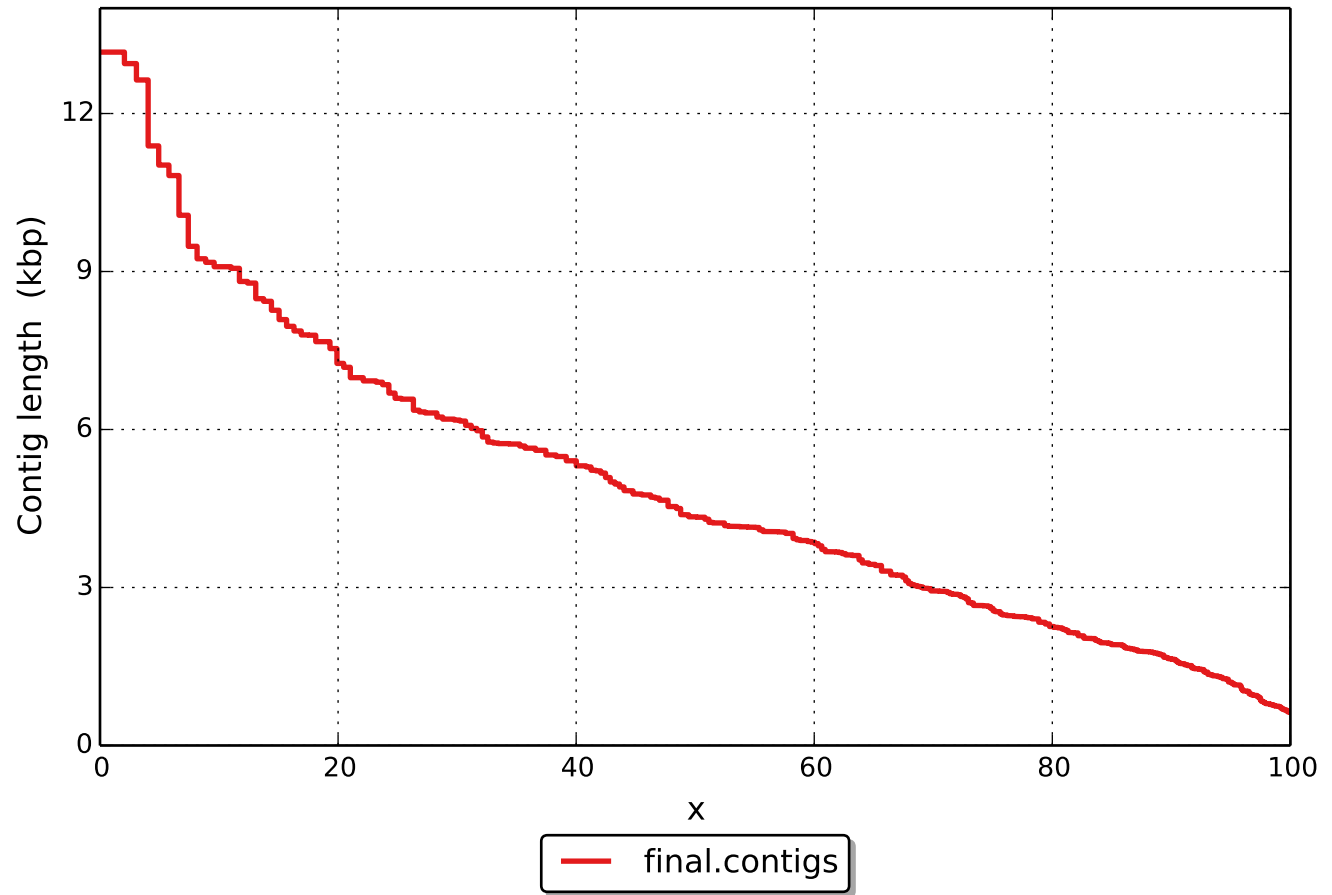
Cumulative length

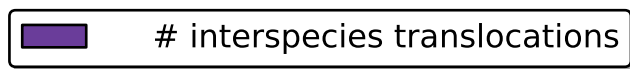
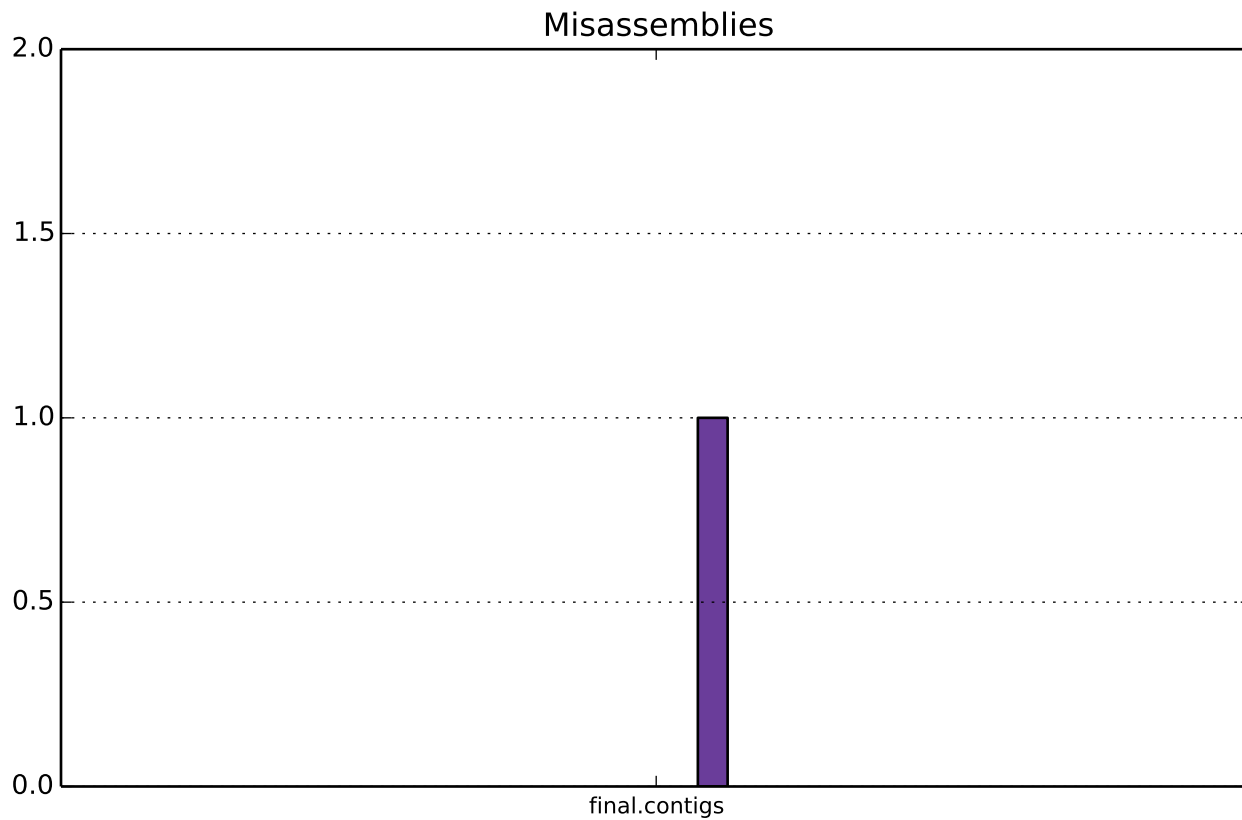




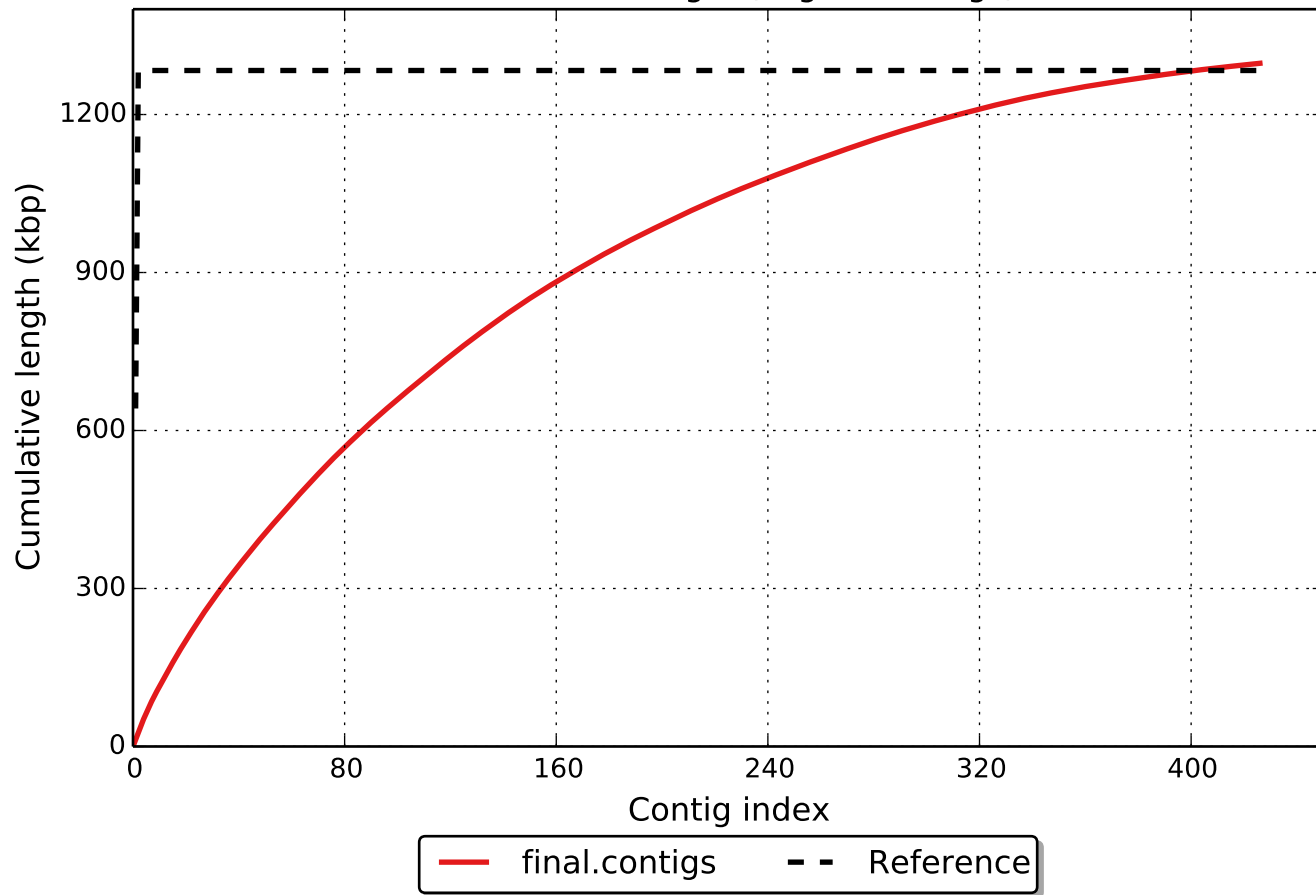


NGx

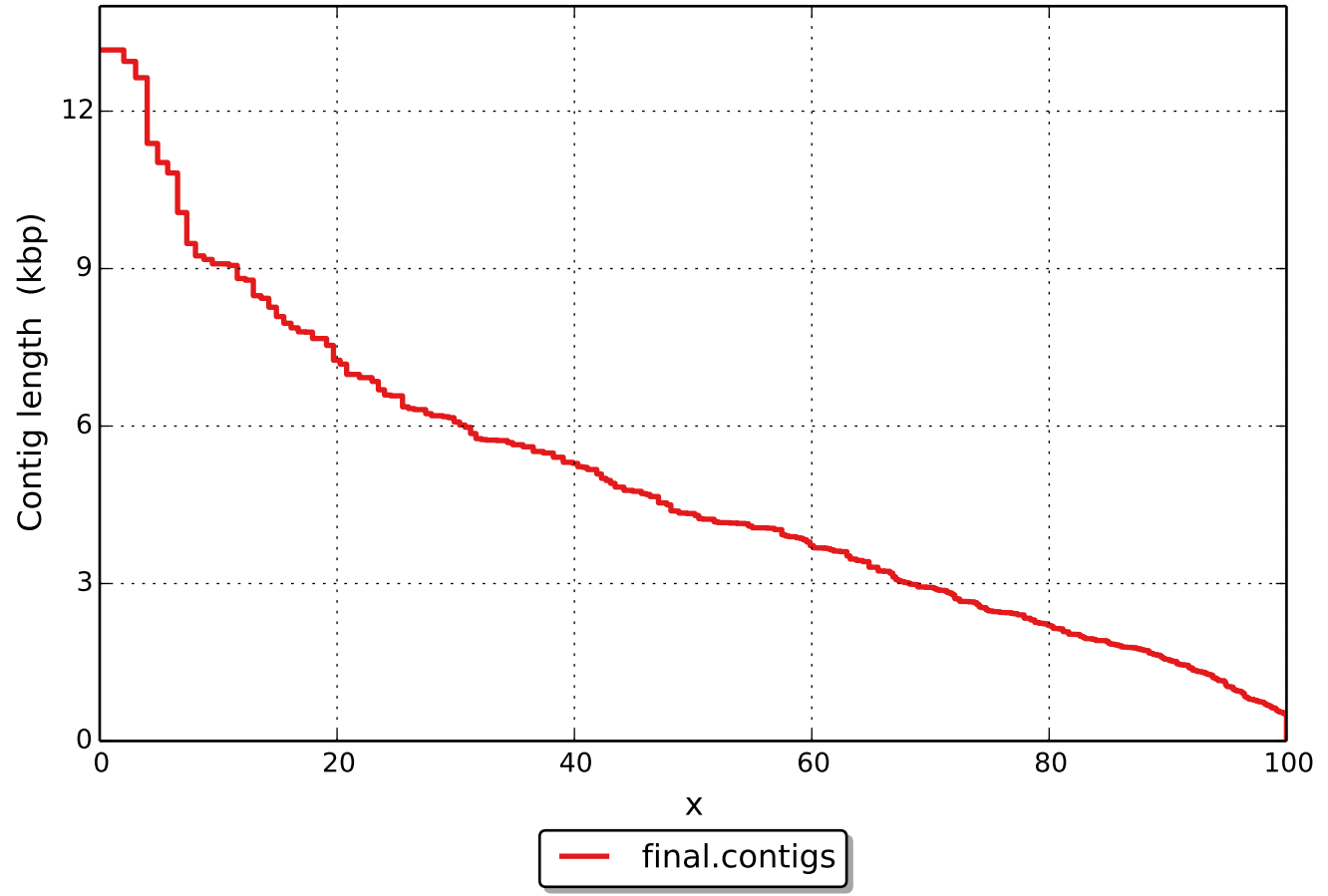




Cumulative length (aligned contigs)



NAx



NGAx

