

Report

	final.contigs
# contigs (>= 0 bp)	71838
# contigs (>= 1000 bp)	1462
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29195863
Total length (>= 1000 bp)	2036512
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8312
Largest contig	4275
Total length	6384066
Reference length	4641652
GC (%)	50.69
Reference GC (%)	50.79
N50	751
NG50	929
N75	567
NG75	705
L50	2803
LG50	1757
L75	5290
LG75	3201
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	786
# local misassemblies	1
# unaligned contigs	5964 + 43 part
Unaligned length	4015484
Genome fraction (%)	49.169
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	451.61
# indels per 100 kbp	0.35
Largest alignment	4275
NGA50	517
LGA50	2244

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
# misassembled contigs	1
Misassembled contigs length	786
# local misassemblies	1
# mismatches	10307
# indels	8
# short indels	8
# long indels	0
Indels length	9

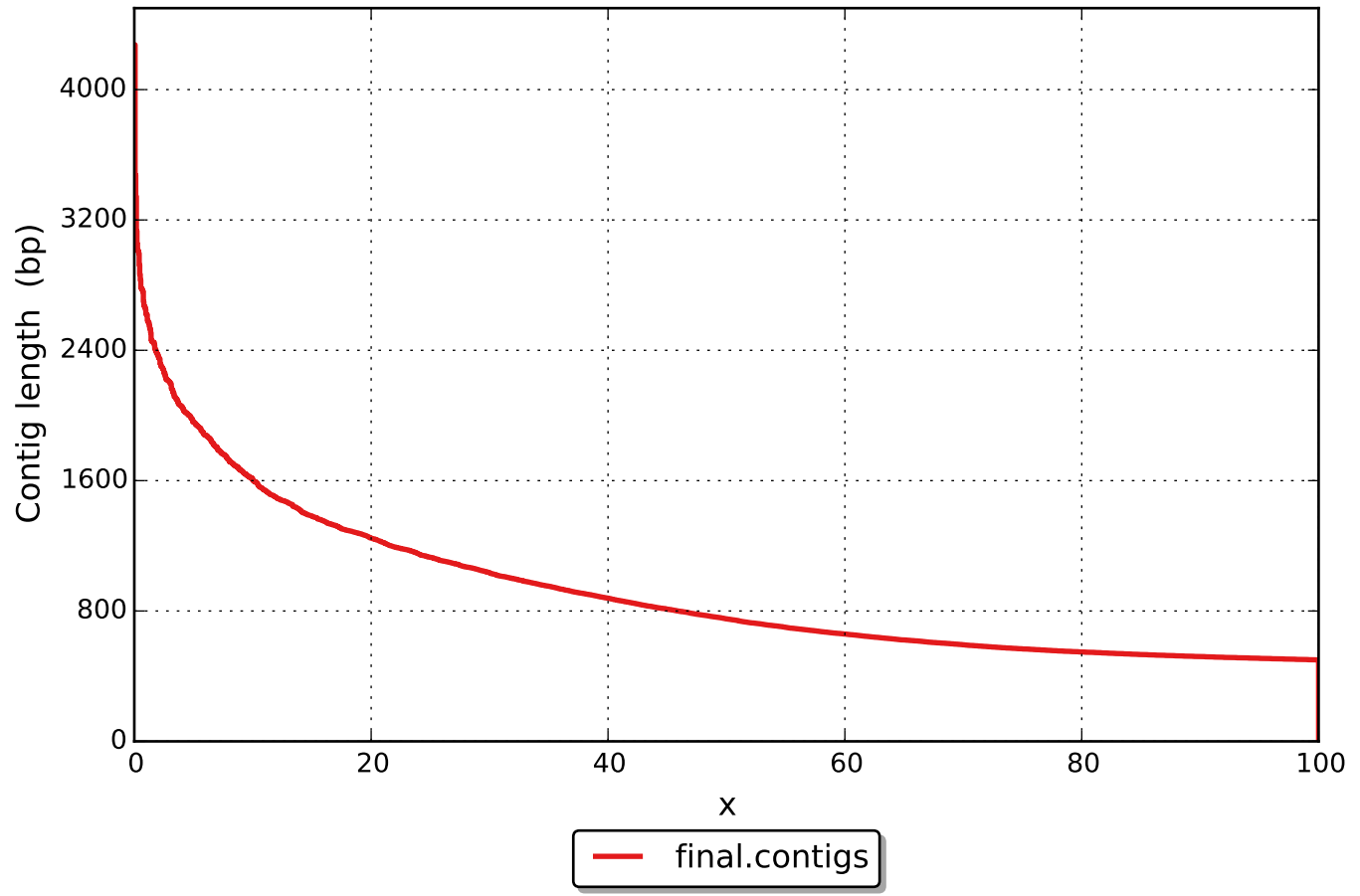
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

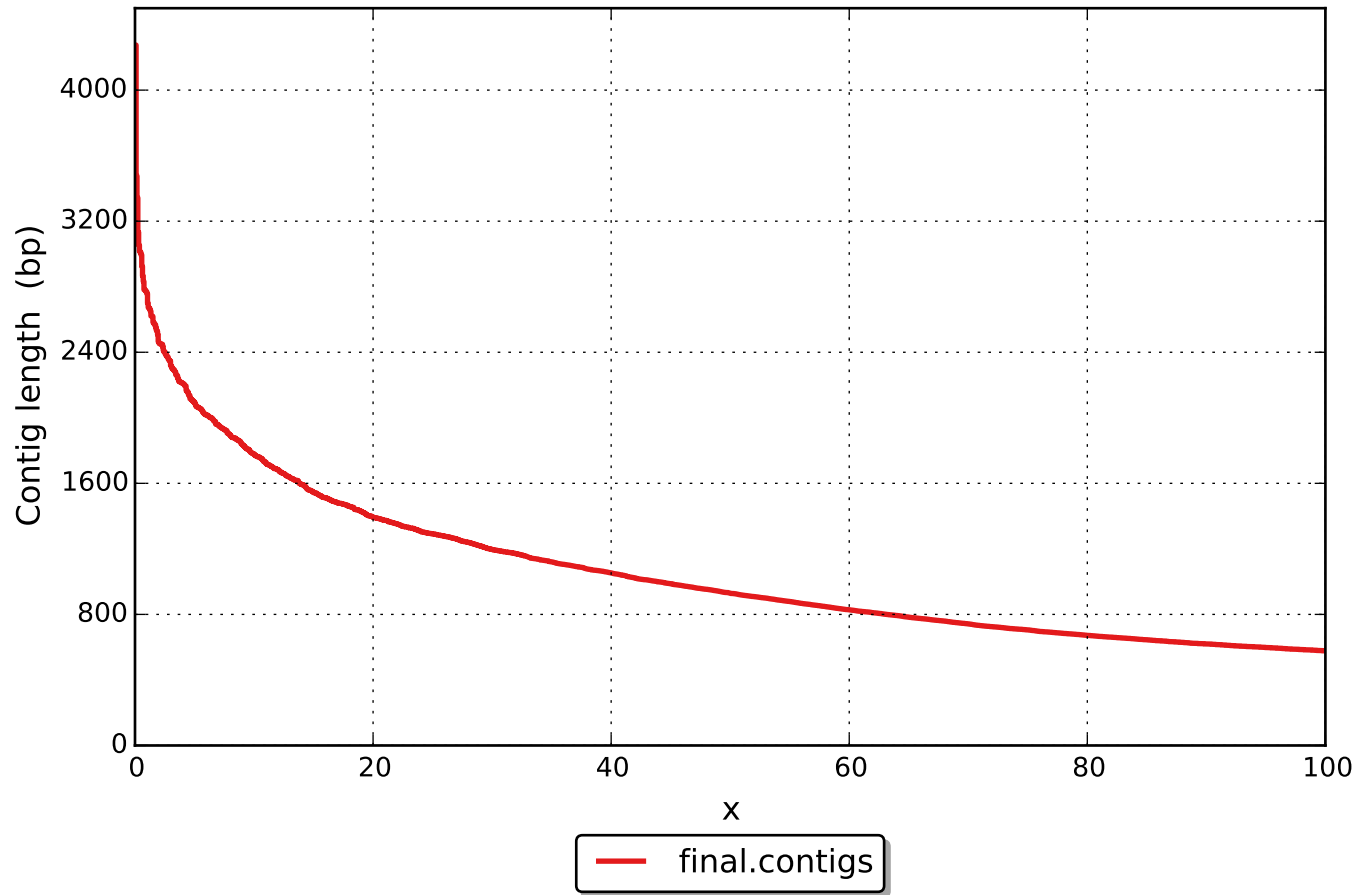
	final.contigs
# fully unaligned contigs	5964
Fully unaligned length	4003289
# partially unaligned contigs	43
# with misassembly	0
# both parts are significant	0
Partially unaligned length	12195
# N's	0

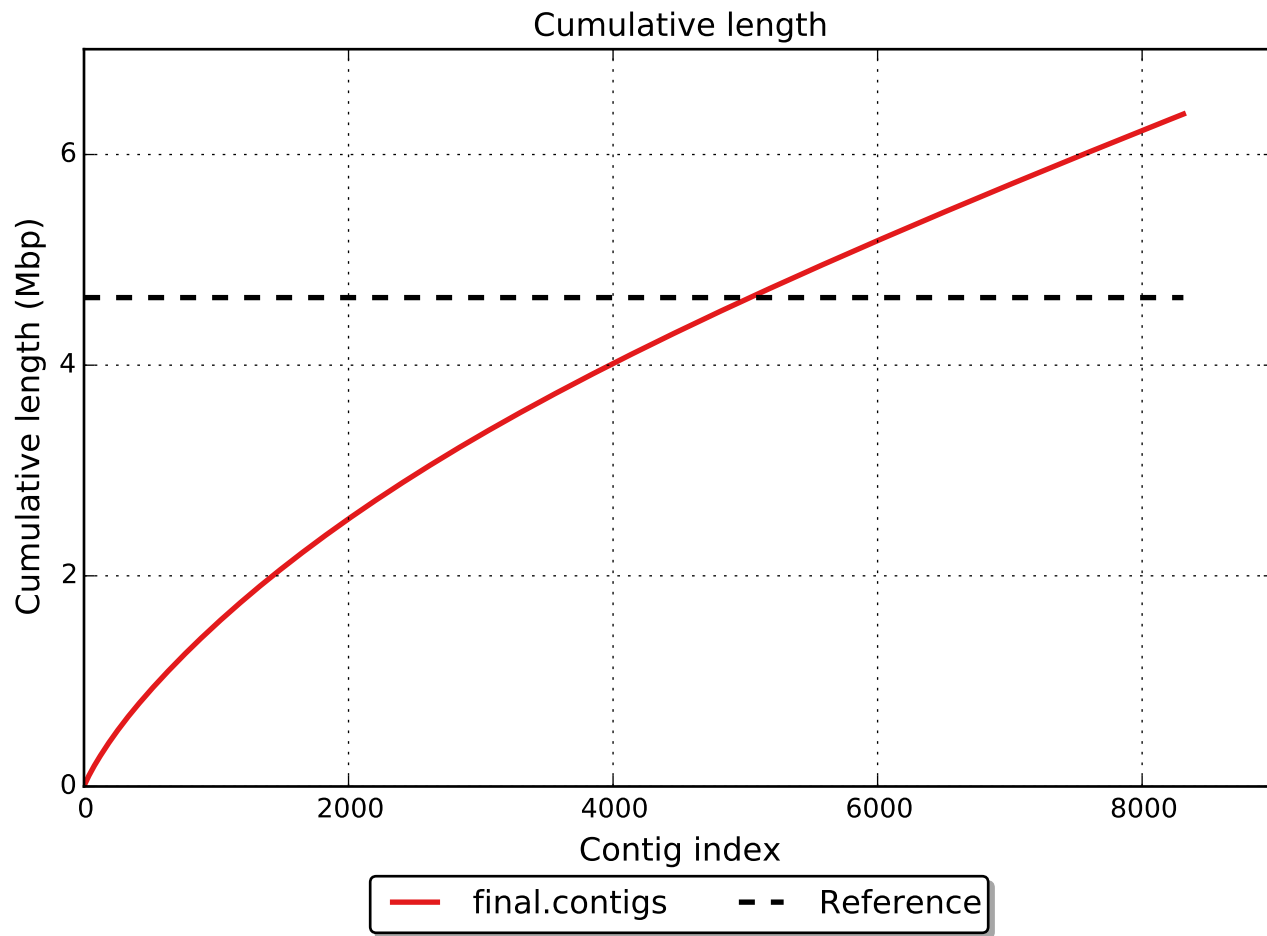
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

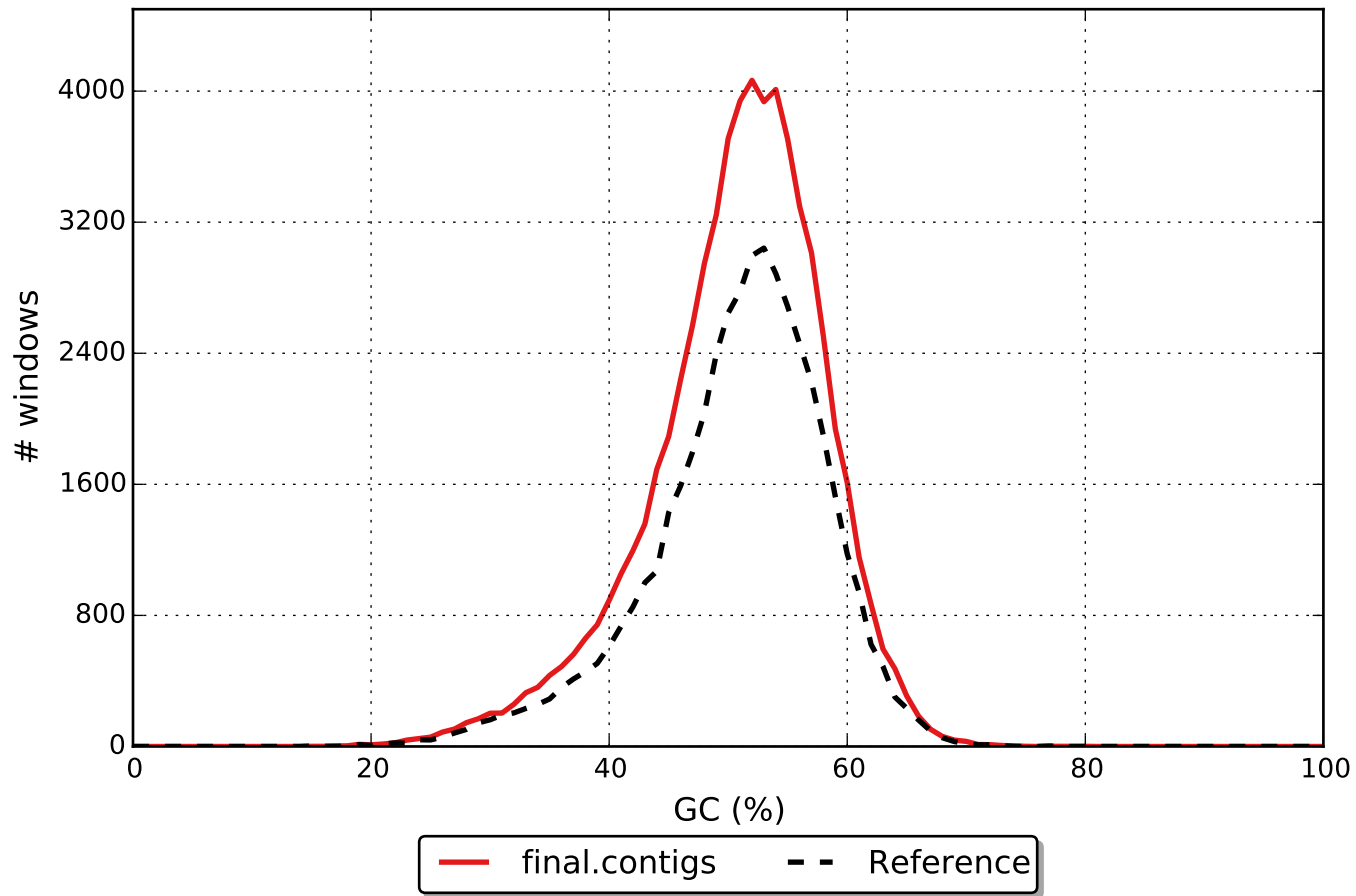


NGx



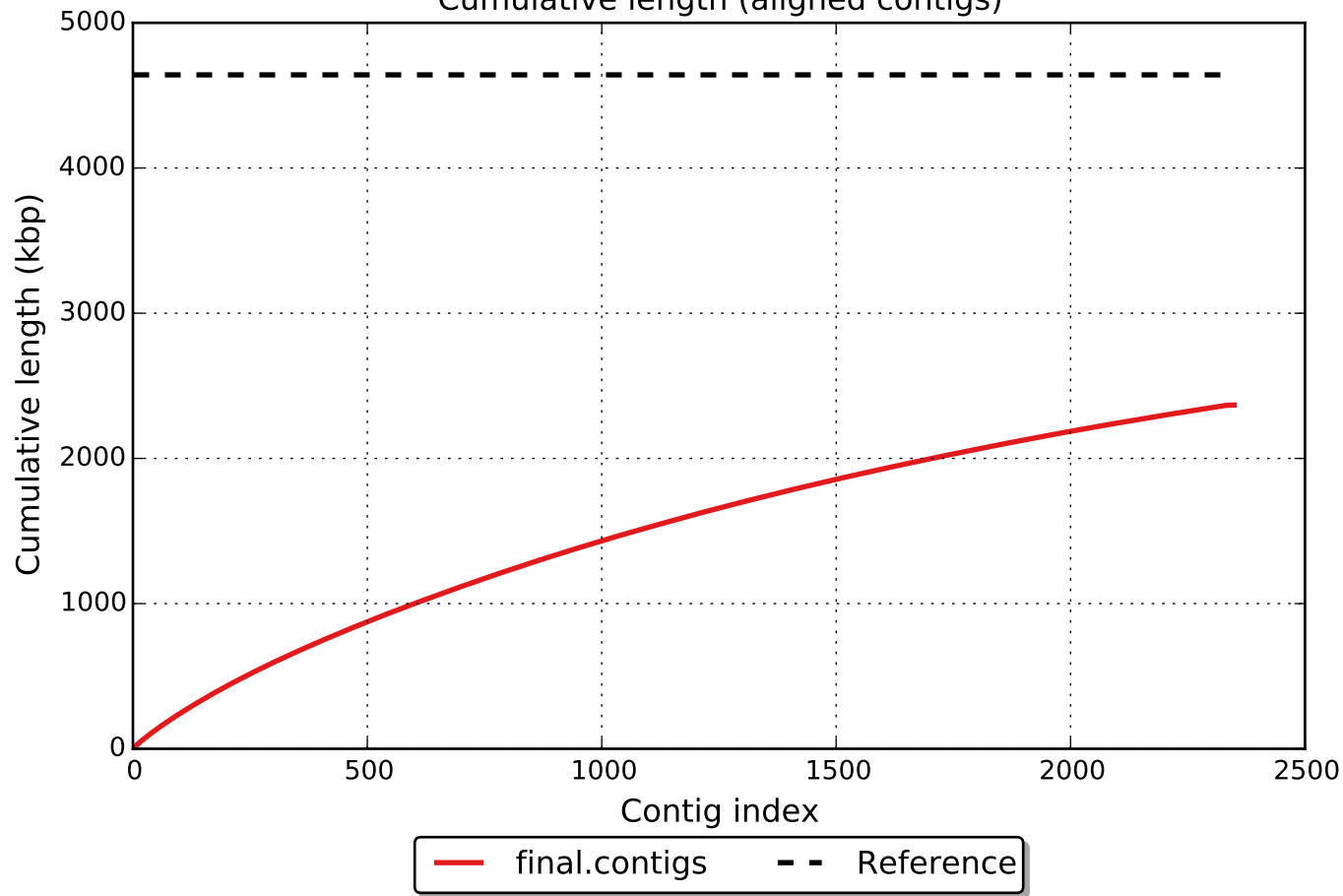


GC content

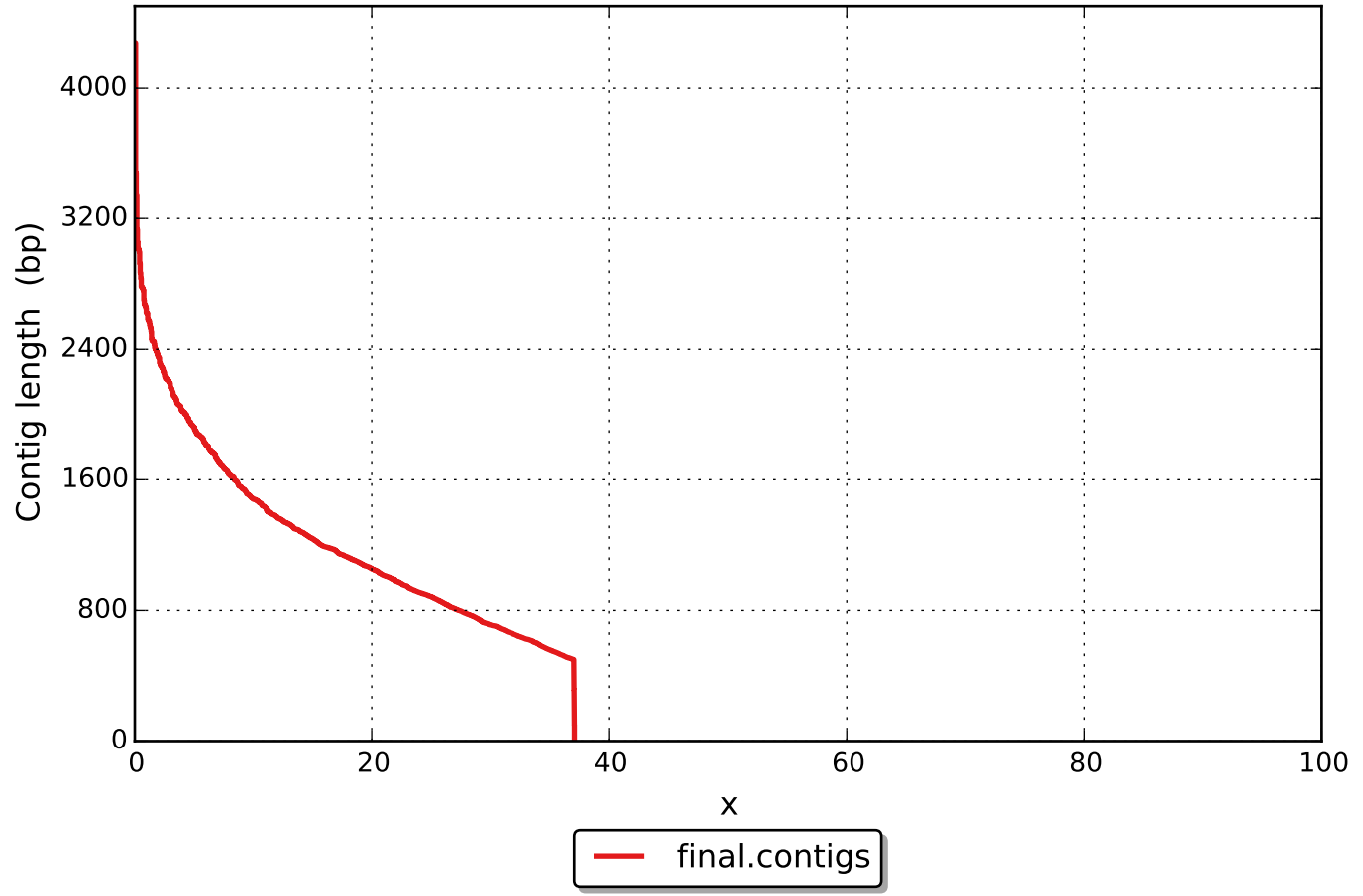




Cumulative length (aligned contigs)



NAx



NGAx

