

# Report

	final.contigs
# contigs (>= 0 bp)	10411
# contigs (>= 1000 bp)	1839
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7076166
Total length (>= 1000 bp)	2660324
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5524
Largest contig	4077
Total length	5261284
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1007
NG50	1091
N75	725
NG75	819
L50	1810
LG50	1515
L75	3350
LG75	2746
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	4540 + 18 part
Unaligned length	3886921
Genome fraction (%)	29.149
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	695.35
# indels per 100 kbp	0.89
Largest alignment	4077
NGA50	-

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9408
# indels	12
# short indels	12
# long indels	0
Indels length	12

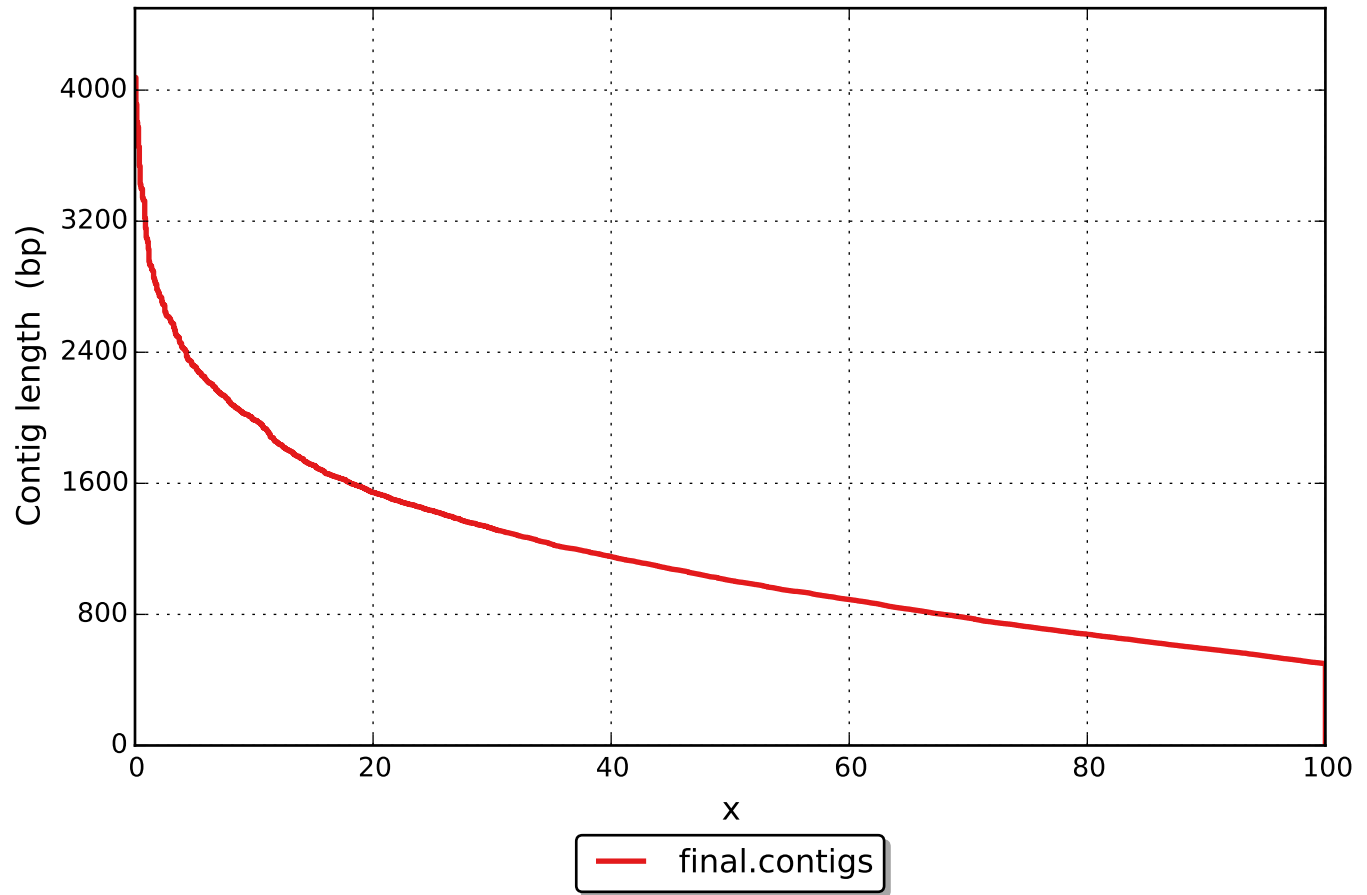
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

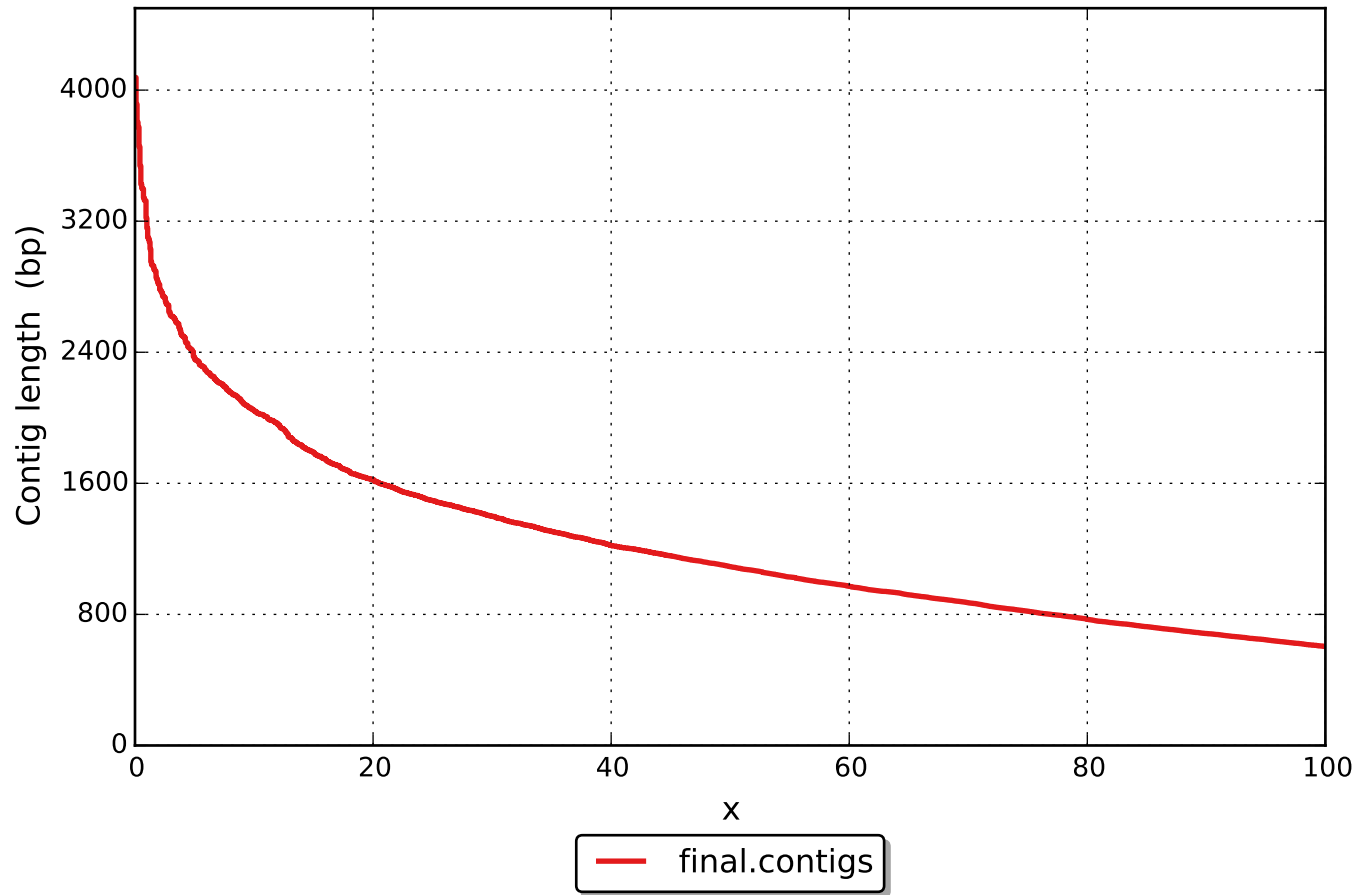
	final.contigs
# fully unaligned contigs	4540
Fully unaligned length	3879732
# partially unaligned contigs	18
# with misassembly	0
# both parts are significant	0
Partially unaligned length	7189
# N's	0

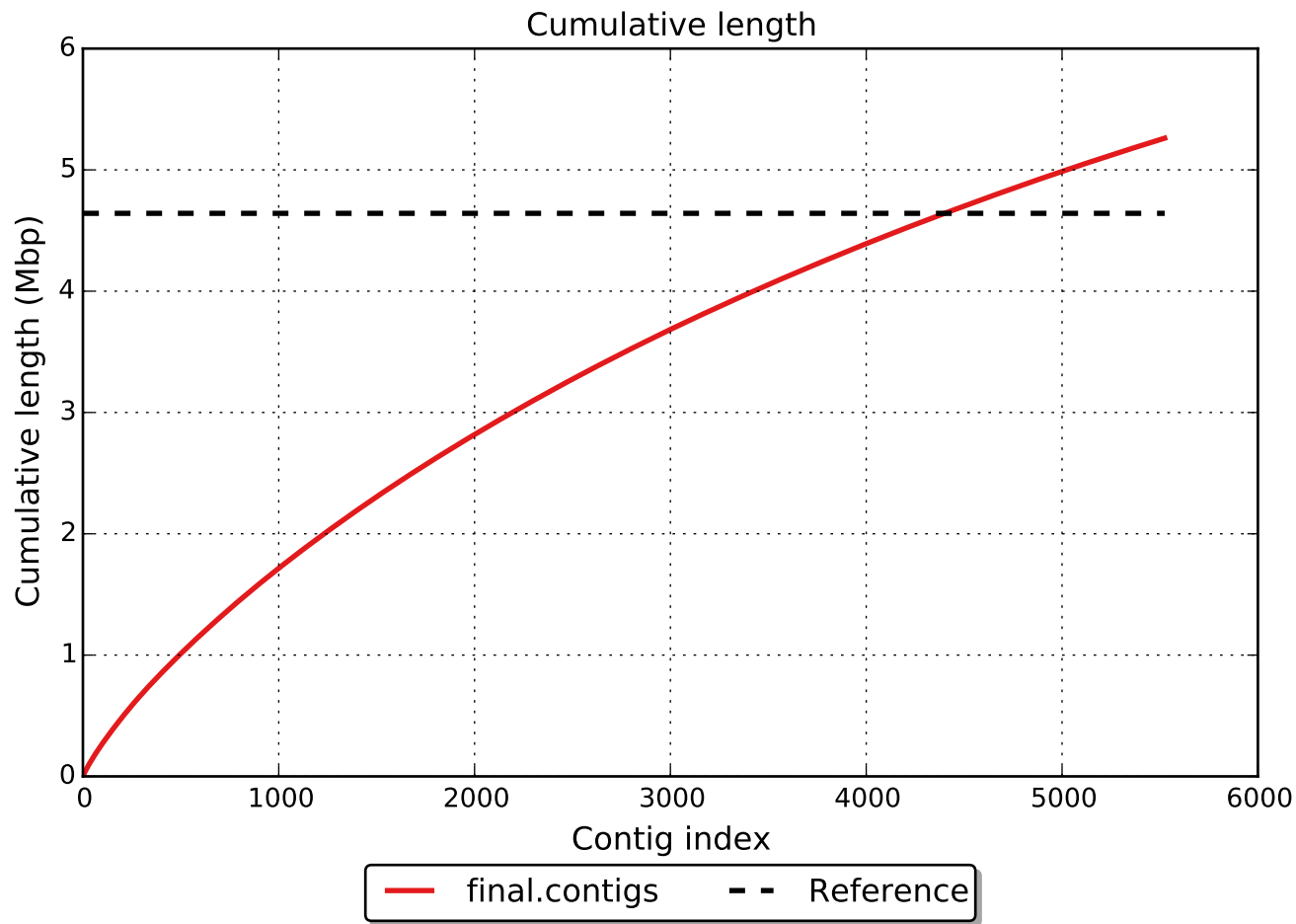
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

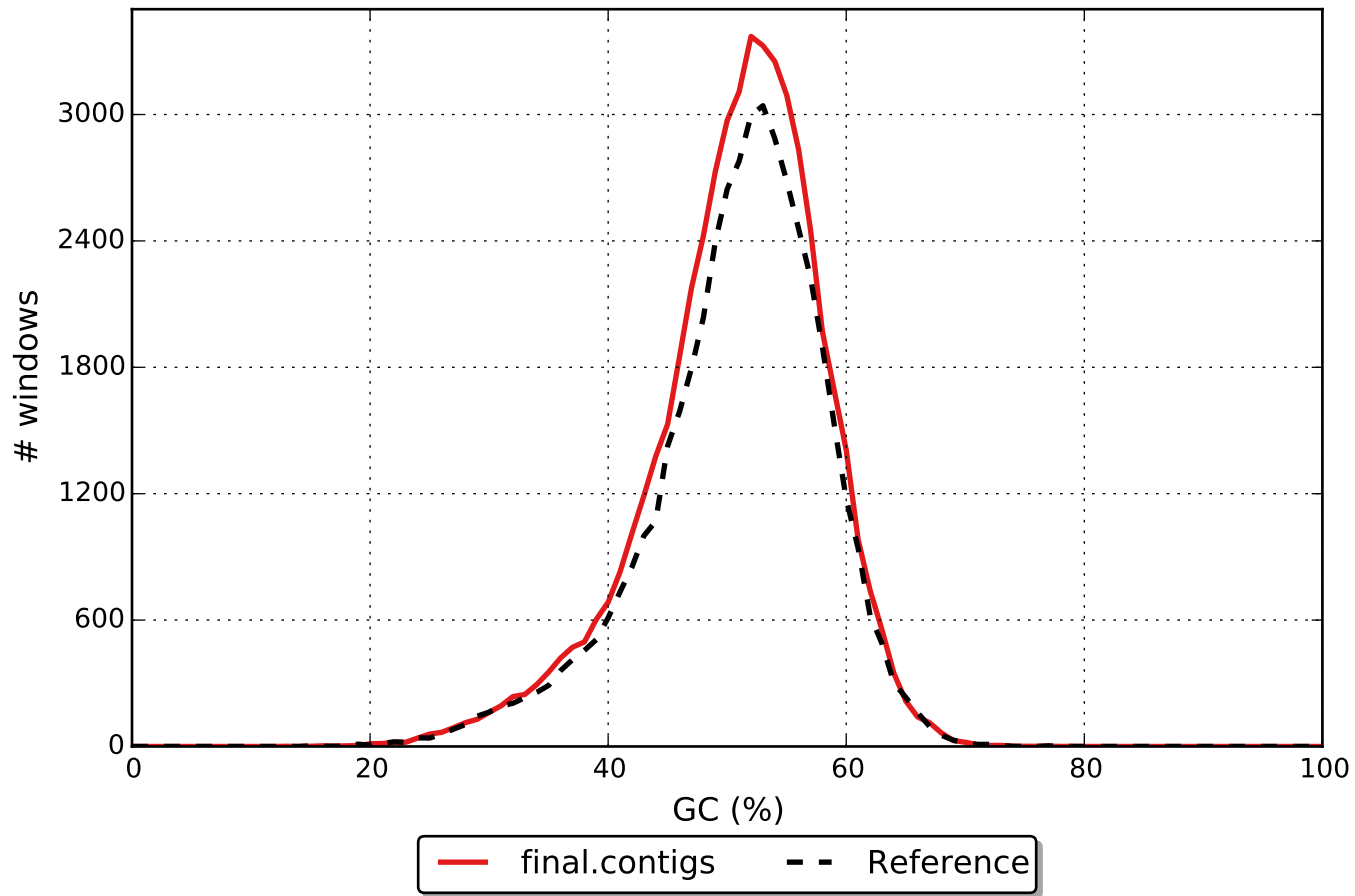


NGx





GC content

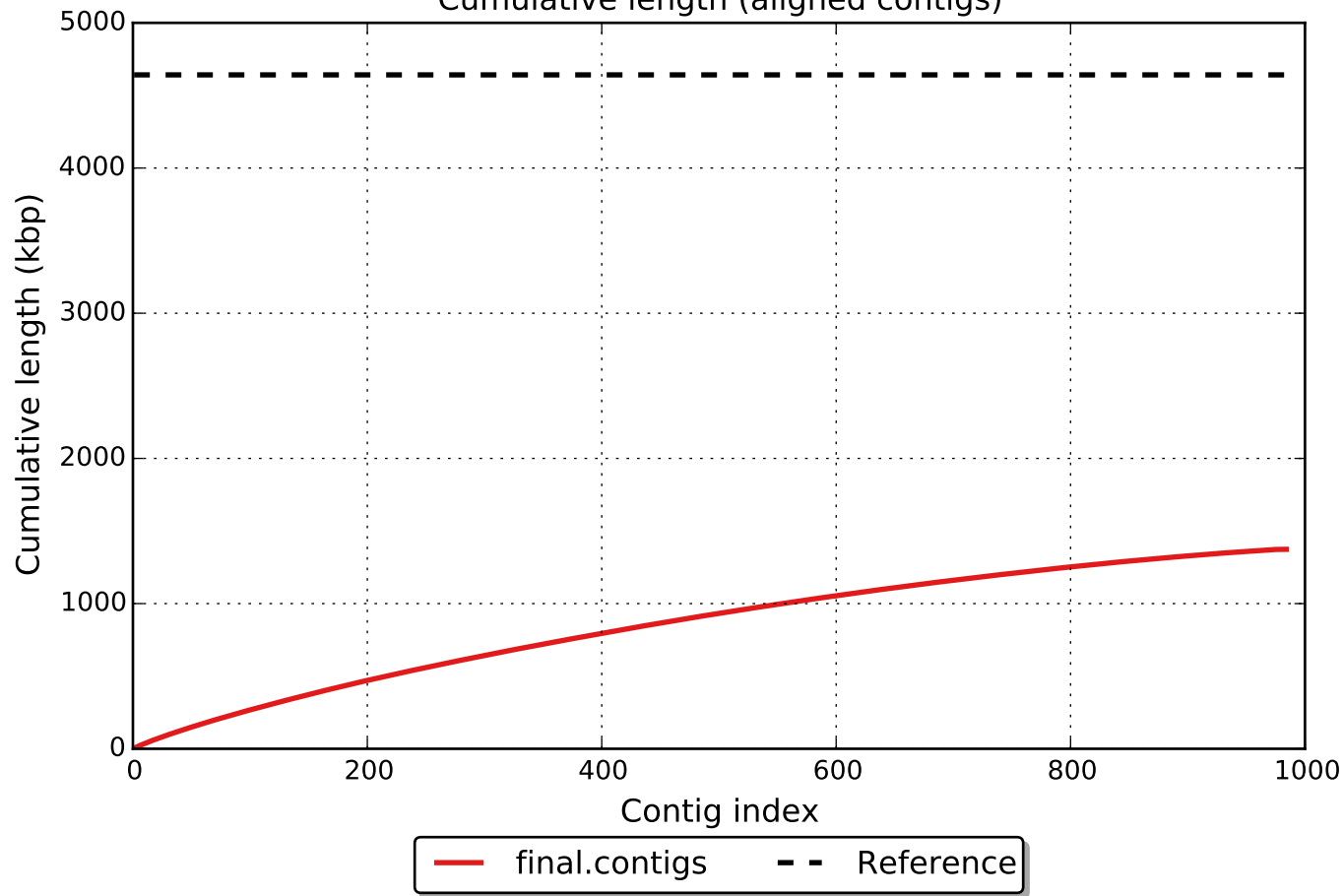


# Misassemblies

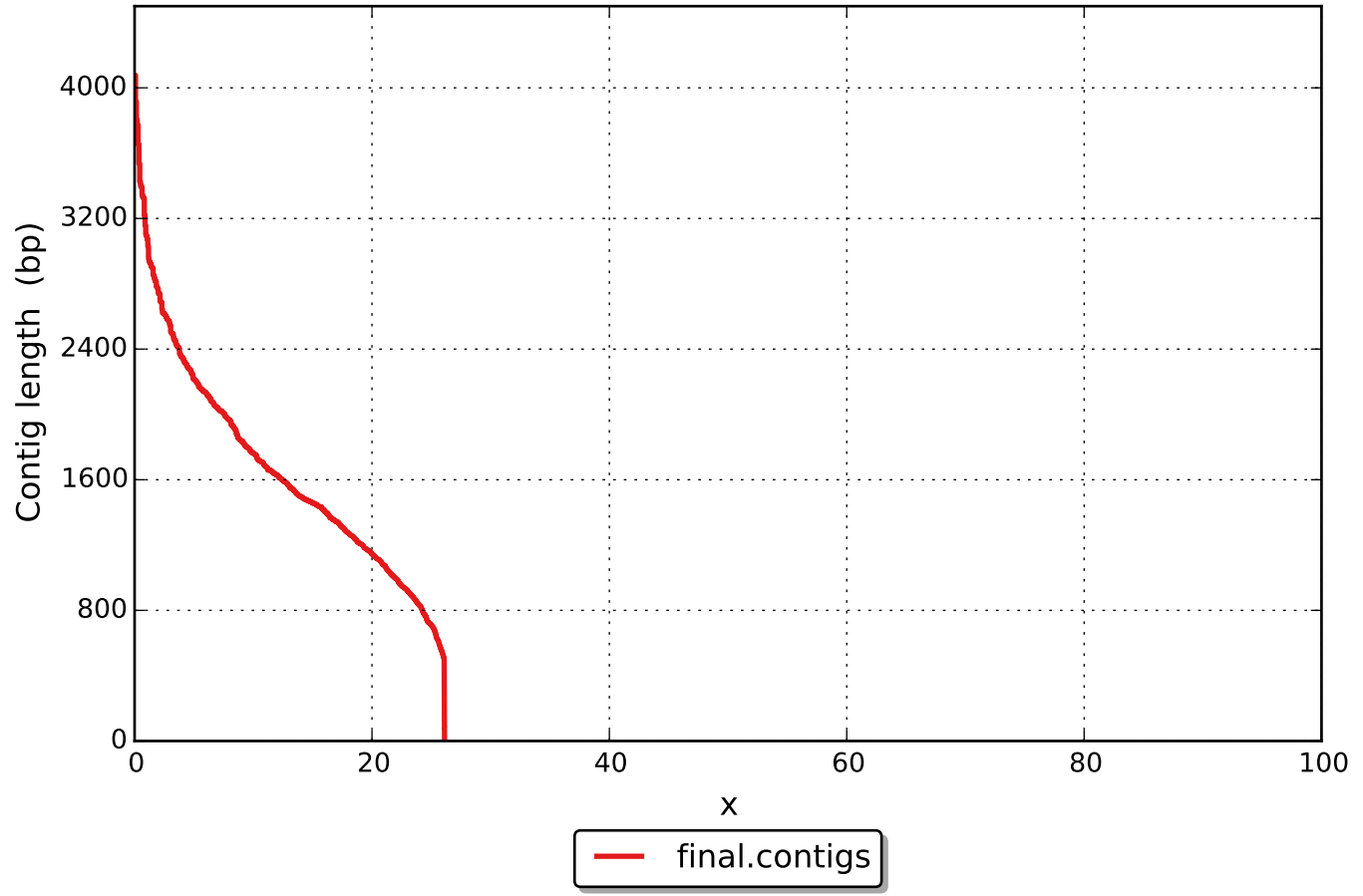




Cumulative length (aligned contigs)



NAx



NGAx

