

Report

	final.contigs
# contigs (>= 0 bp)	3217
# contigs (>= 1000 bp)	112
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1646637
Total length (>= 1000 bp)	143662
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1253
Largest contig	4453
Total length	882296
Reference length	4641652
GC (%)	50.85
Reference GC (%)	50.79
N50	682
N75	581
L50	488
L75	841
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	9862
# local misassemblies	4
# unaligned contigs	1 + 8 part
Unaligned length	1291
Genome fraction (%)	18.909
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1332.37
# indels per 100 kbp	1.60
Largest alignment	4453
NA50	679
NGA50	-
NA75	578
LA50	490
LA75	845

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	9
# relocations	9
# translocations	0
# inversions	0
# misassembled contigs	9
Misassembled contigs length	9862
# local misassemblies	4
# mismatches	11694
# indels	14
# short indels	14
# long indels	0
Indels length	14

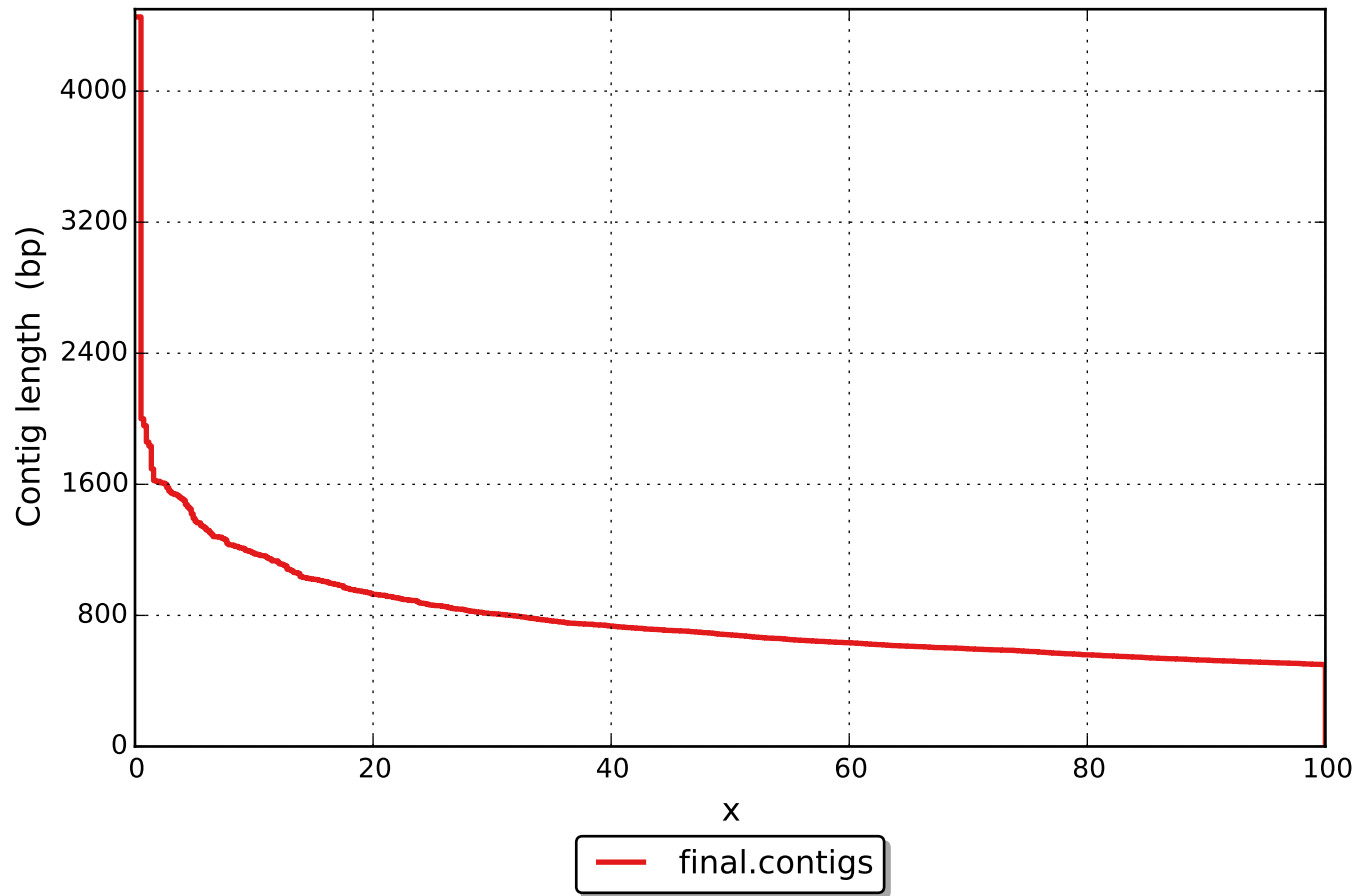
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

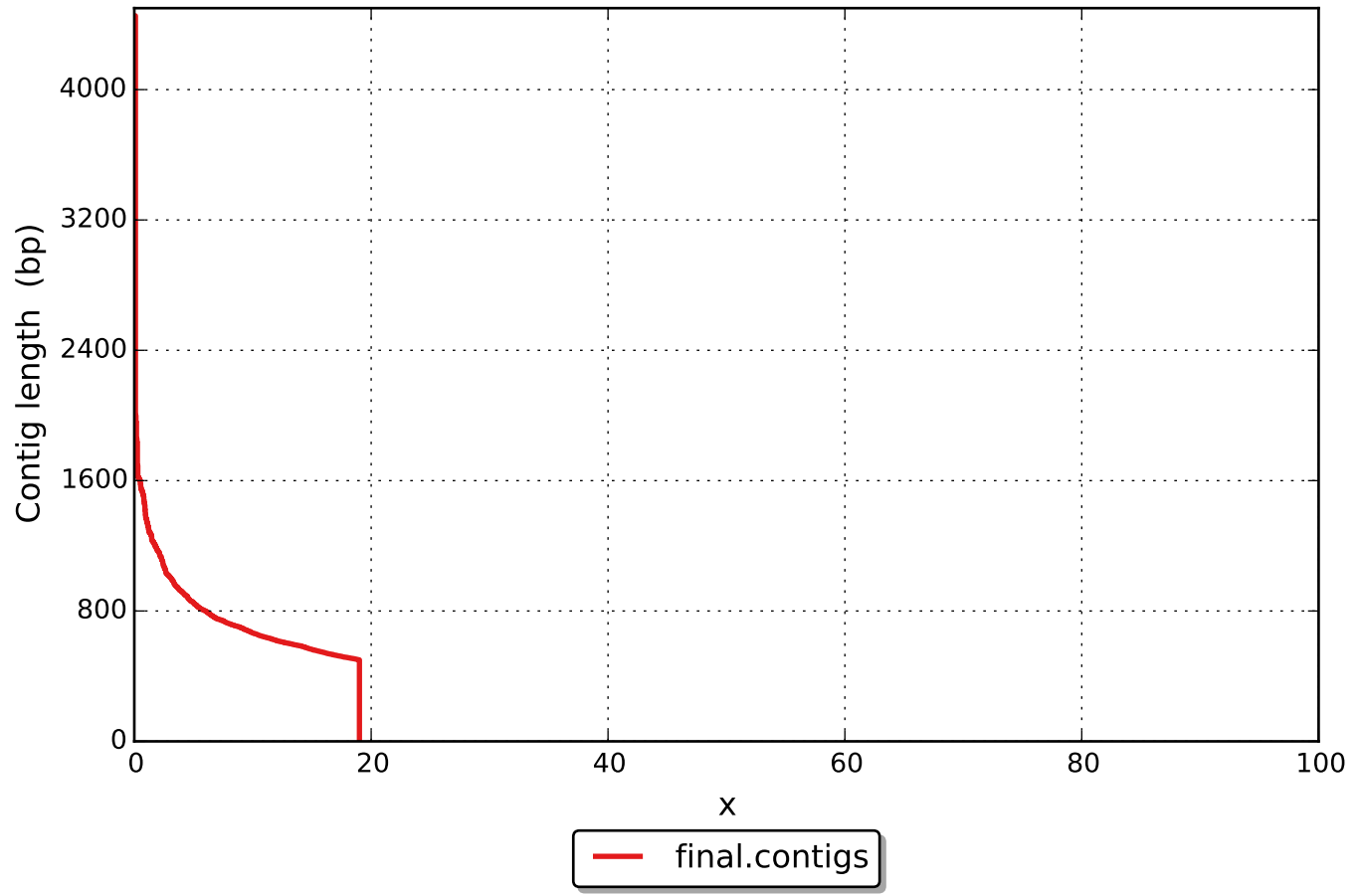
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	625
# partially unaligned contigs	8
# with misassembly	0
# both parts are significant	0
Partially unaligned length	666
# N's	0

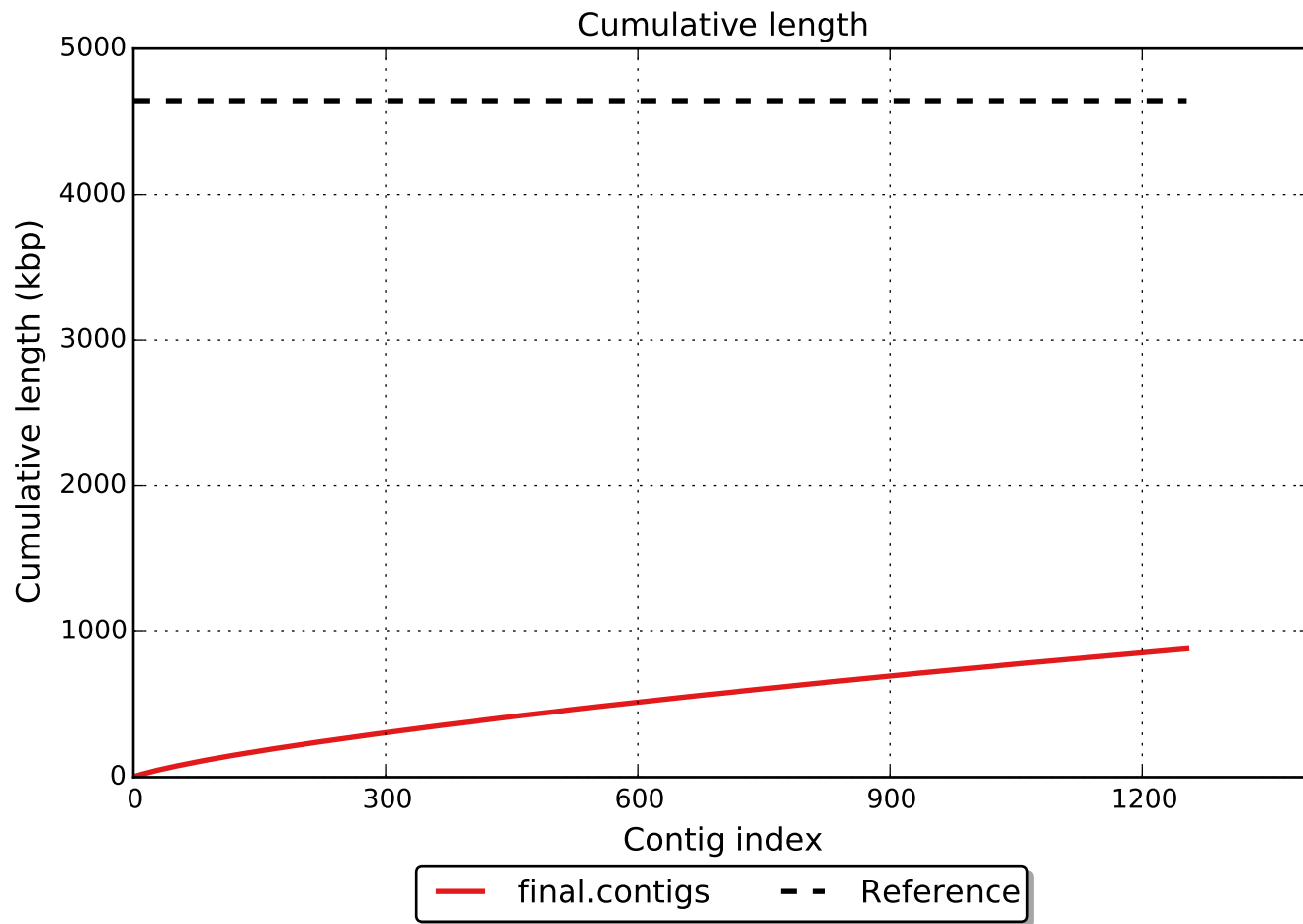
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

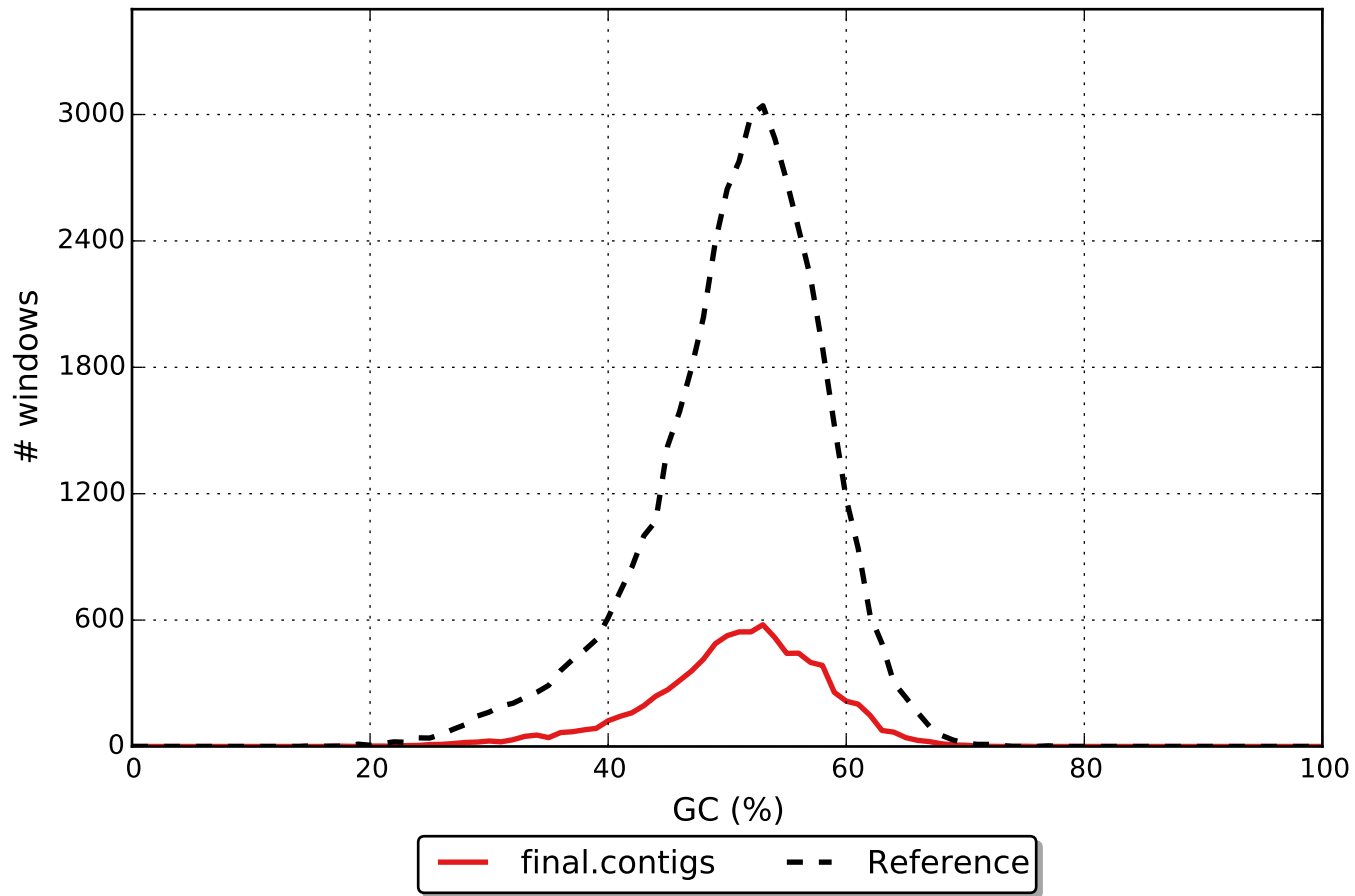


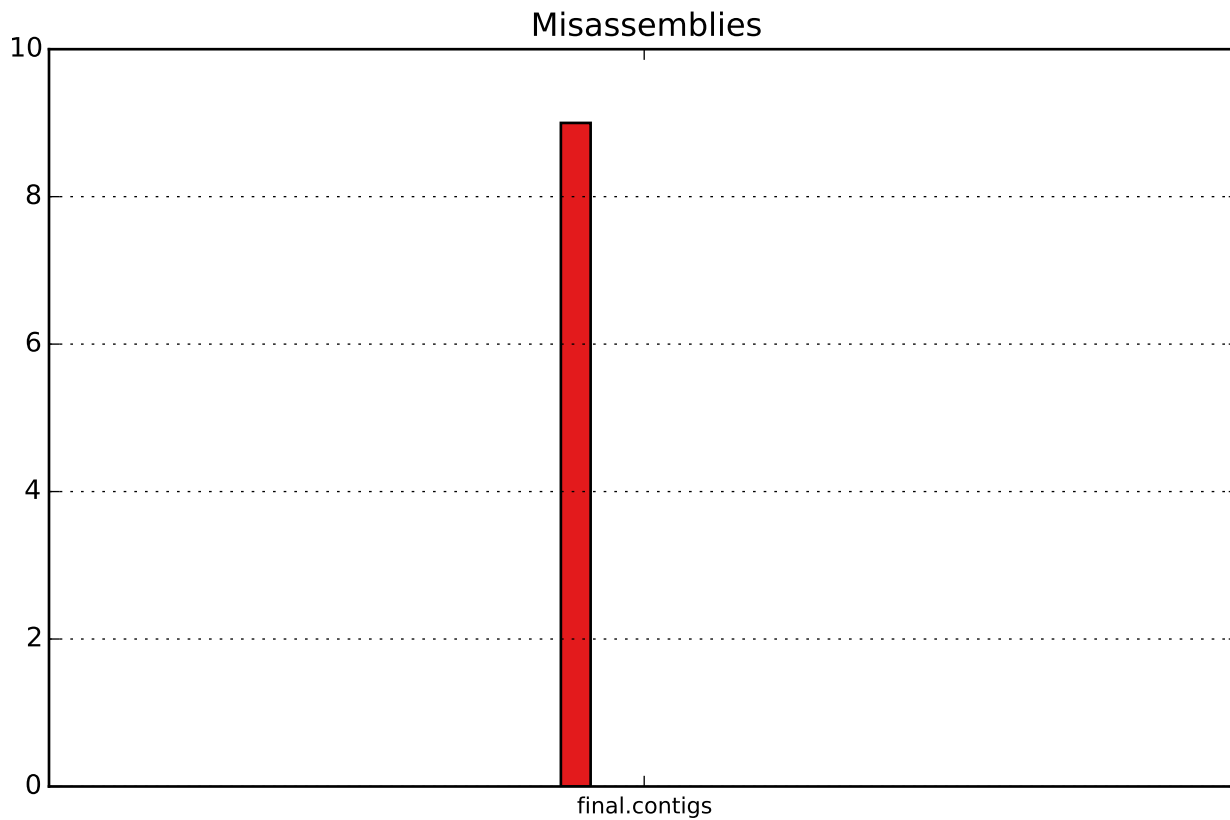
NGx



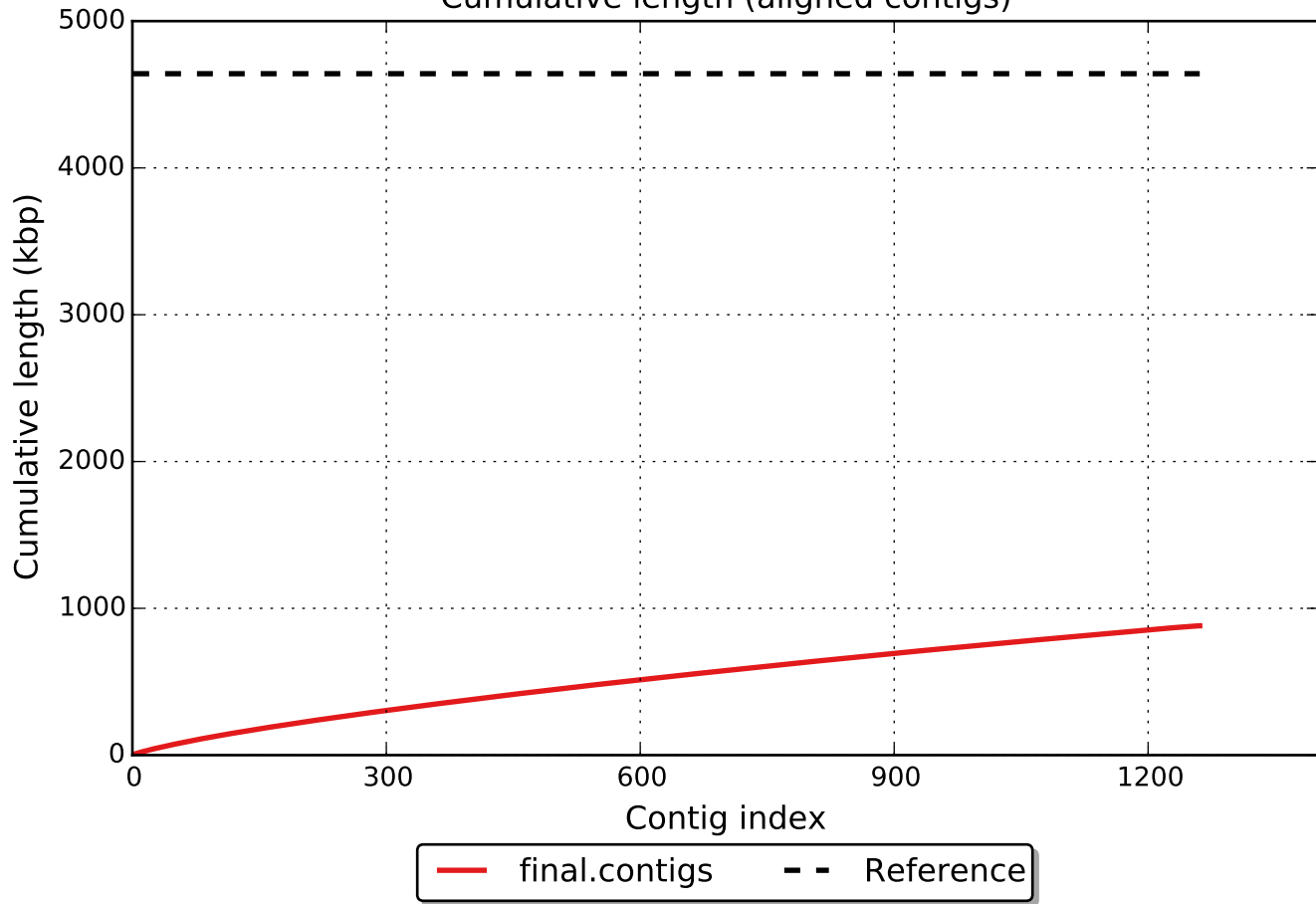


GC content

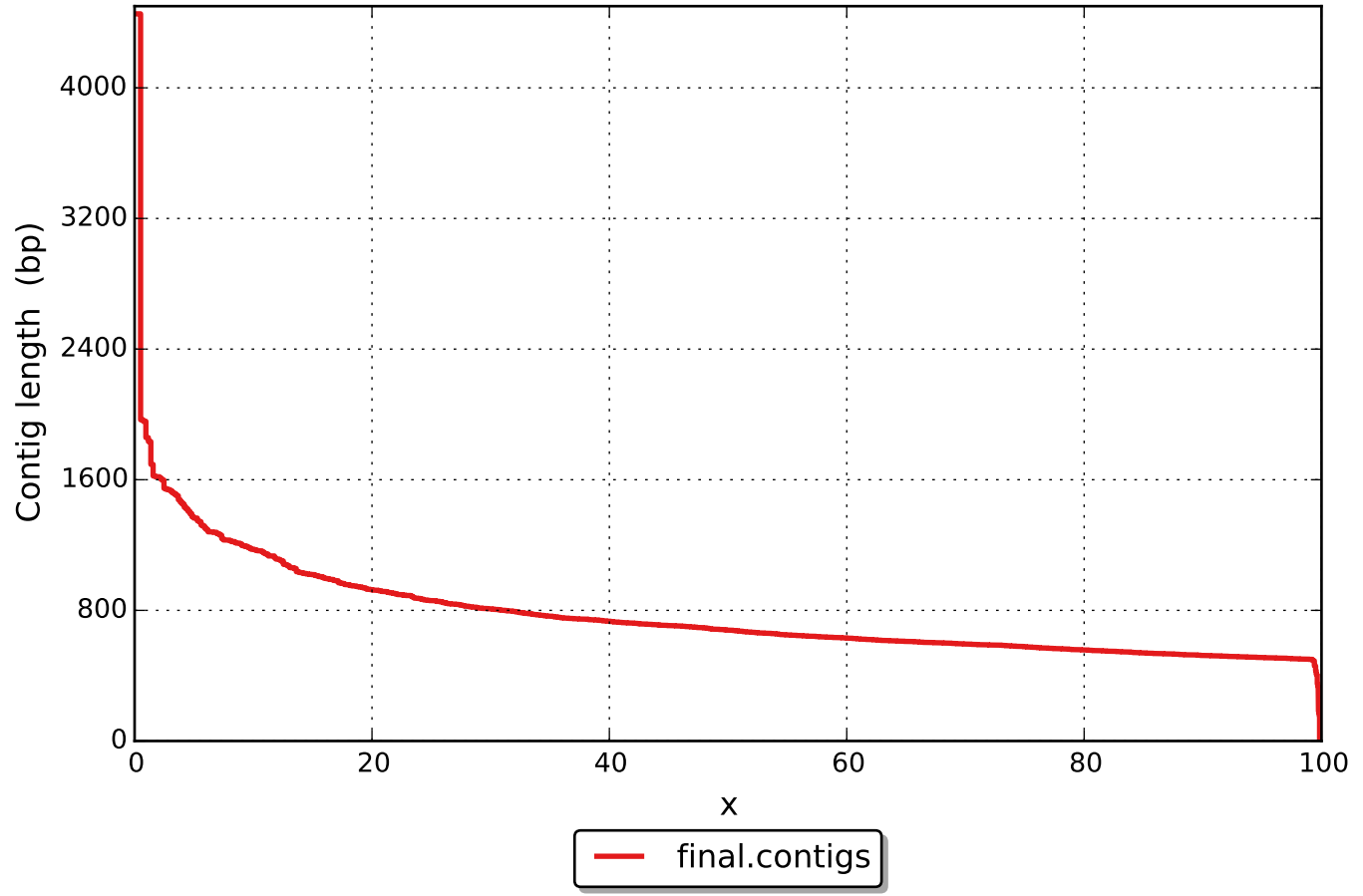




Cumulative length (aligned contigs)



NAx



NGAx

