

Report

	final.contigs
# contigs (≥ 1000 bp)	293
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	380096
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1906
Largest contig	3225
Total length	1460764
Reference length	4641652
GC (%)	50.82
Reference GC (%)	50.79
N50	764
N75	607
L50	700
L75	1241
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	8370
# local misassemblies	0
# unaligned contigs	0 + 5 part
Unaligned length	273
Genome fraction (%)	31.440
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	218.87
# indels per 100 kbp	10.35
Largest alignment	3225
NA50	761
NGA50	-
NA75	606
LA50	702
LA75	1244

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	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	8370
# local misassemblies	0
# mismatches	3194
# indels	151
# short indels	147
# long indels	4
Indels length	357

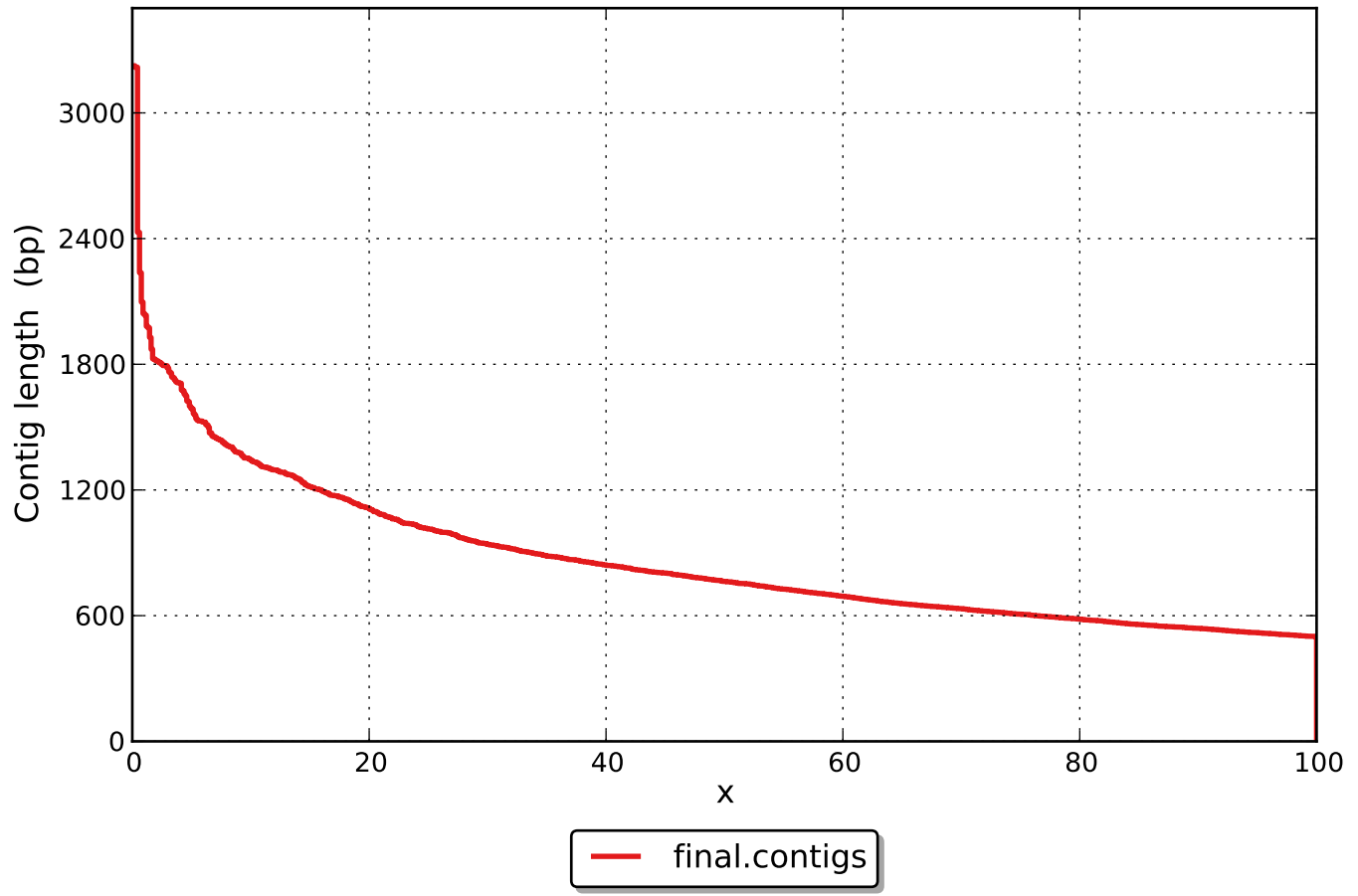
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

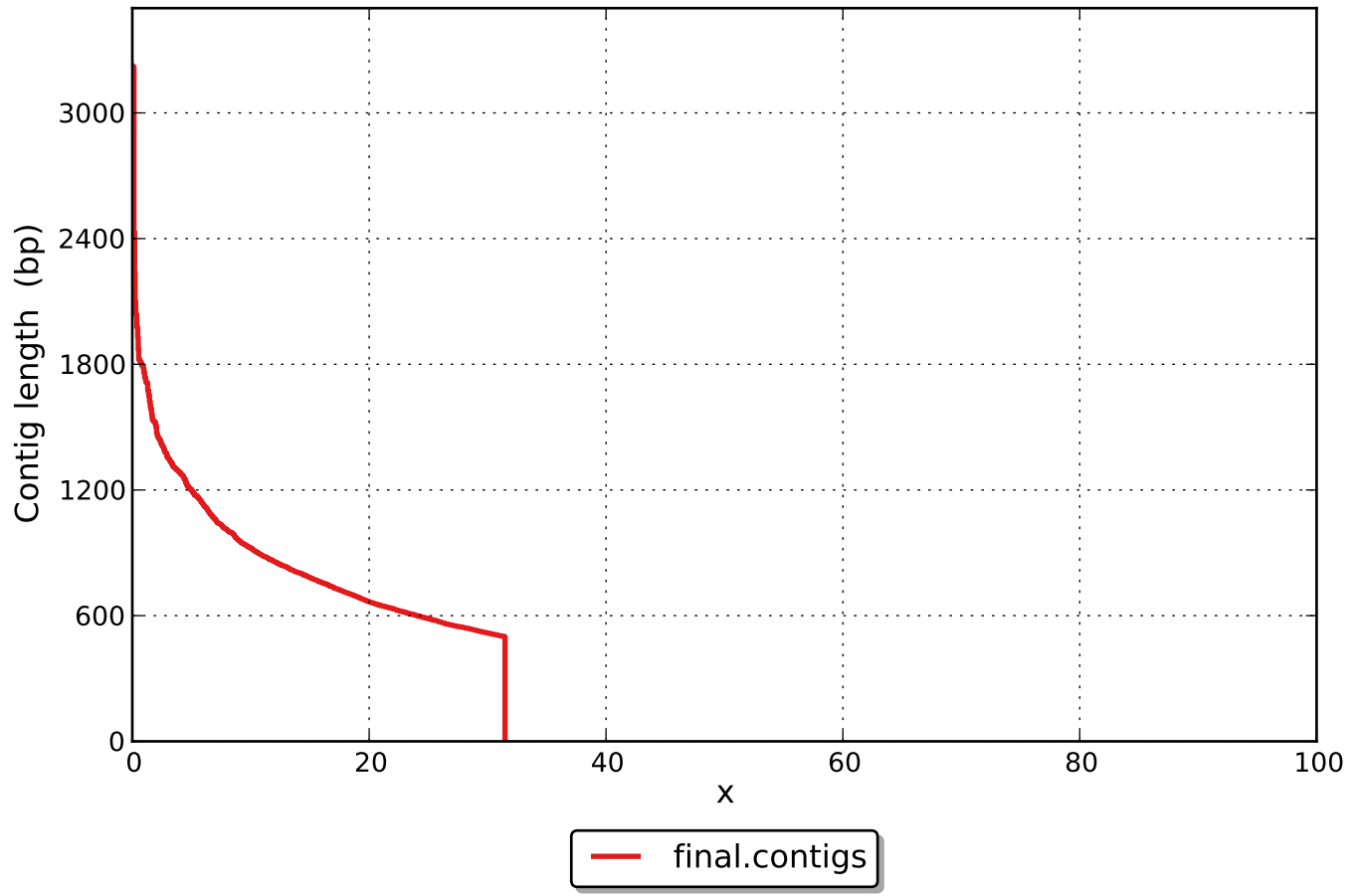
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	0
Partially unaligned length	273
# N's	0

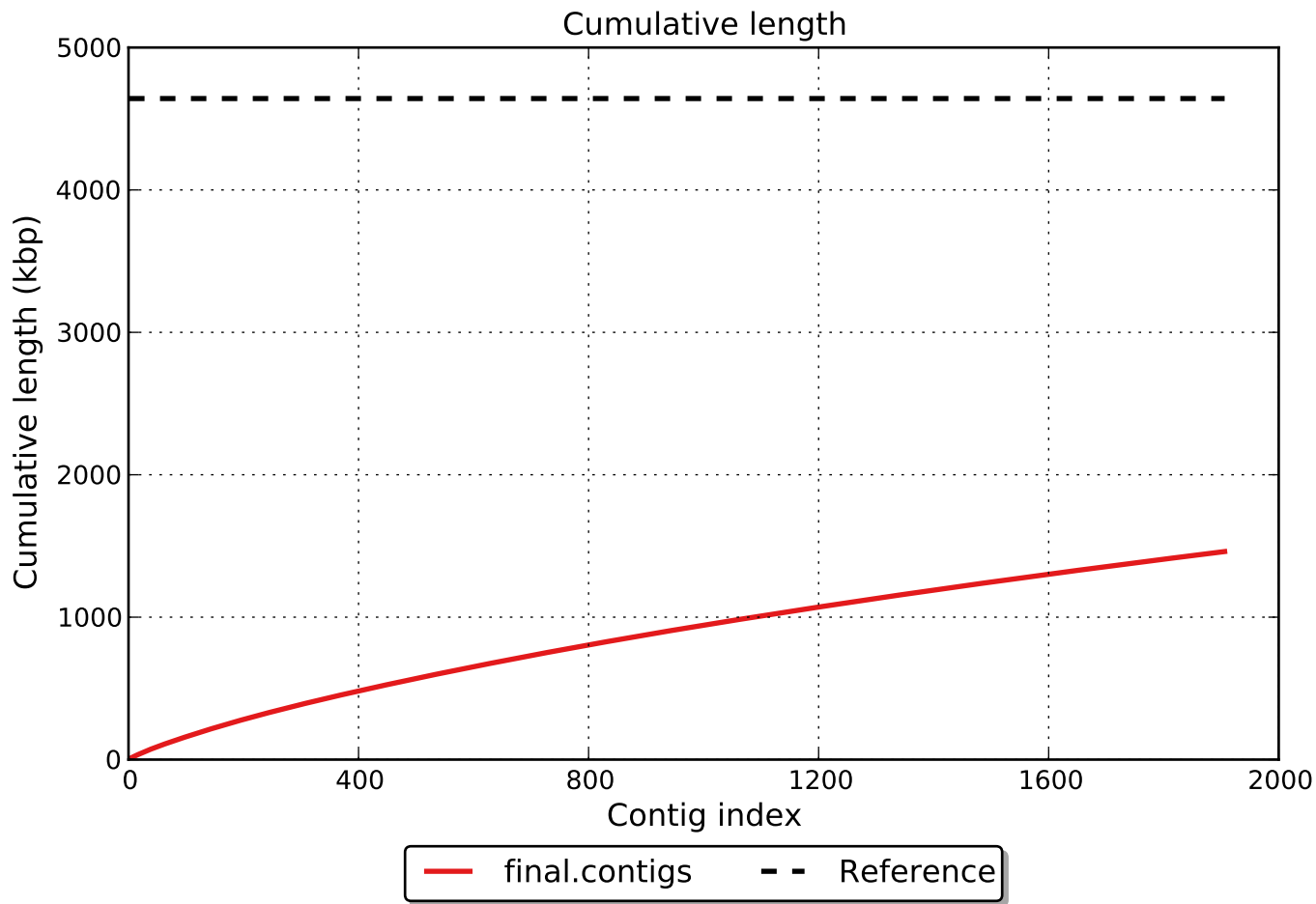
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

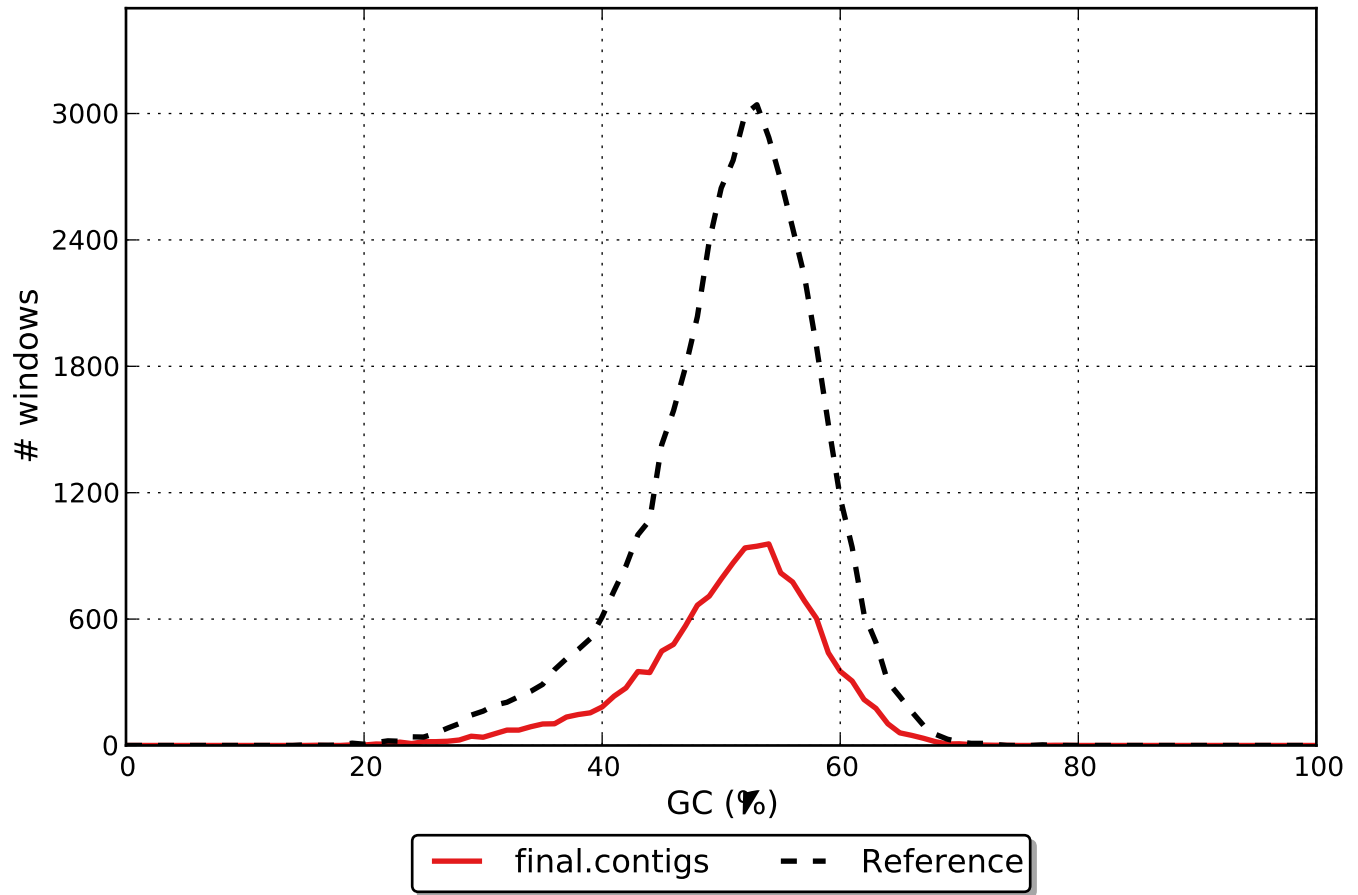


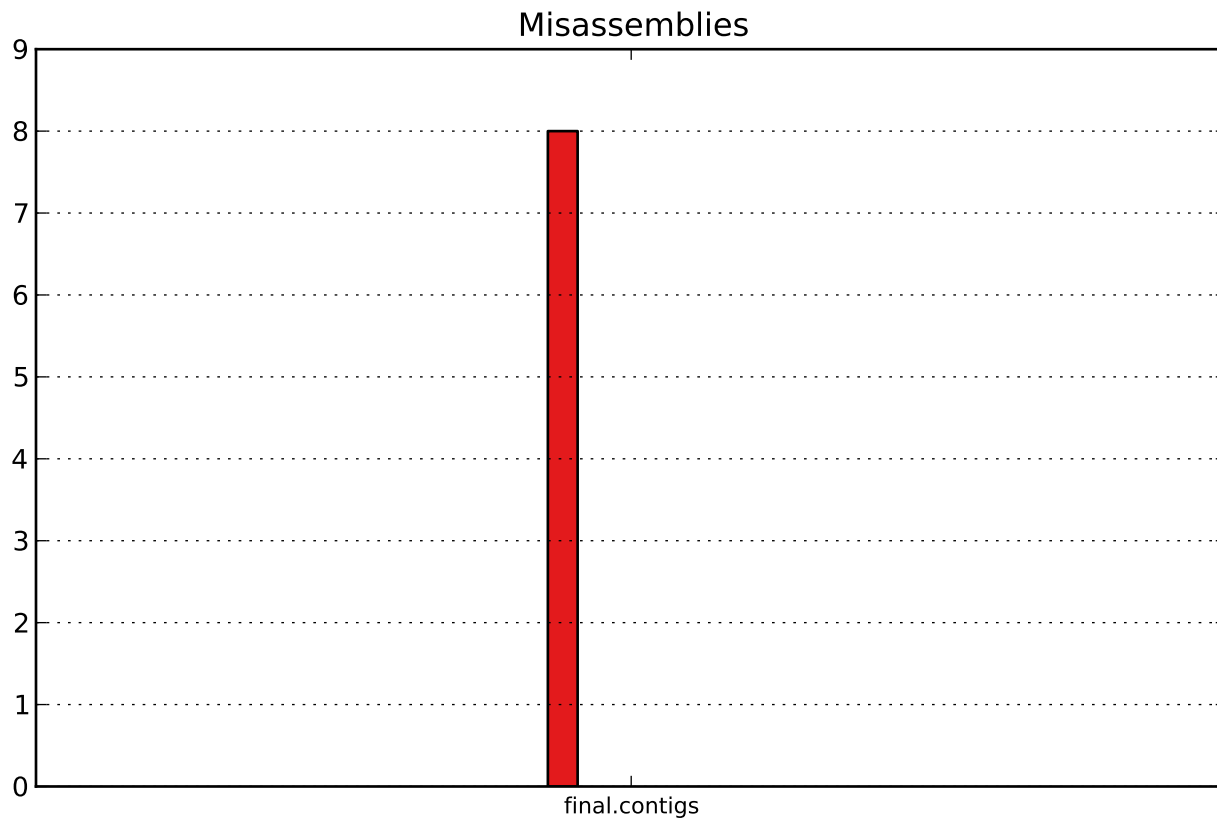
NGx



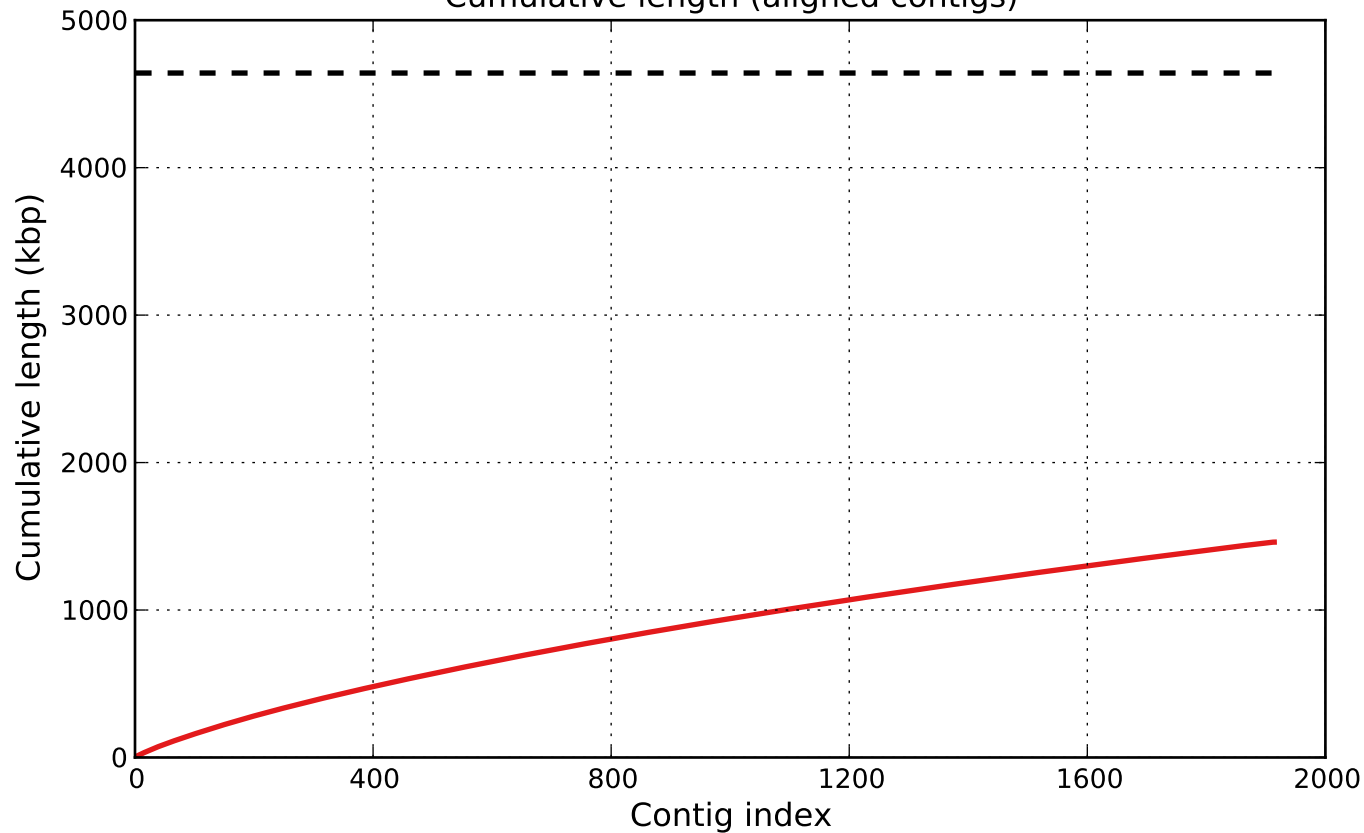


GC content



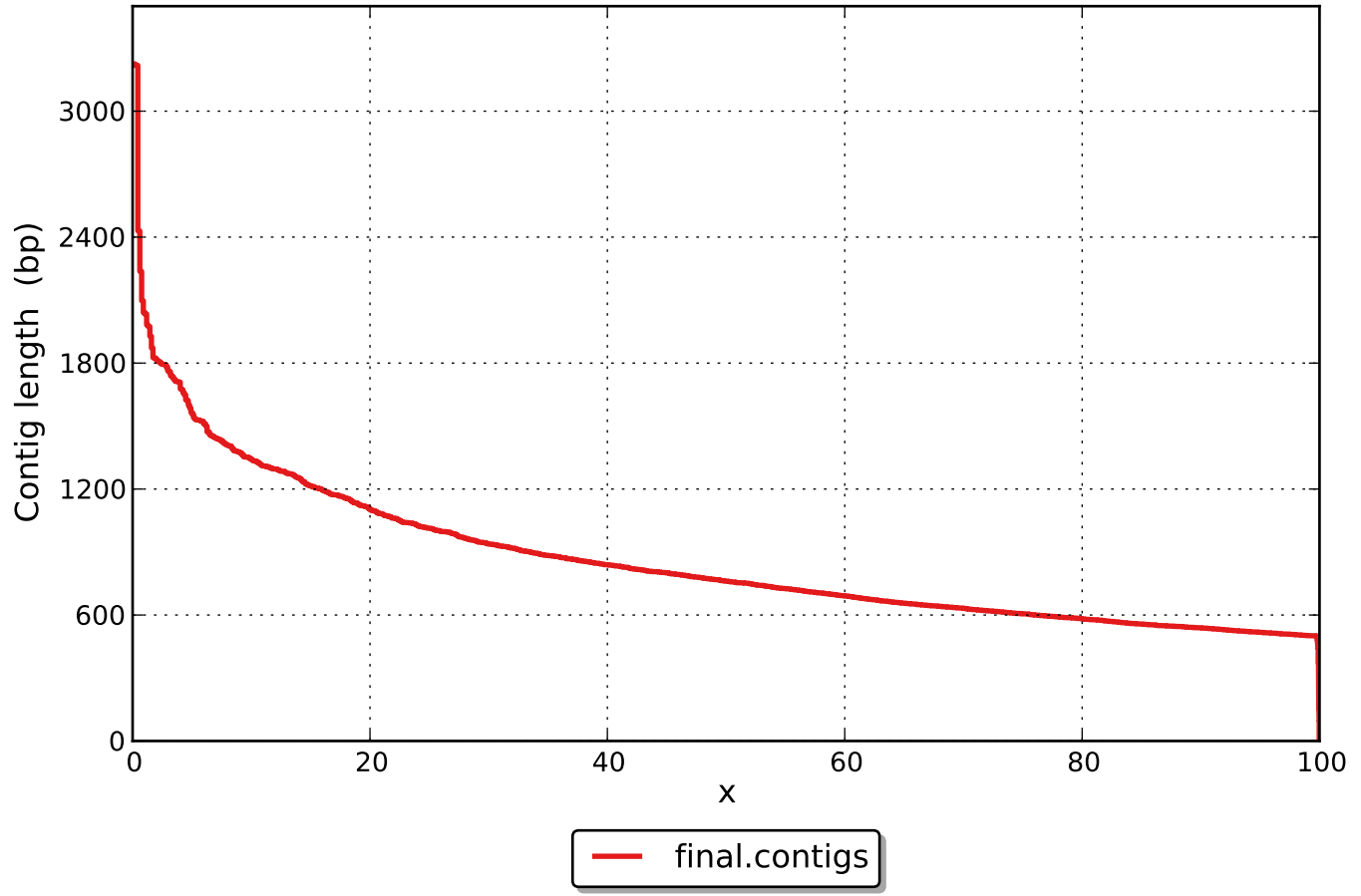


Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx



NGAx

