

Report

	final.contigs
# contigs (≥ 0 bp)	1025
# contigs (≥ 1000 bp)	302
Total length (≥ 0 bp)	945995
Total length (≥ 1000 bp)	432774
# contigs	1025
Largest contig	4169
Total length	945995
Reference length	641799
GC (%)	26.40
Reference GC (%)	26.30
N50	935
NG50	1150
N75	714
NG75	928
L50	344
LG50	199
L75	633
LG75	353
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	14988
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.975
Duplication ratio	1.620
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1169.93
# indels per 100 kbp	1.37
Largest alignment	4169
NA50	929
NGA50	1147
NA75	708
NGA75	924
LA50	347
LGA50	201
LA75	637
LGA75	356

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	12
# relocations	12
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	12
Misassembled contigs length	14988
# local misassemblies	0
# mismatches	6831
# indels	8
# short indels	8
# long indels	0
Indels length	8

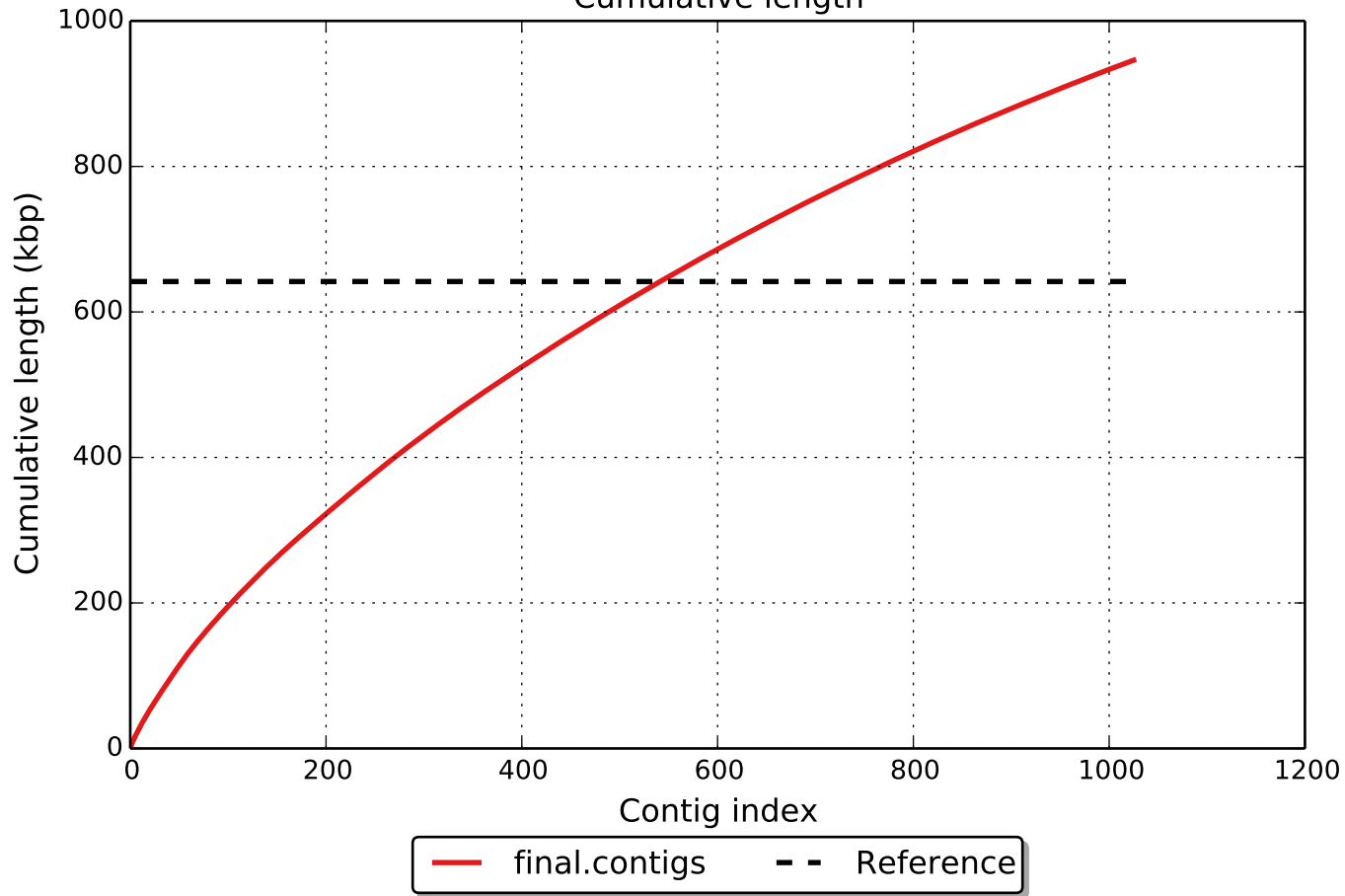
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

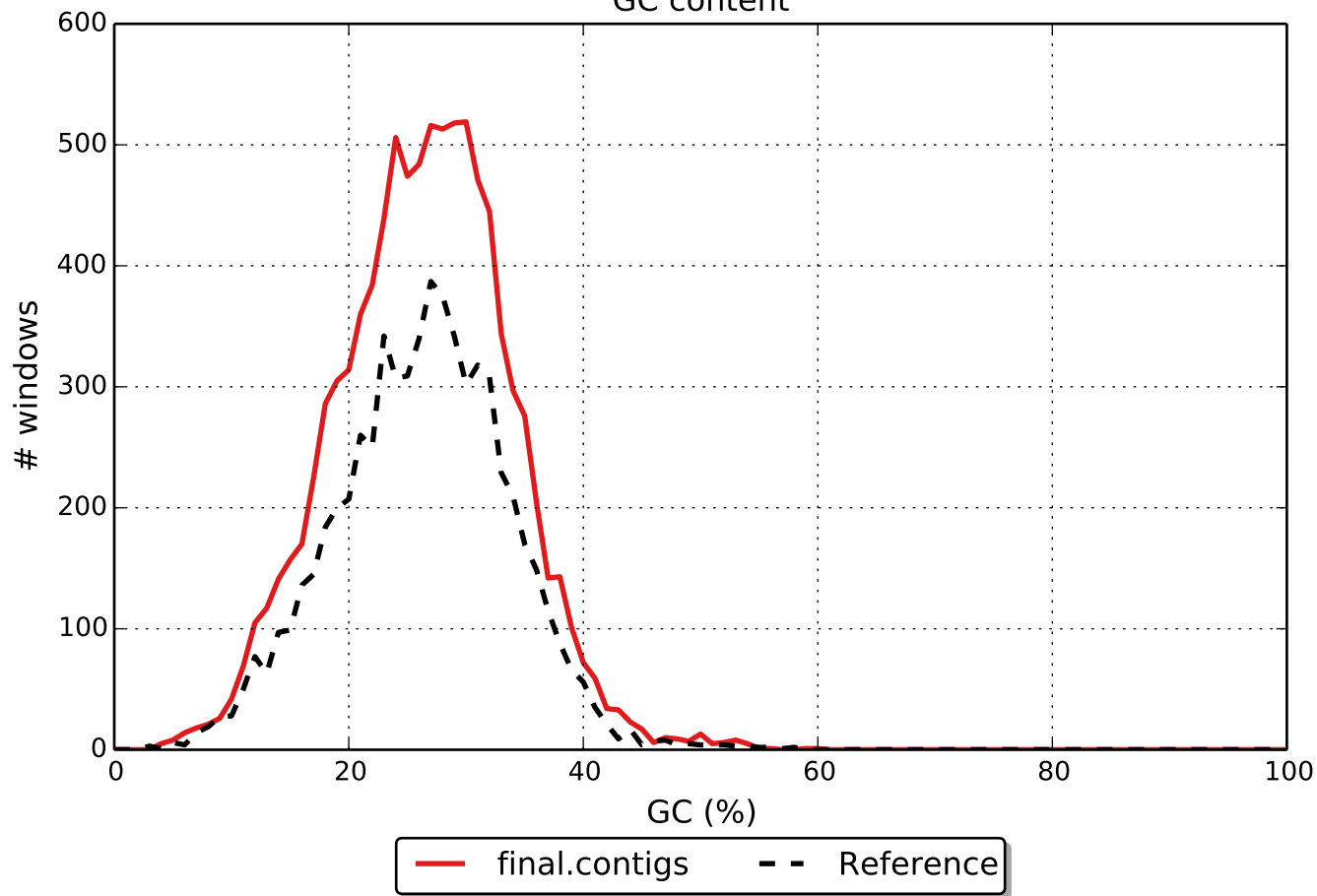
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

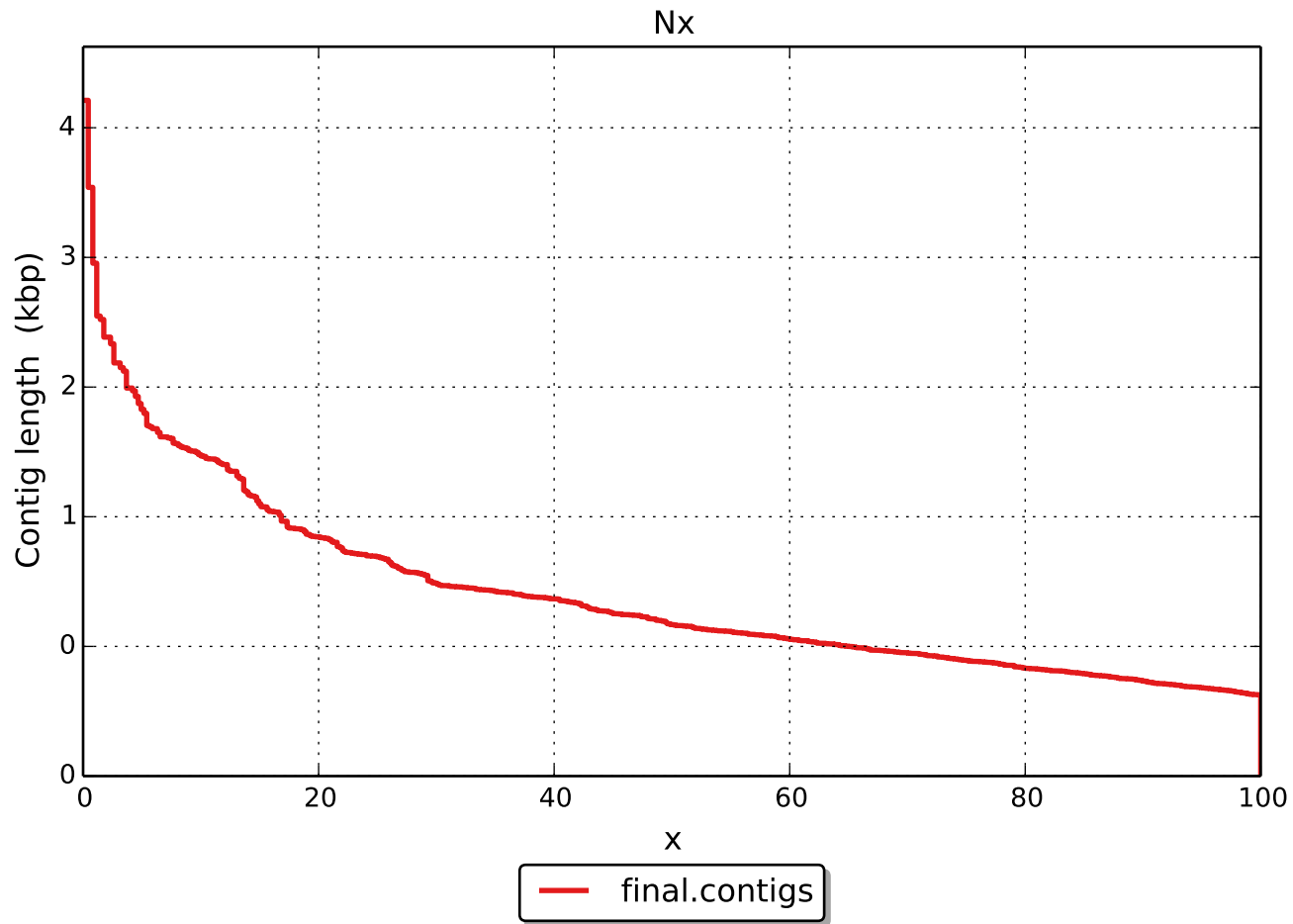
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

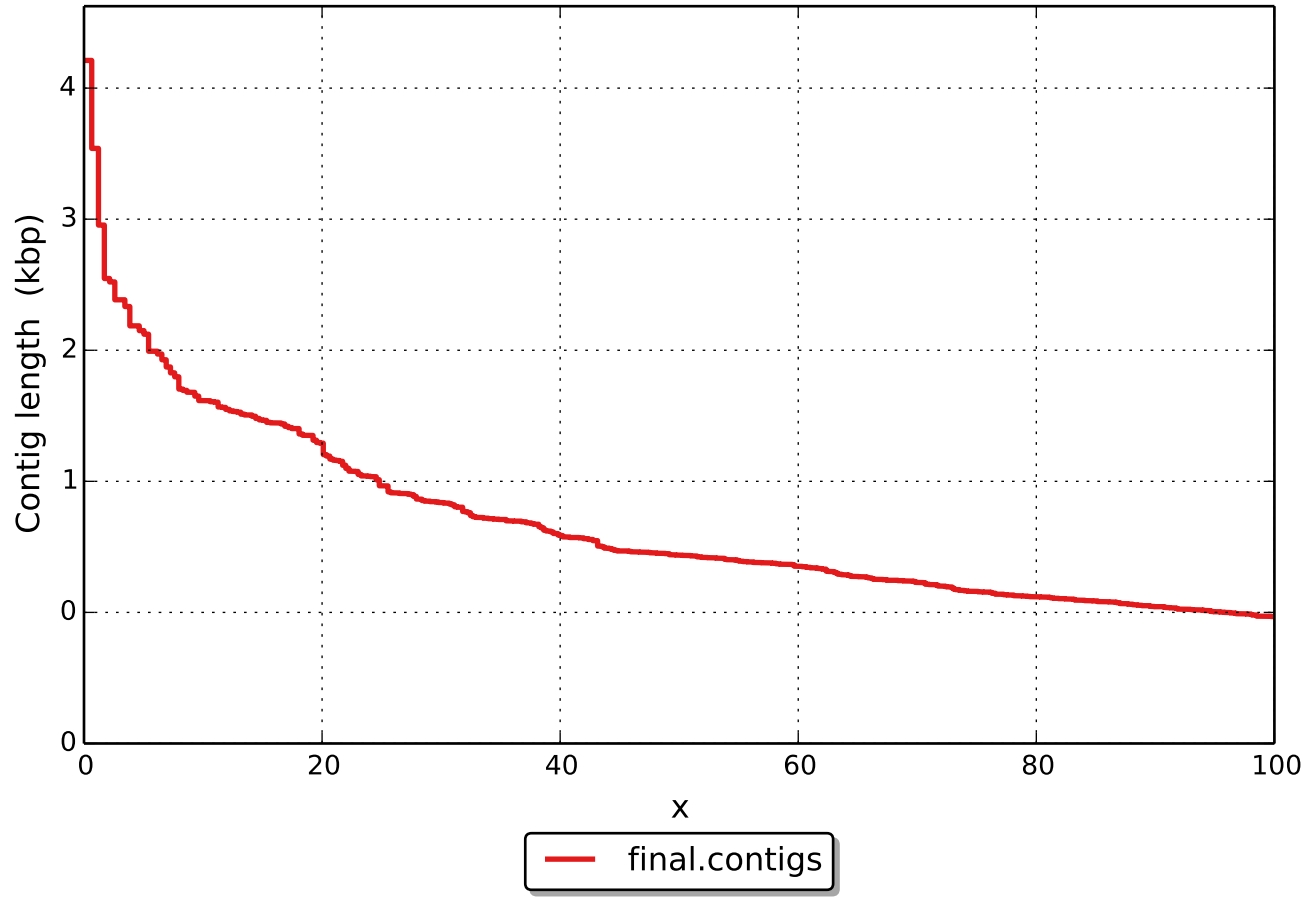


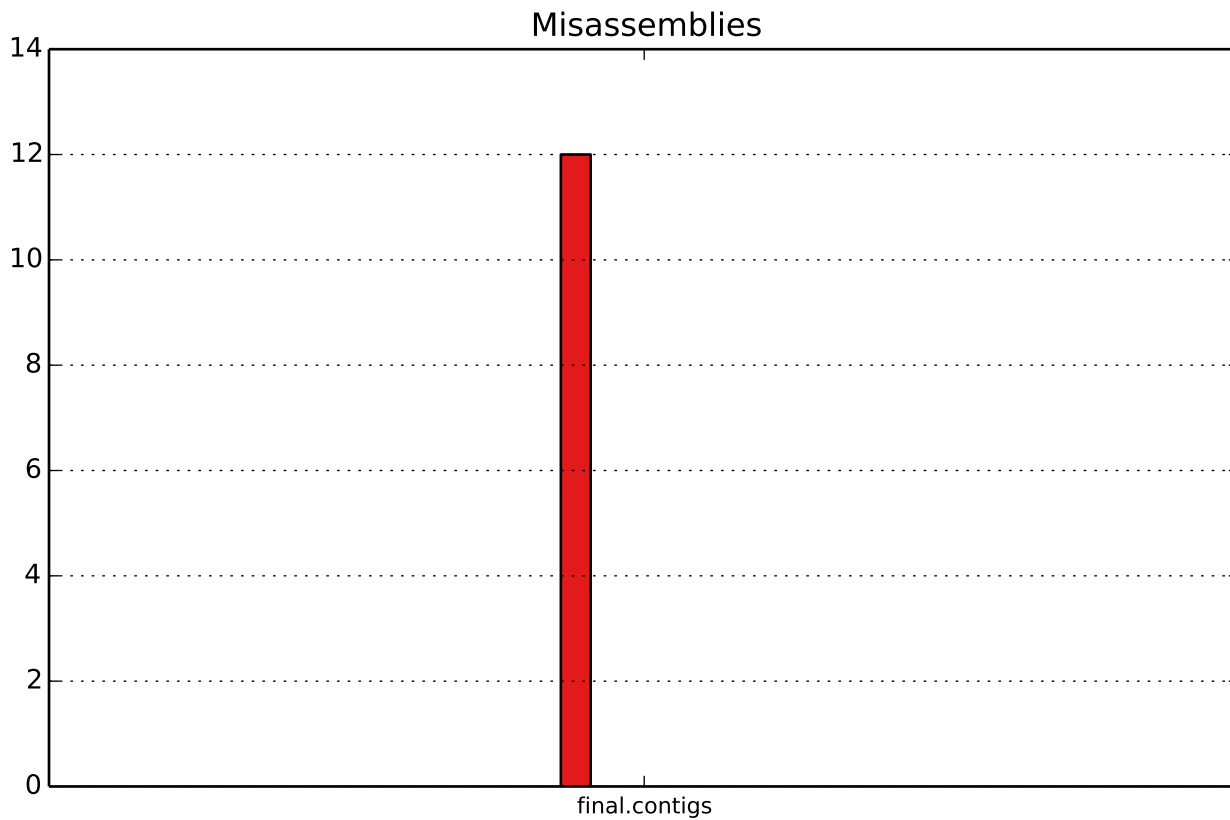
GC content



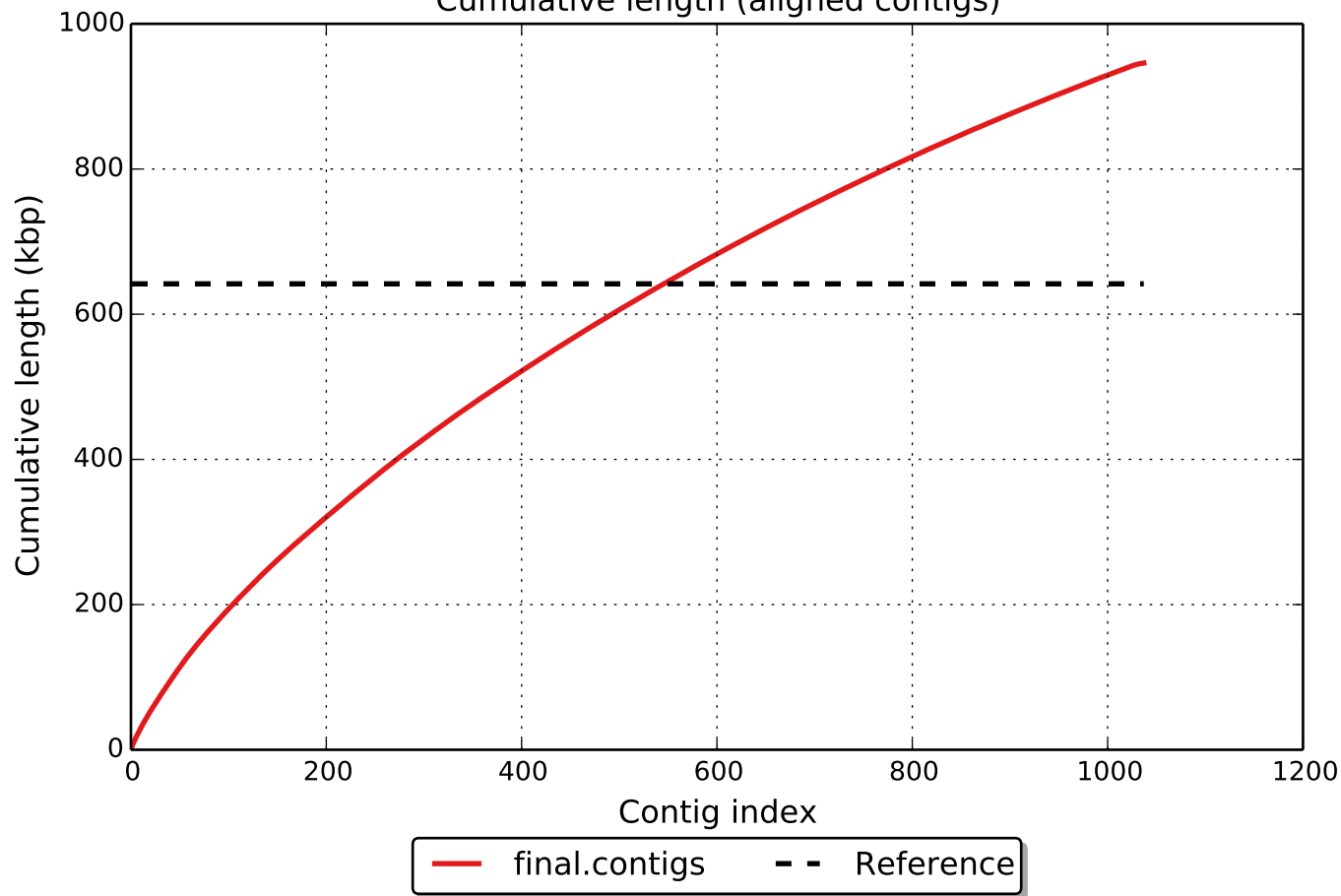


NGx

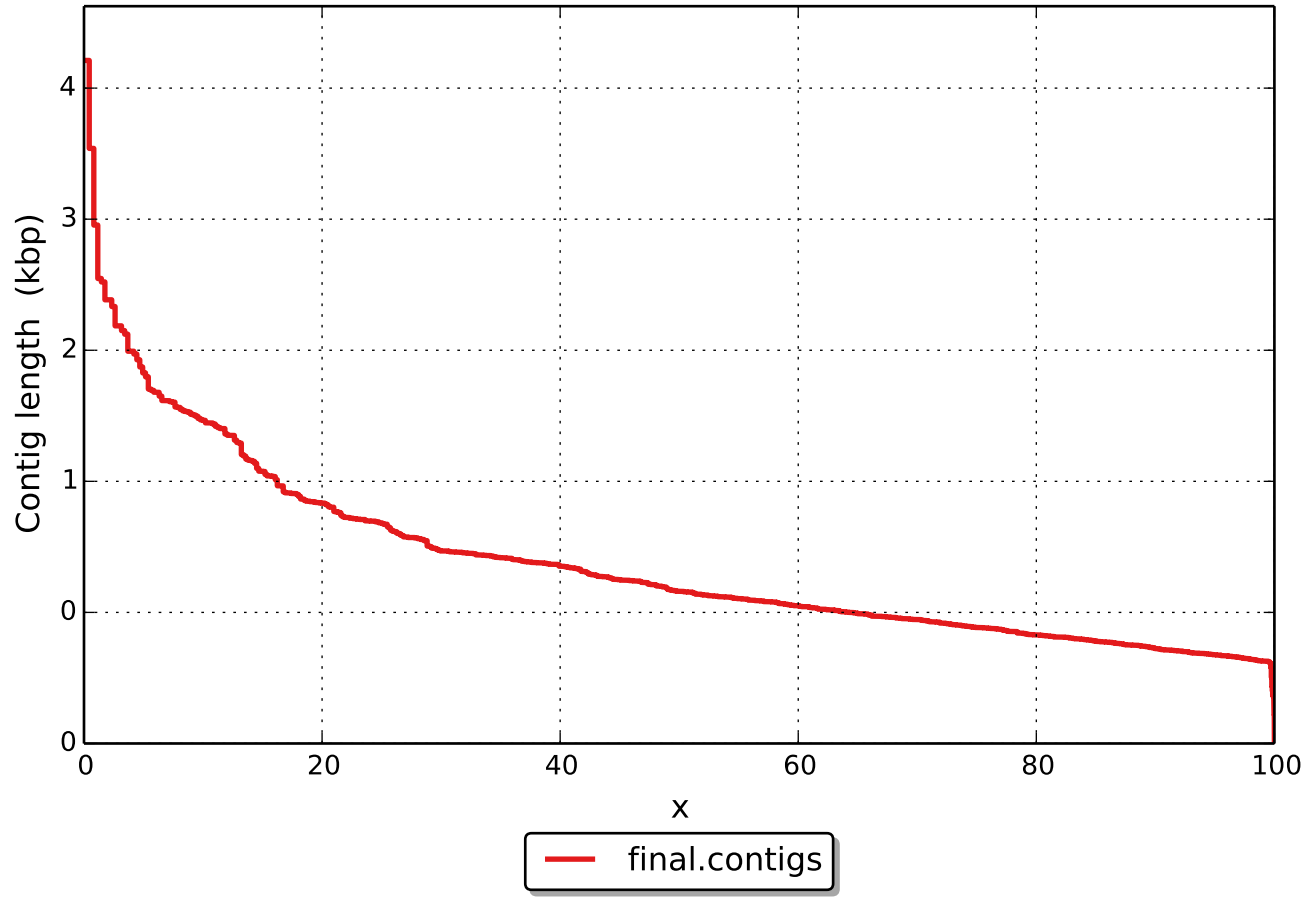




Cumulative length (aligned contigs)



NAx



NGAx

