

Report

	final.contigs
# contigs (>= 0 bp)	973
# contigs (>= 1000 bp)	457
Total length (>= 0 bp)	1166229
Total length (>= 1000 bp)	792152
# contigs	973
Largest contig	8192
Total length	1166229
Reference length	615980
GC (%)	25.44
Reference GC (%)	25.35
N50	1355
NG50	2022
N75	878
NG75	1658
L50	276
LG50	112
L75	545
LG75	196
# misassemblies	27
# misassembled contigs	27
Misassembled contigs length	48365
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	920
Genome fraction (%)	92.952
Duplication ratio	2.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1562.09
# indels per 100 kbp	0.87
Largest alignment	8192
NA50	1285
NGA50	1966
NA75	852
NGA75	1599
LA50	285
LGA50	115
LA75	564
LGA75	201

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

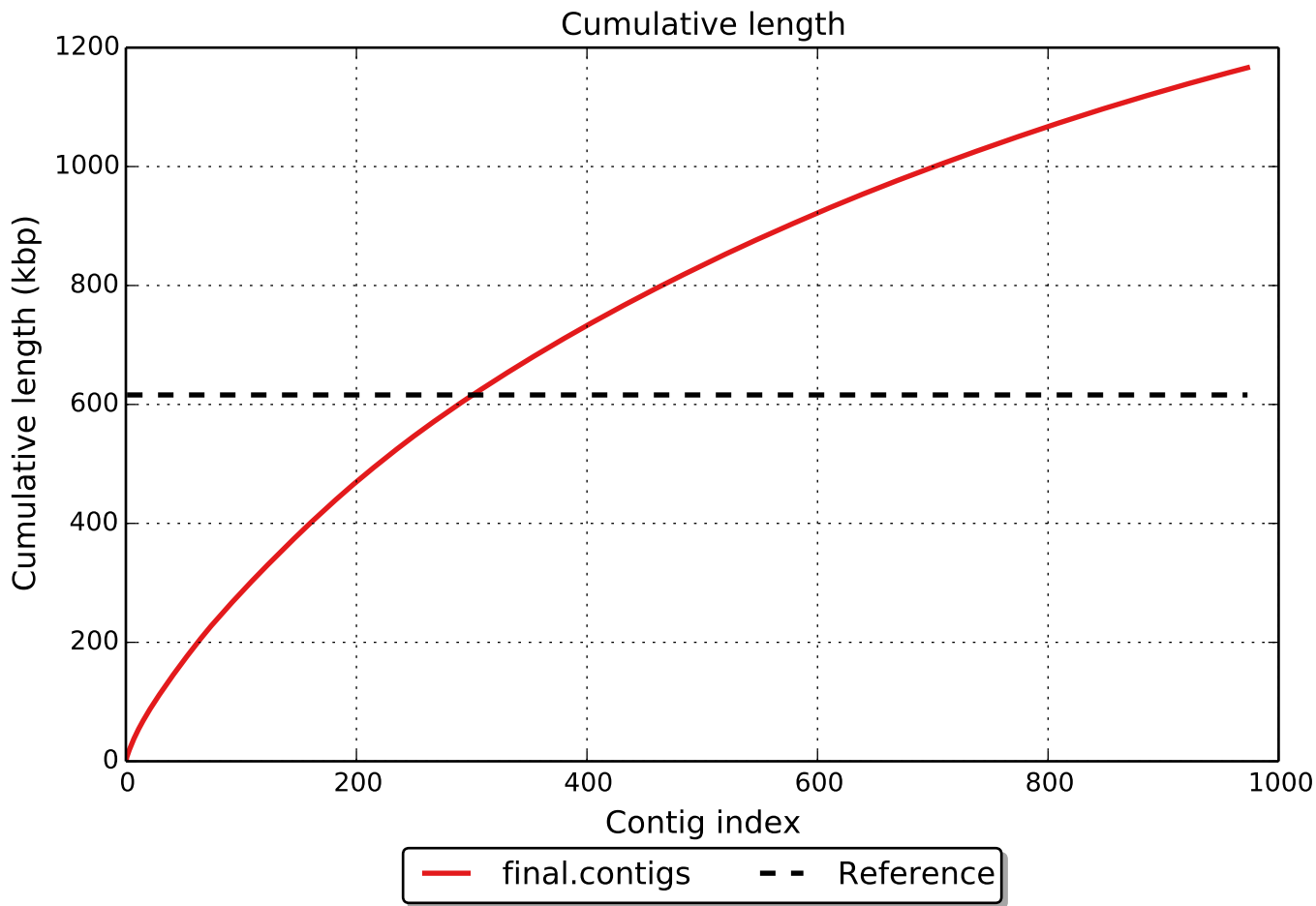
	final.contigs
# misassemblies	27
# relocations	27
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	27
Misassembled contigs length	48365
# local misassemblies	0
# mismatches	8944
# indels	5
# short indels	5
# long indels	0
Indels length	5

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).

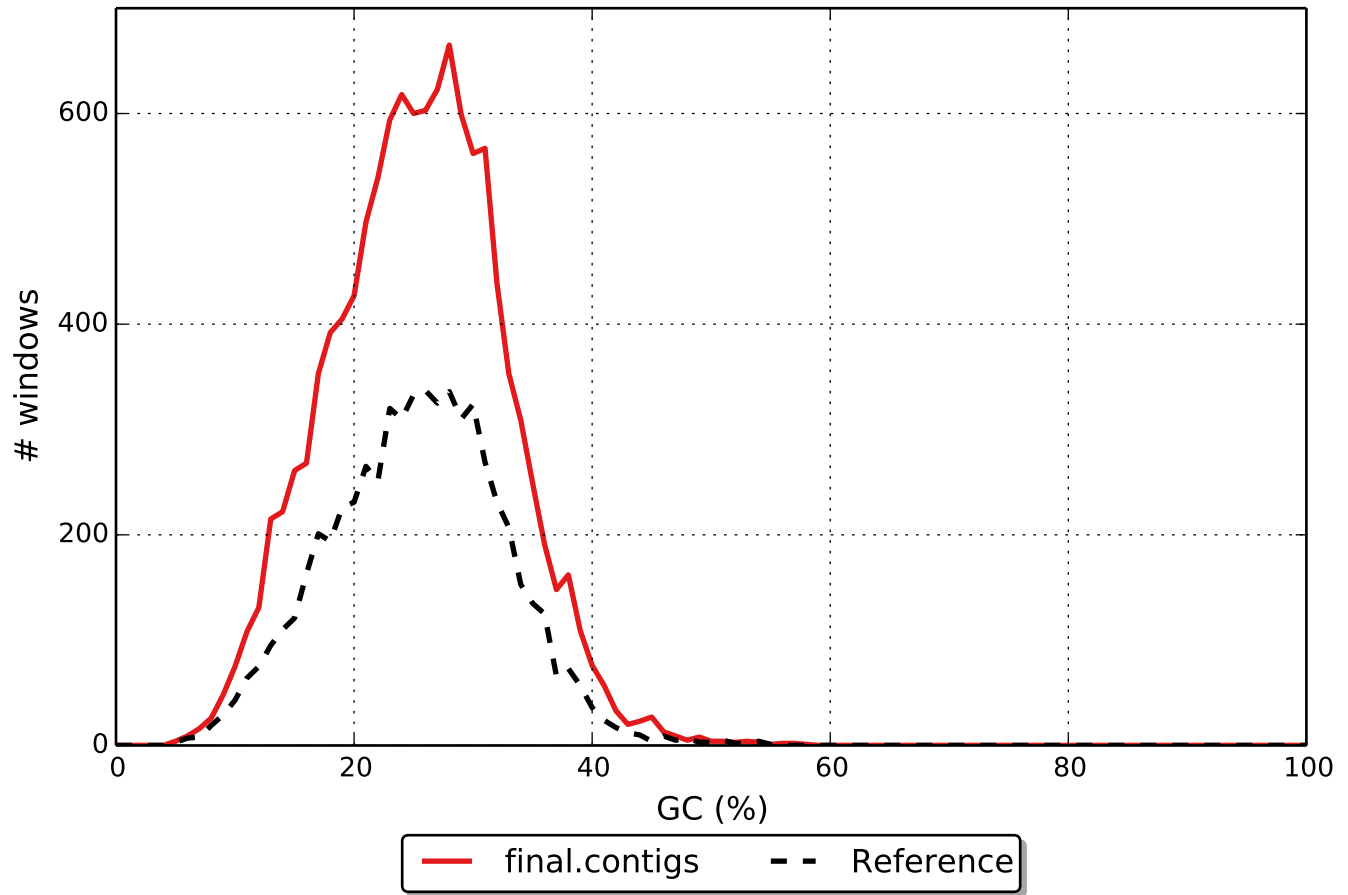
Unaligned report

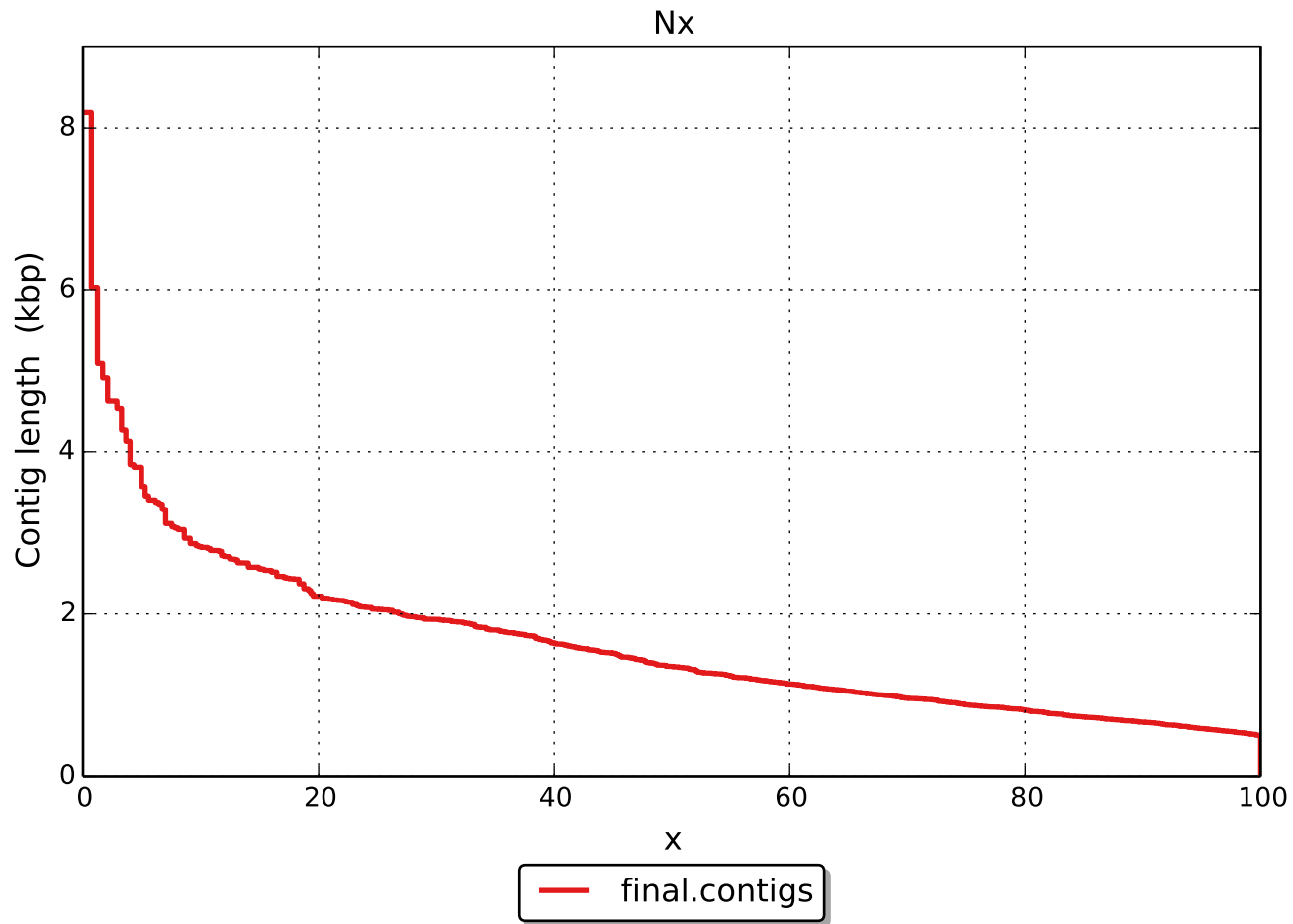
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	920
# N's	0

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).

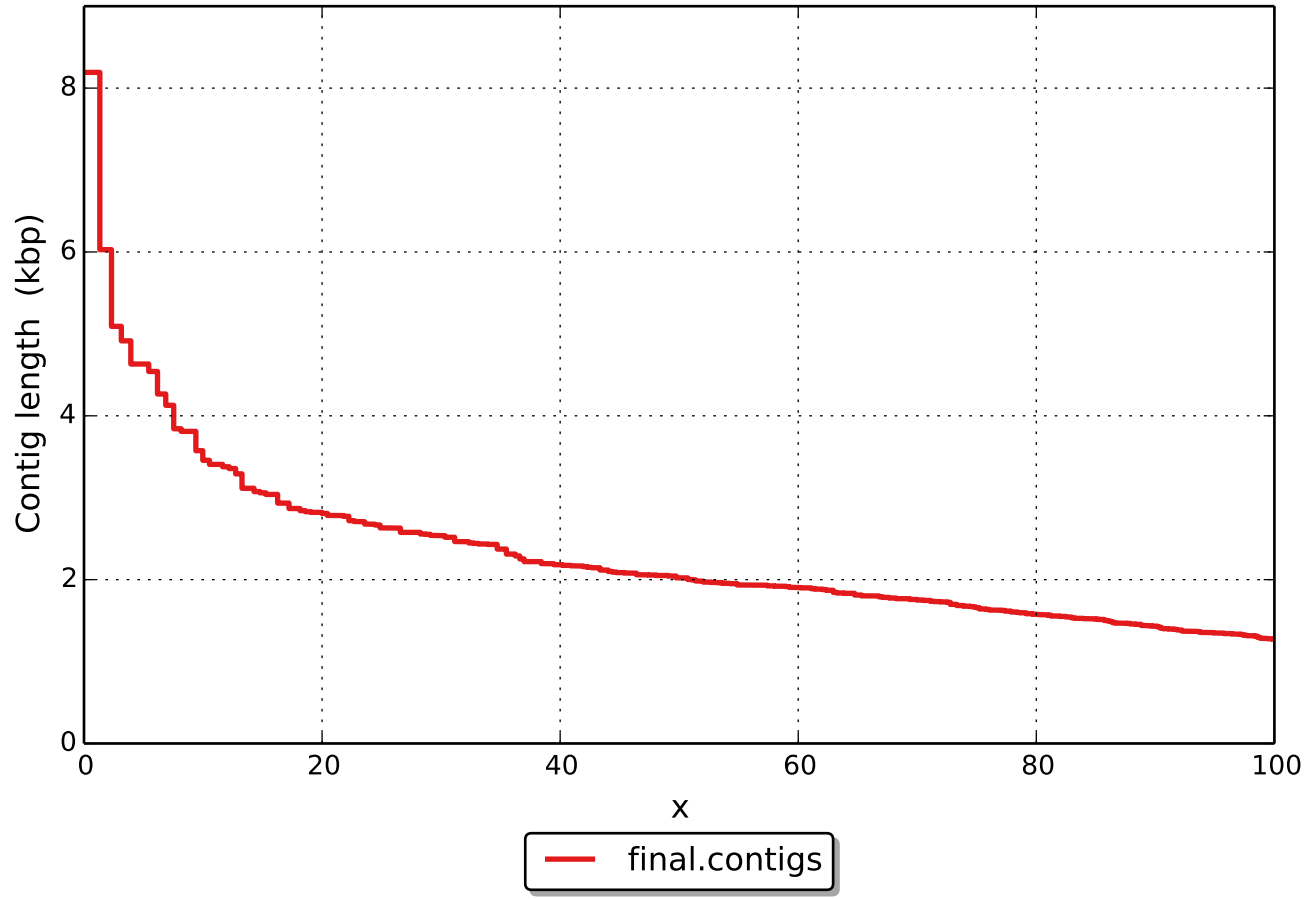


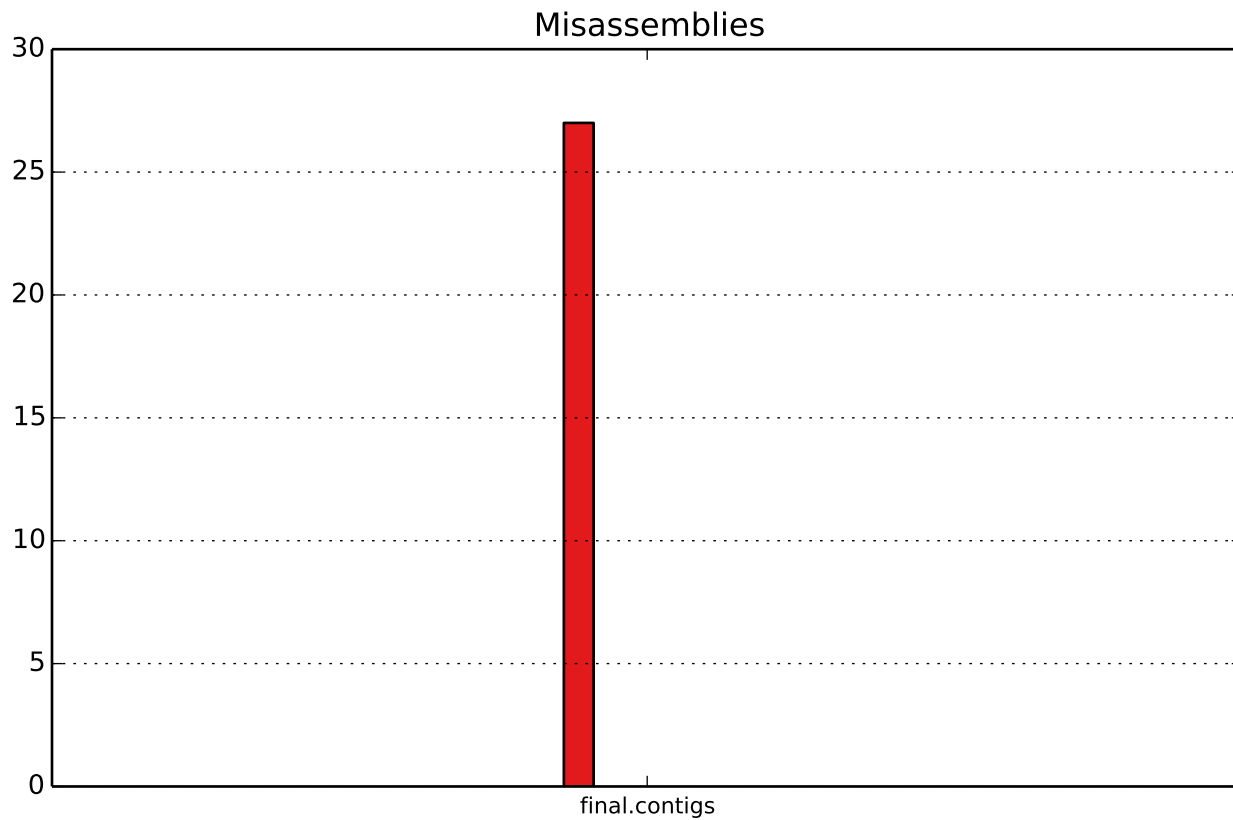
GC content



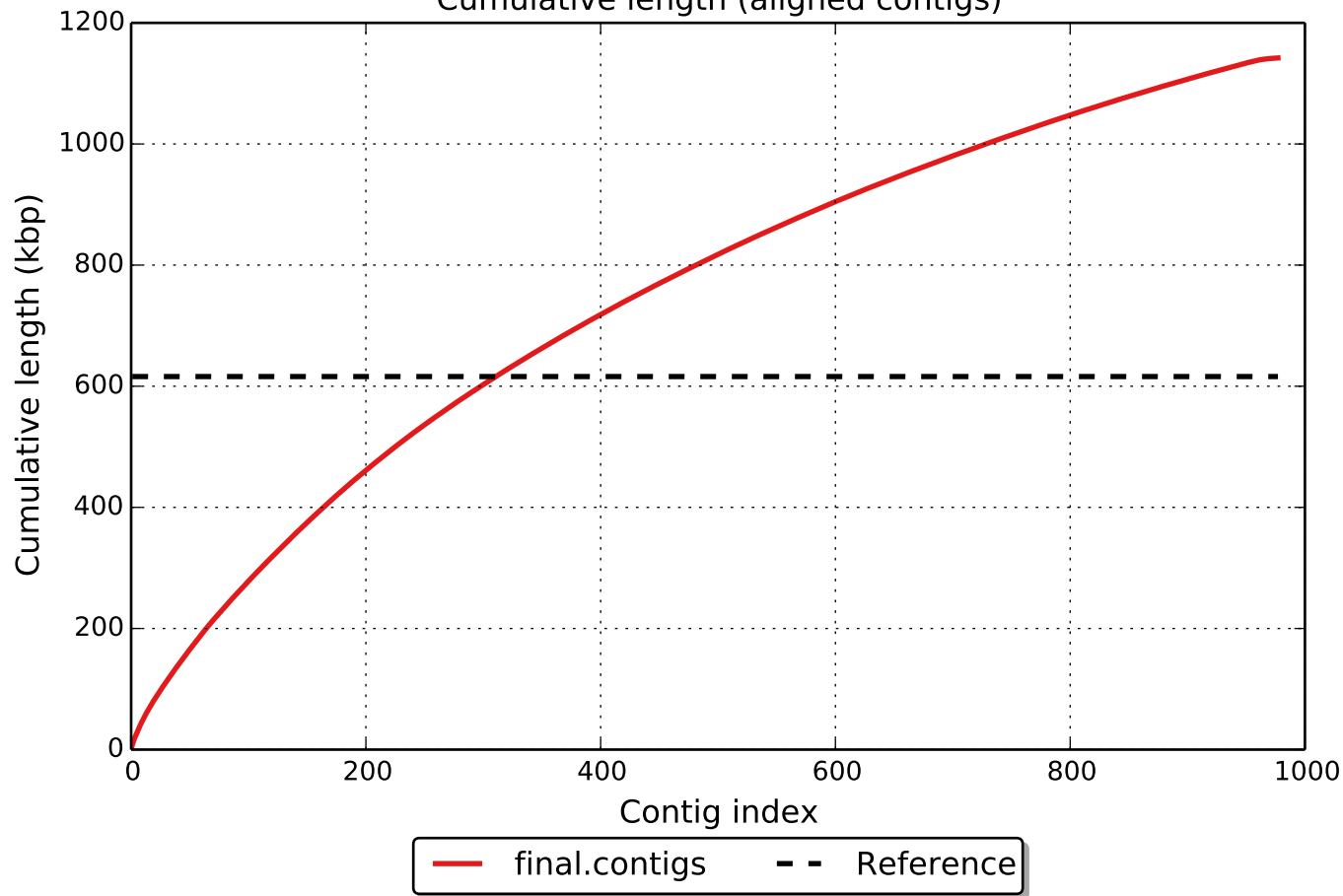


NGx

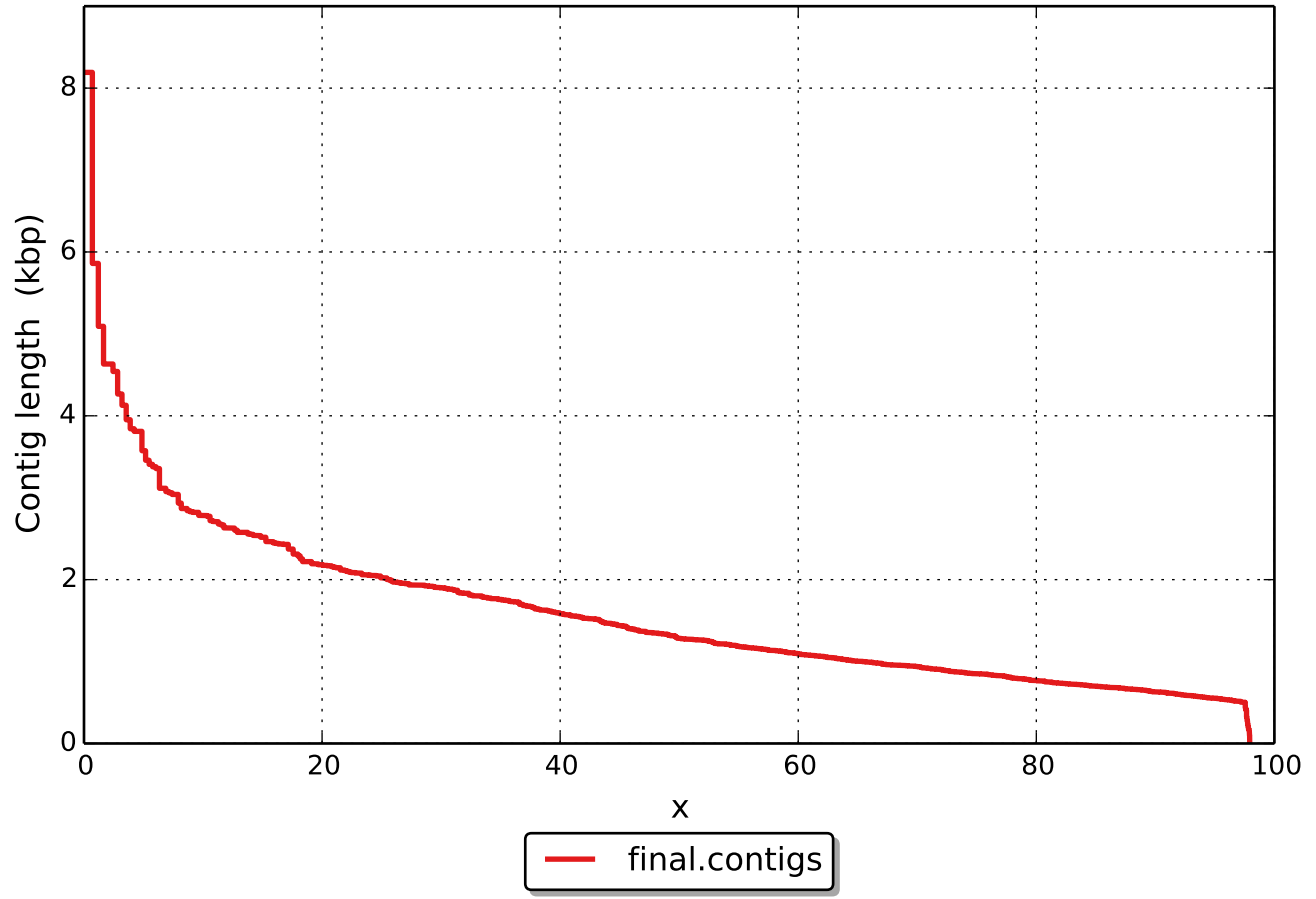




Cumulative length (aligned contigs)



NAx



NGAx

