

## Report

	final.contigs
# contigs (>= 1000 bp)	1865
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3548413
Total length (>= 5000 bp)	113410
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3301
Largest contig	6813
Total length	4584558
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1664
NG50	1647
N75	1050
NG75	1032
L50	884
LG50	901
L75	1758
LG75	1799
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	9298
# local misassemblies	5
# unaligned contigs	0 + 16 part
Unaligned length	729
Genome fraction (%)	92.589
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	503.90
# indels per 100 kbp	9.89
Largest alignment	6813
NA50	1659
NGA50	1645
NA75	1048
NGA75	1027
LA50	884
LGA50	902
LA75	1761
LGA75	1803

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

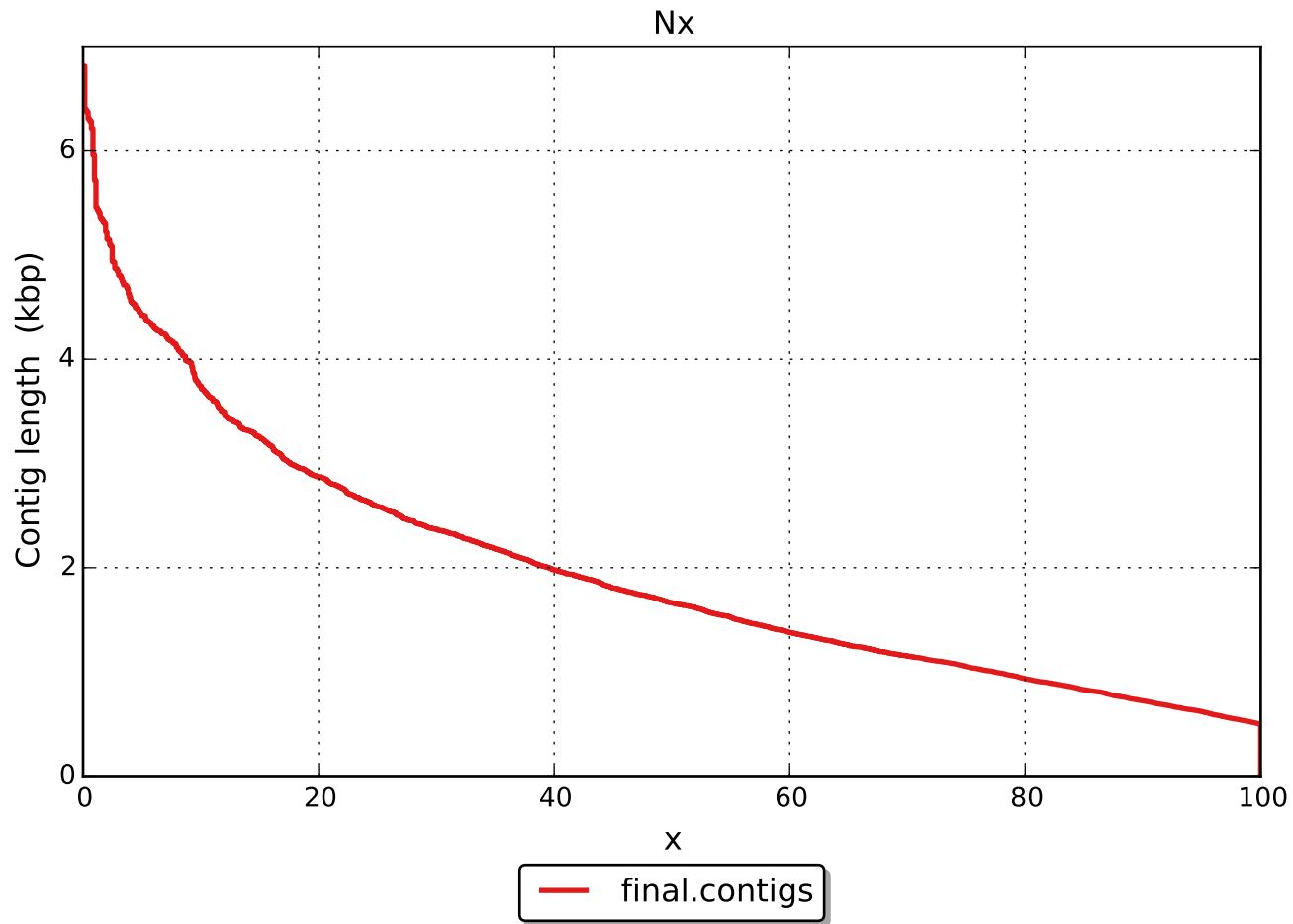
	final.contigs
# misassemblies	6
# relocations	5
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	6
Misassembled contigs length	9298
# local misassemblies	5
# mismatches	21656
# indels	425
# short indels	423
# long indels	2
Indels length	640

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).

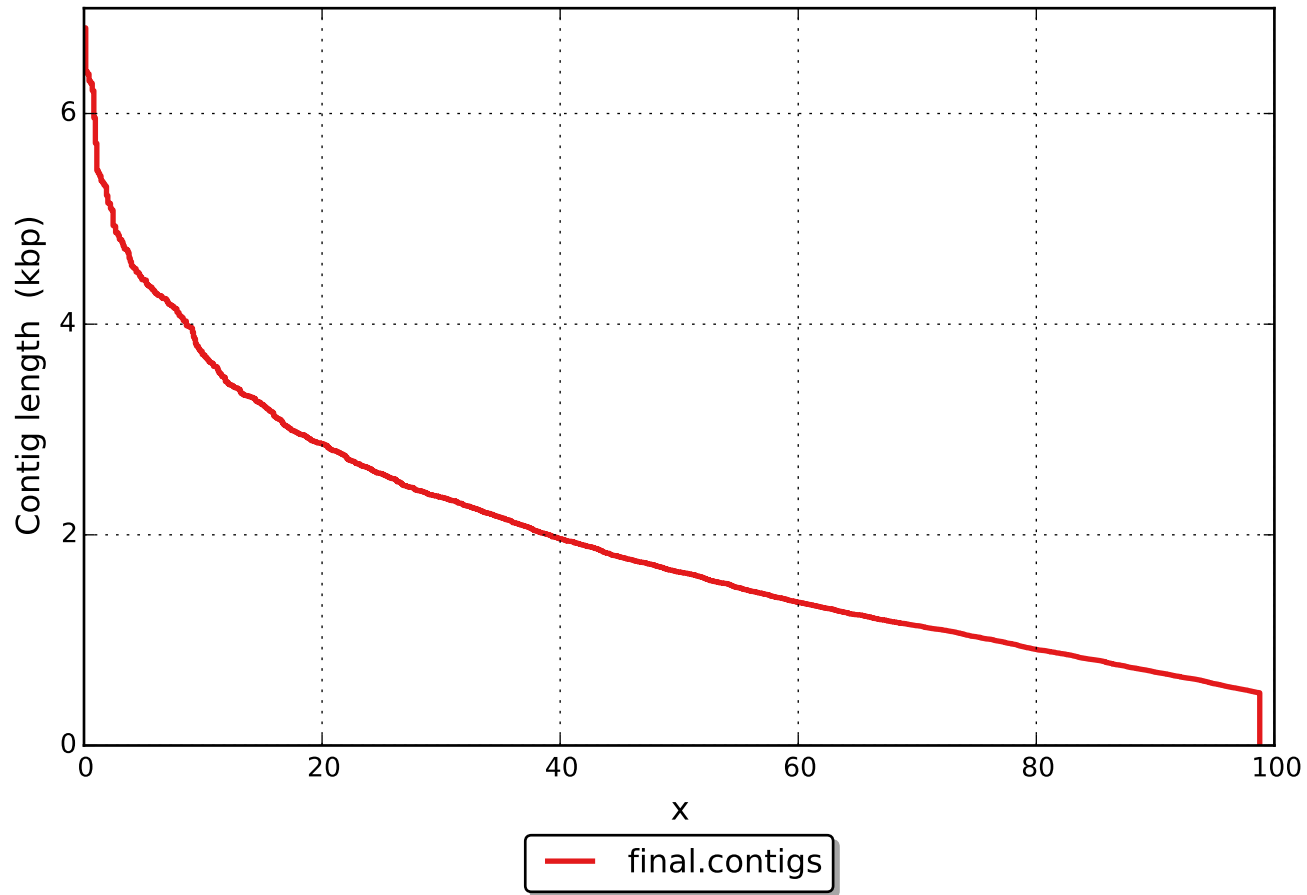
## Unaligned report

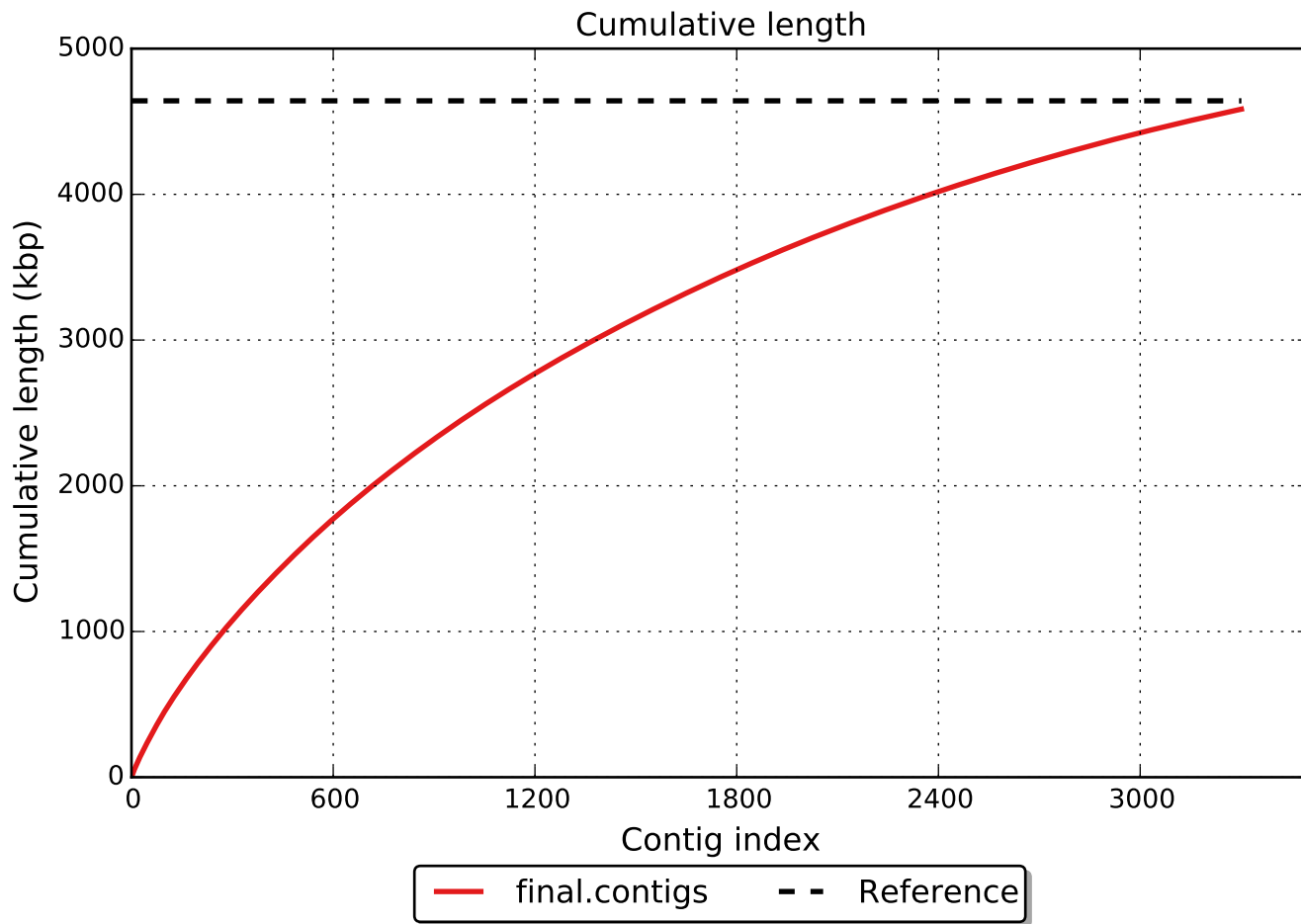
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
# with misassembly	0
# both parts are significant	0
Partially unaligned length	729
# N's	0

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).

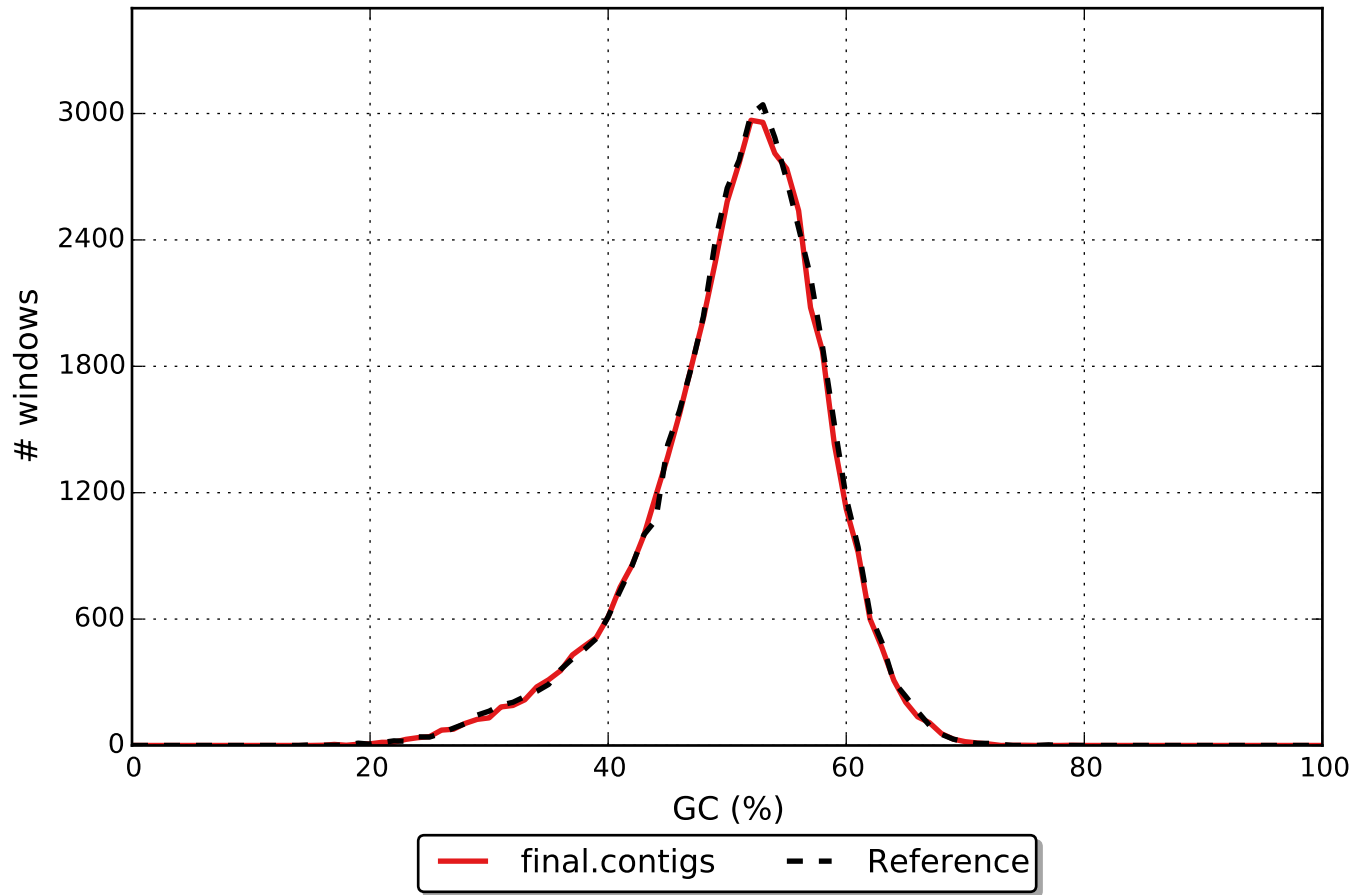


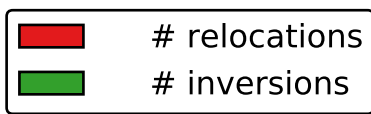
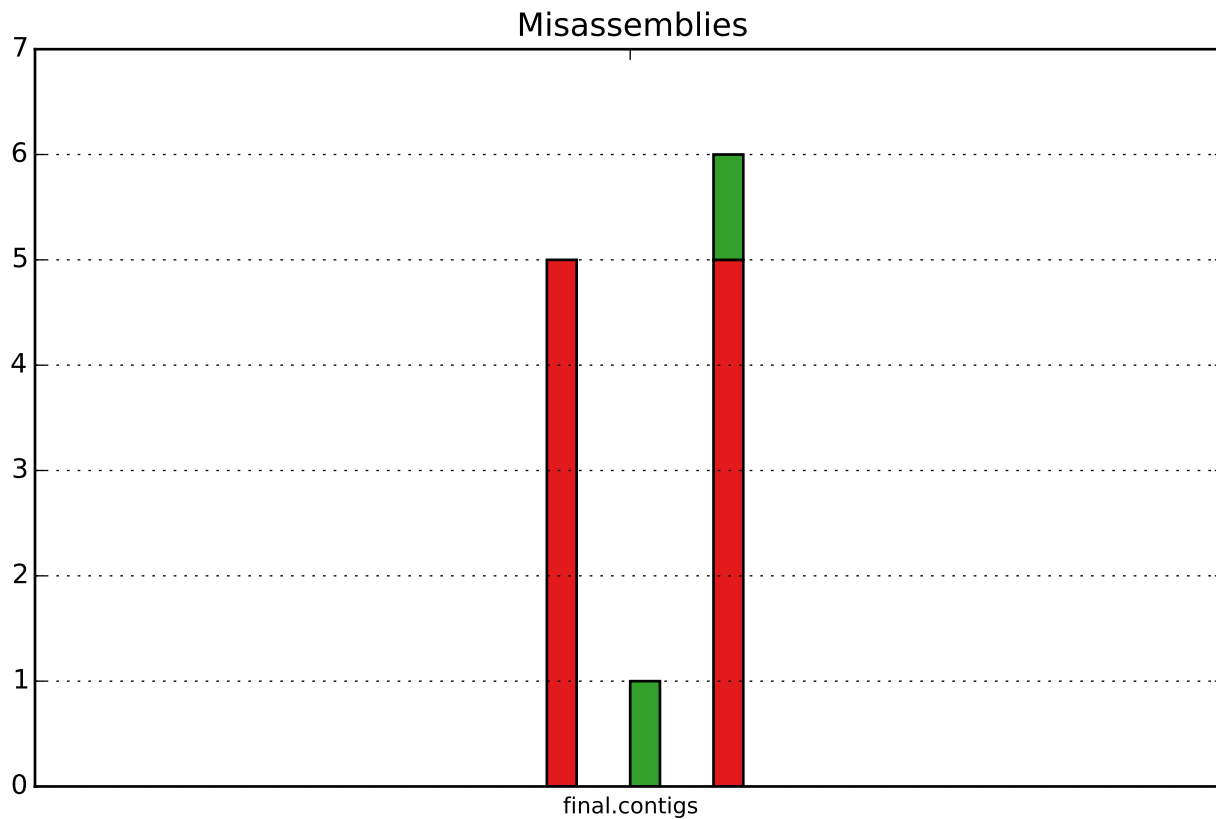
NGx





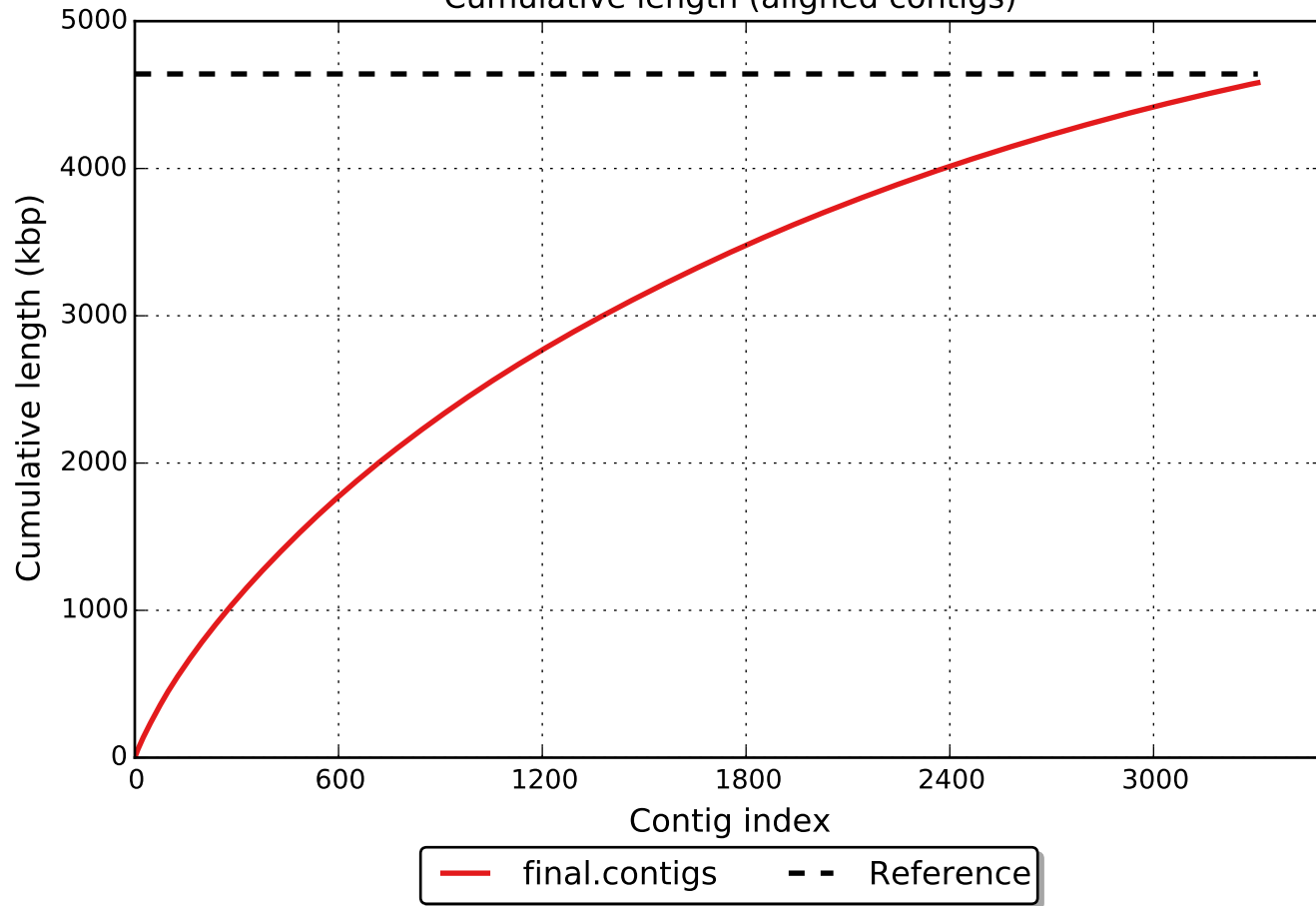
GC content



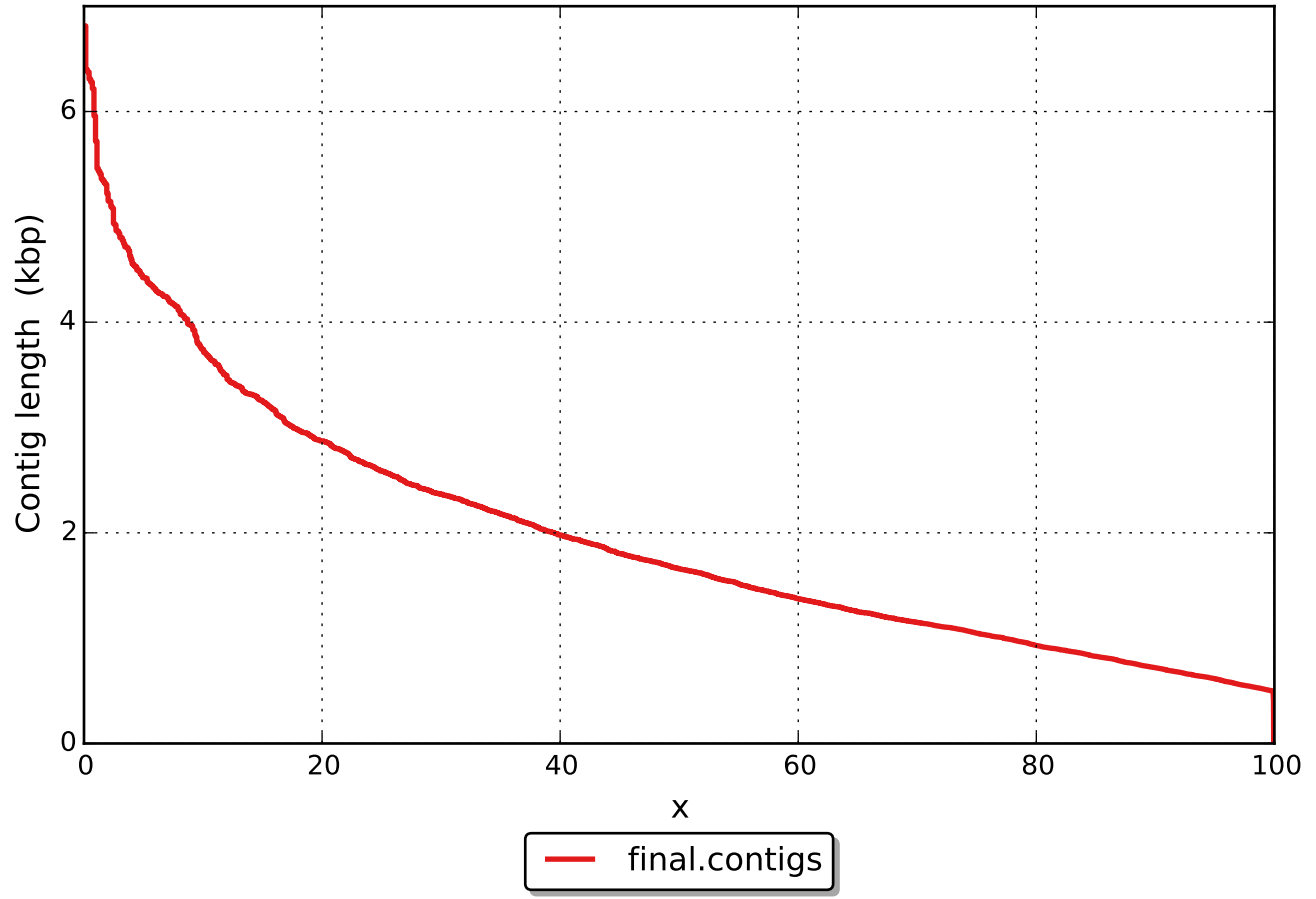




Cumulative length (aligned contigs)



NAx



NGAx

