

Report

	final.contigs
# contigs (>= 1000 bp)	1817
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3051310
Total length (>= 5000 bp)	21511
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3816
Largest contig	5692
Total length	4494320
Reference length	4857432
GC (℥)	52.22
Reference GC (℥)	52.22
N50	1322
NG50	1238
N75	883
NG75	796
L50	1115
LG50	1257
L75	2158
LG75	2482
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	88.758
Duplication ratio	1.042
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.96
# indels per 100 kbp	0.05
Largest alignment	5692
NA50	1322
NGA50	1238
NA75	882
NGA75	796
LA50	1115
LGA50	1257
LA75	2158
LGA75	2482

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

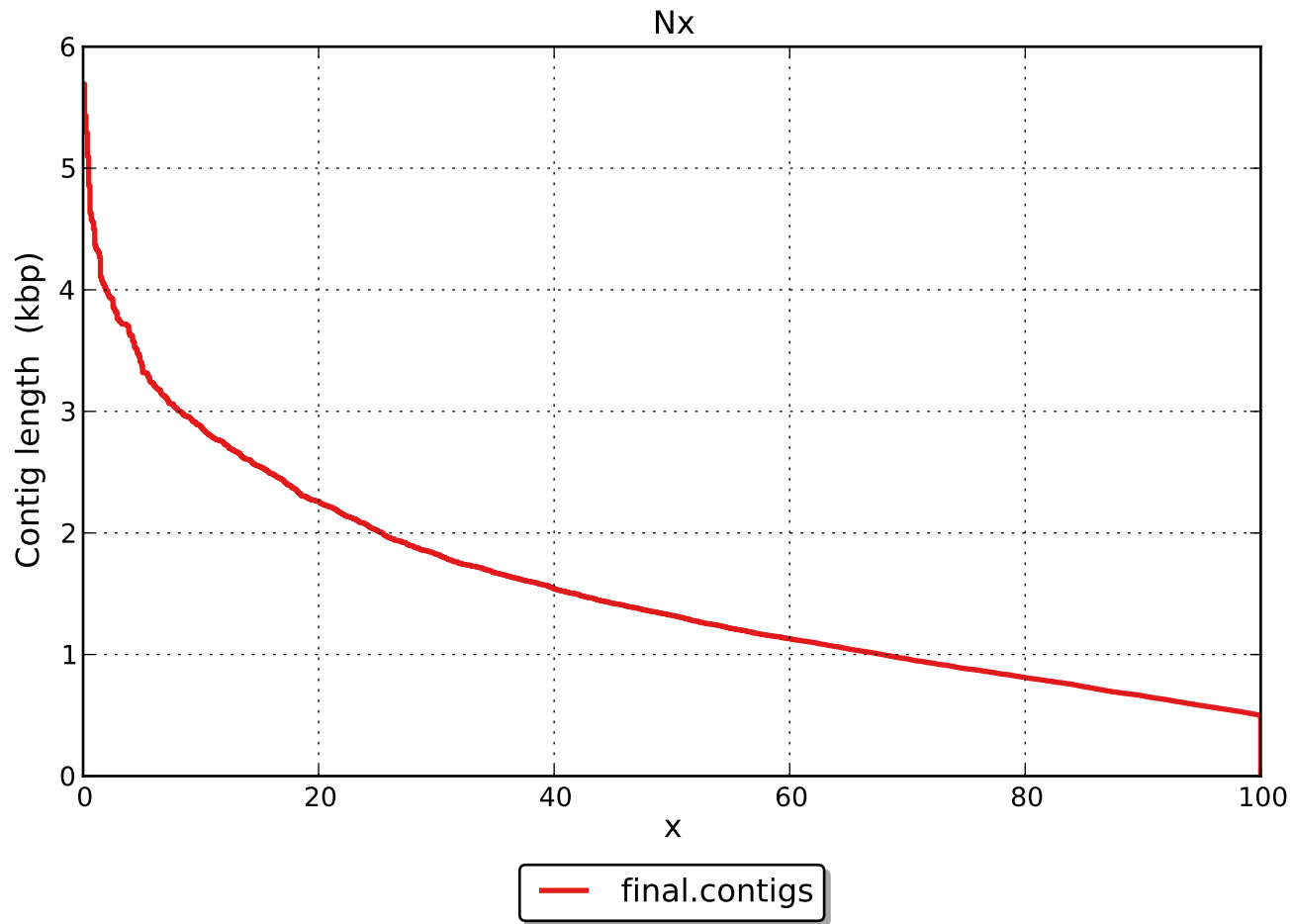
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	990
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

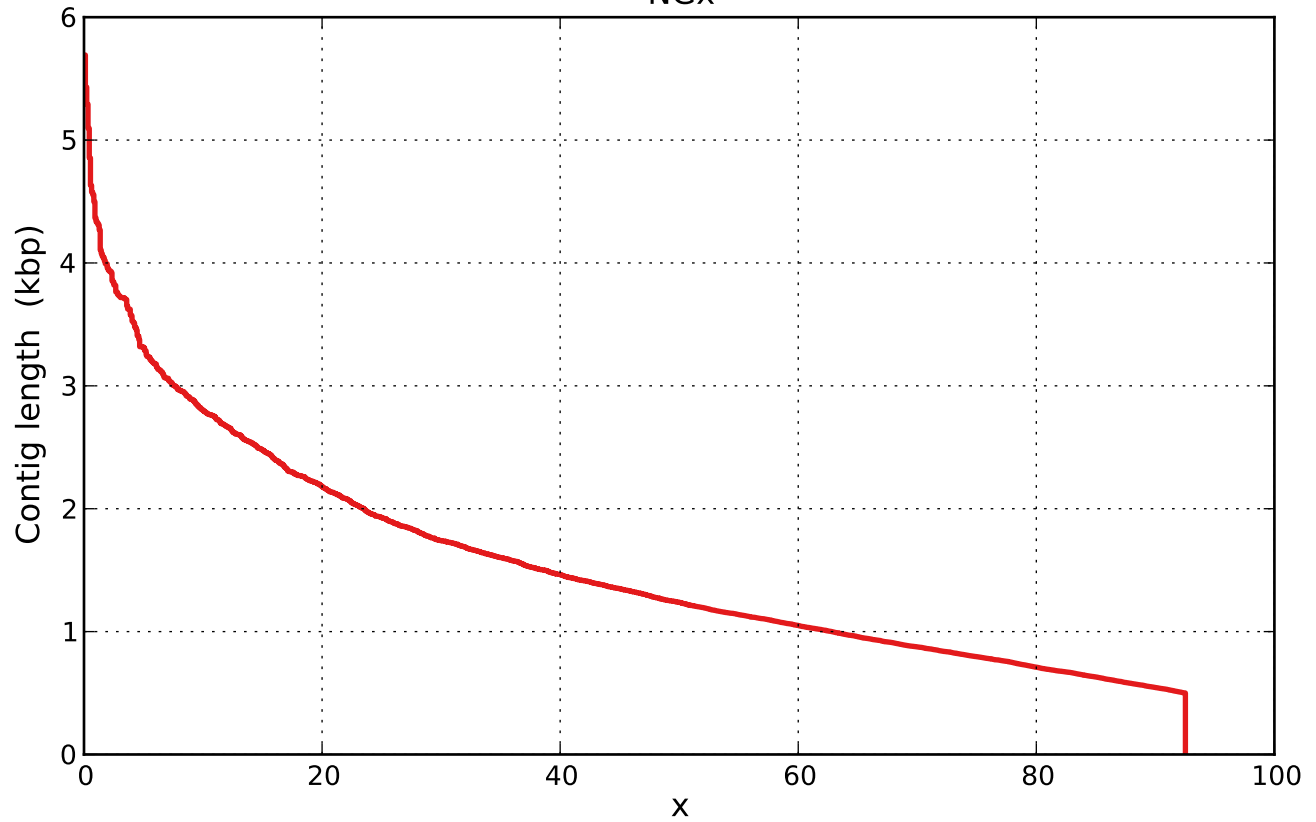
## Unaligned report

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

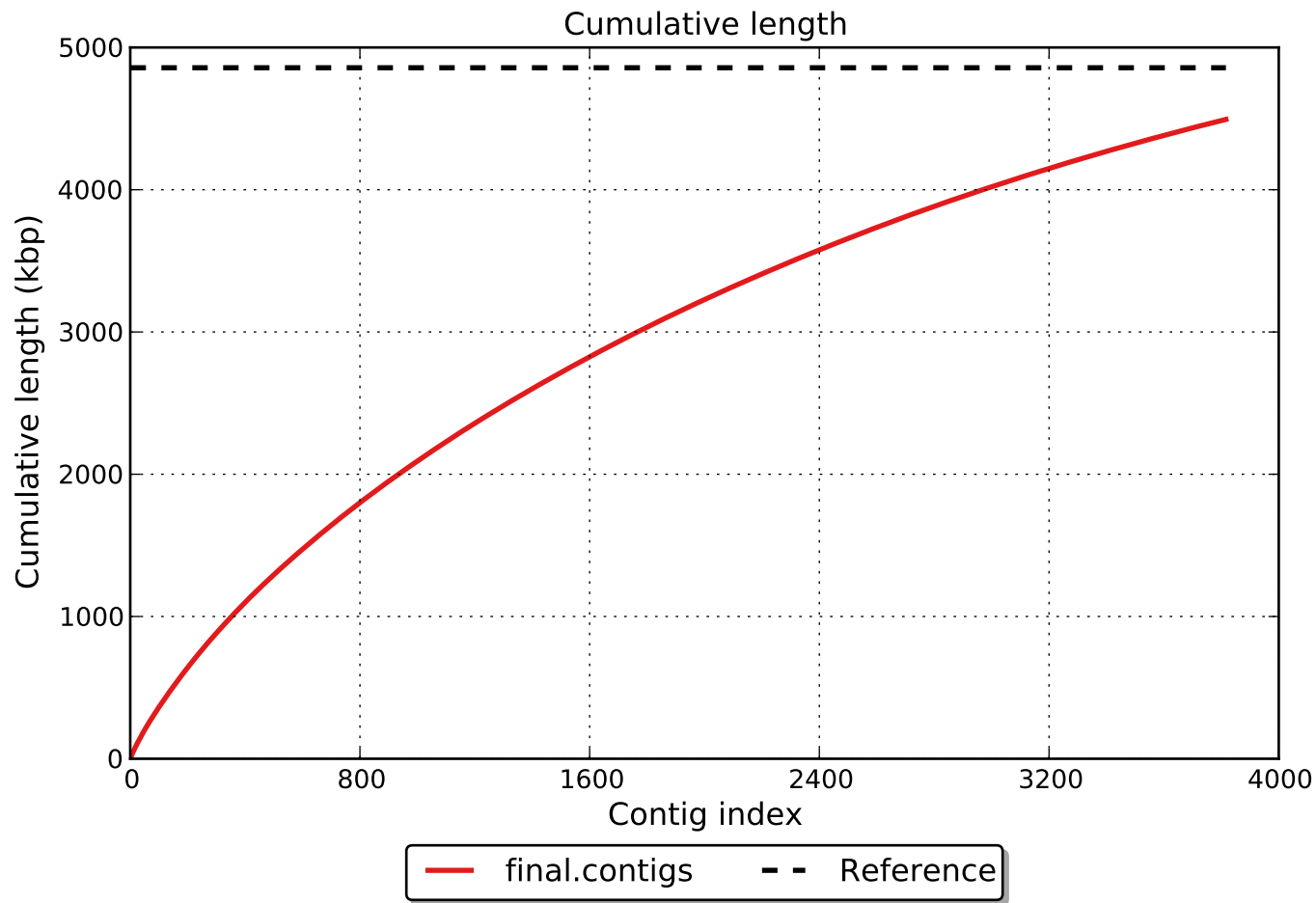
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



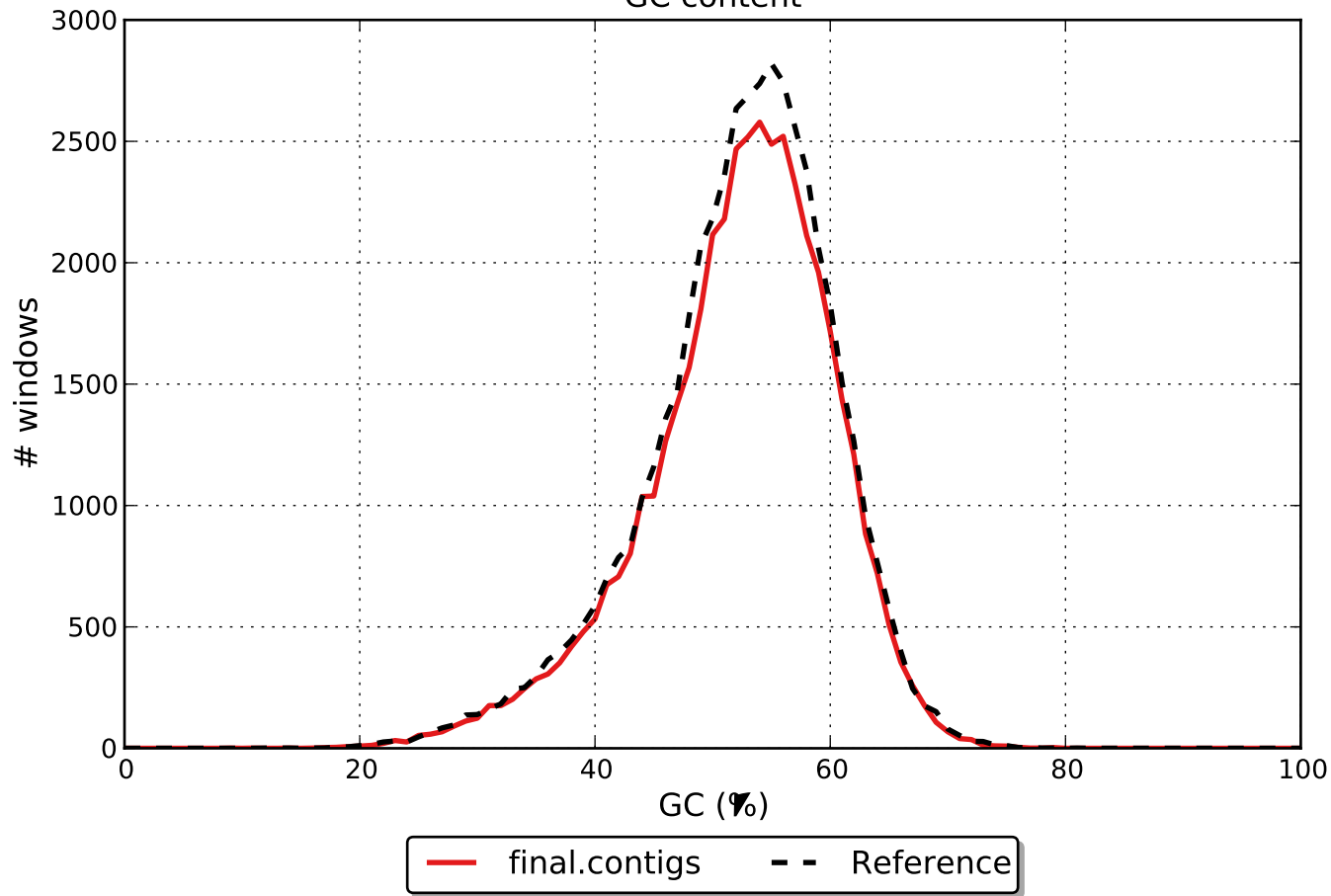
NGx



— final.contigs



GC content

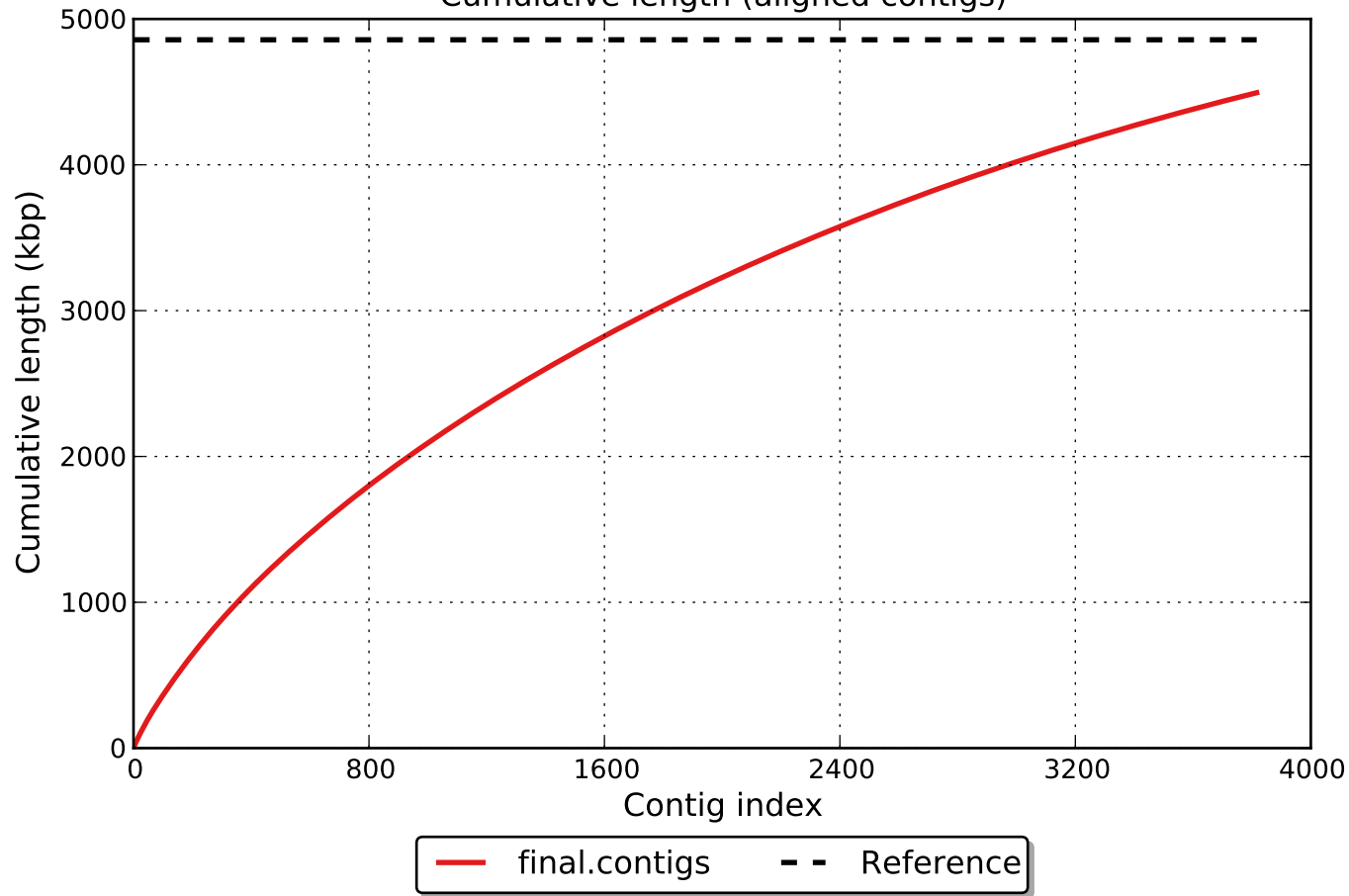


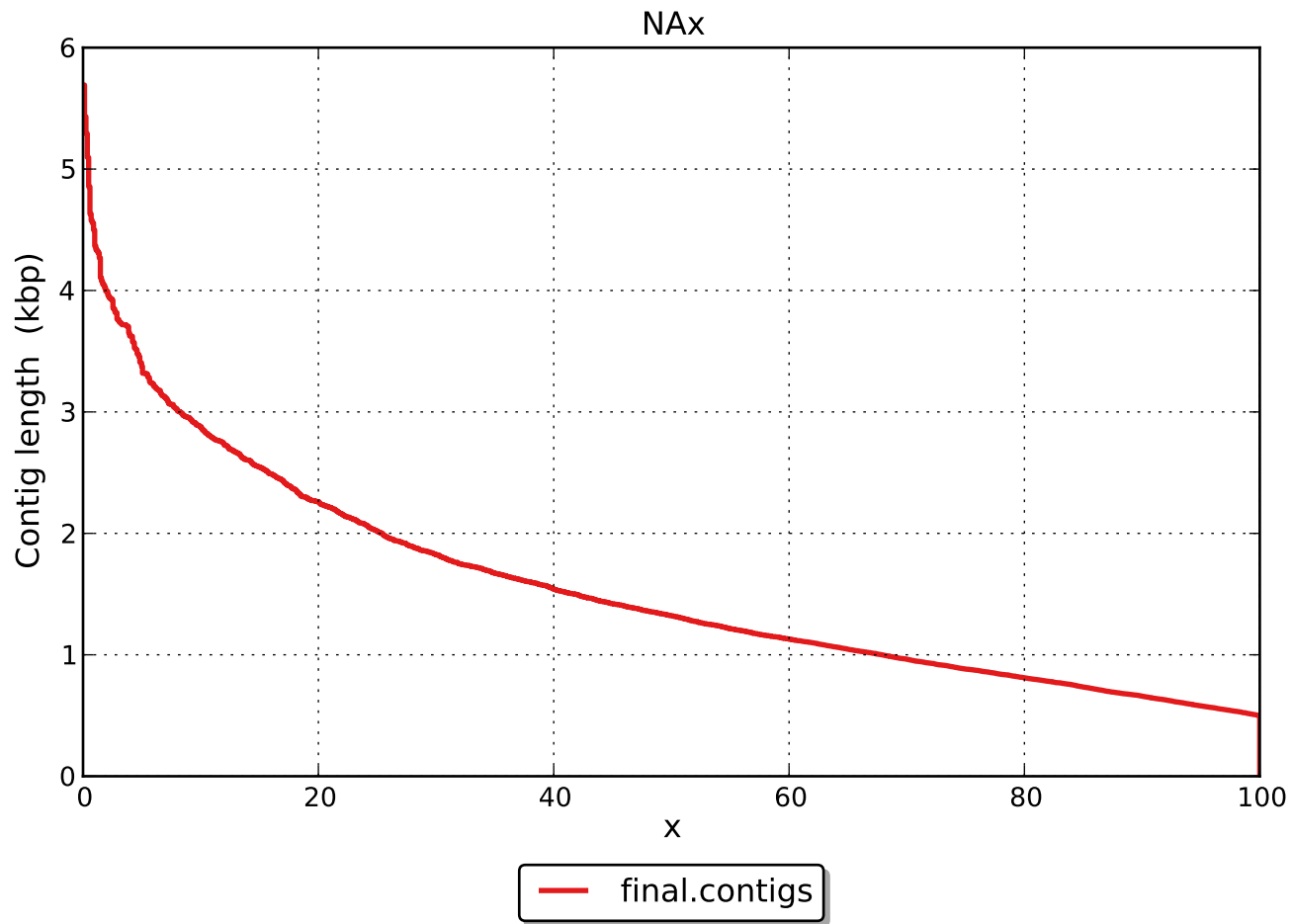
# Misassemblies



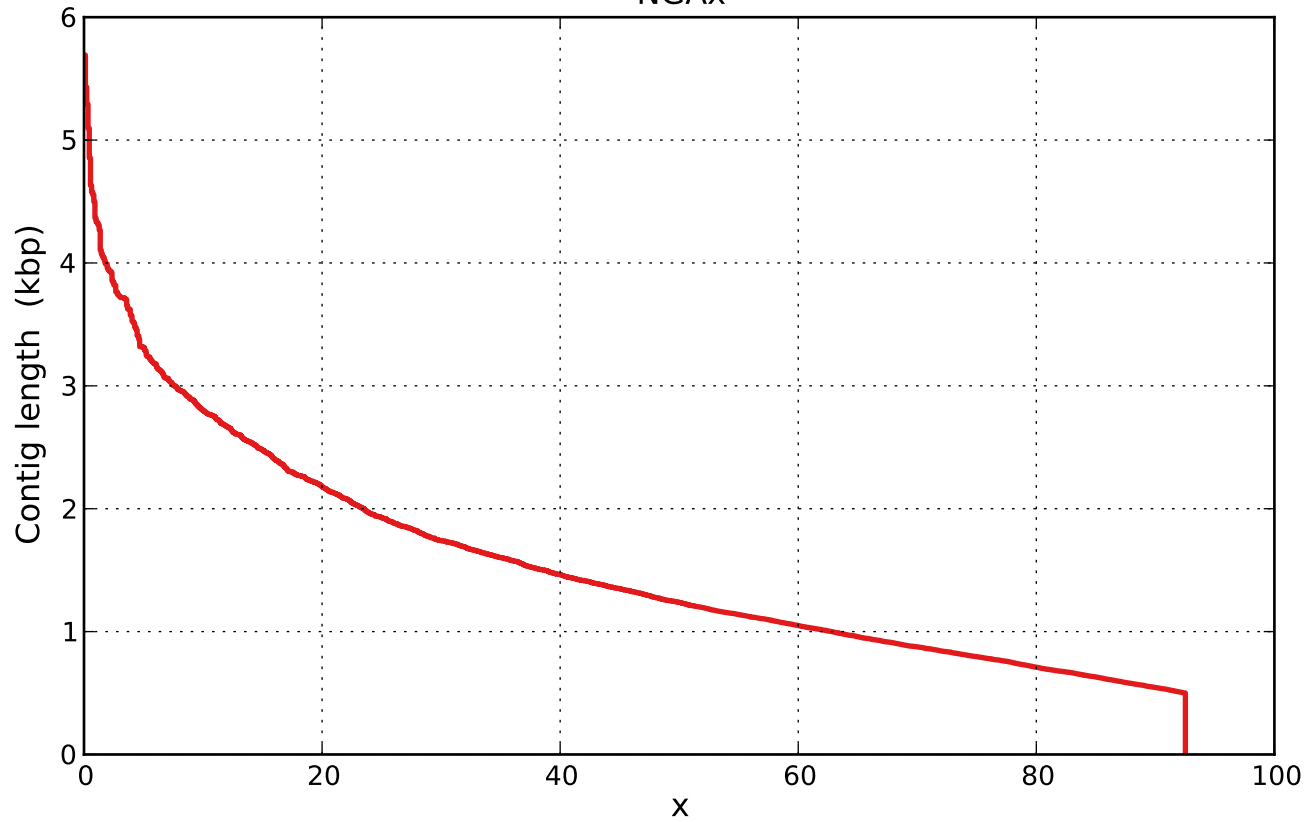


Cumulative length (aligned contigs)





NGAx



— final.contigs