

Report

	final.contigs
# contigs (>= 1000 bp)	1762
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3039207
Total length (>= 5000 bp)	16001
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3675
Largest contig	5370
Total length	4406738
Reference length	4641652
GC (℥)	50.76
Reference GC (℥)	50.78
N50	1391
NG50	1337
N75	899
NG75	831
L50	1056
LG50	1142
L75	2043
LG75	2247
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	90.858
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.46
# indels per 100 kbp	0.00
Largest alignment	5370
NA50	1391
NGA50	1337
NA75	899
NGA75	831
LA50	1056
LGA50	1142
LA75	2043
LGA75	2247

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

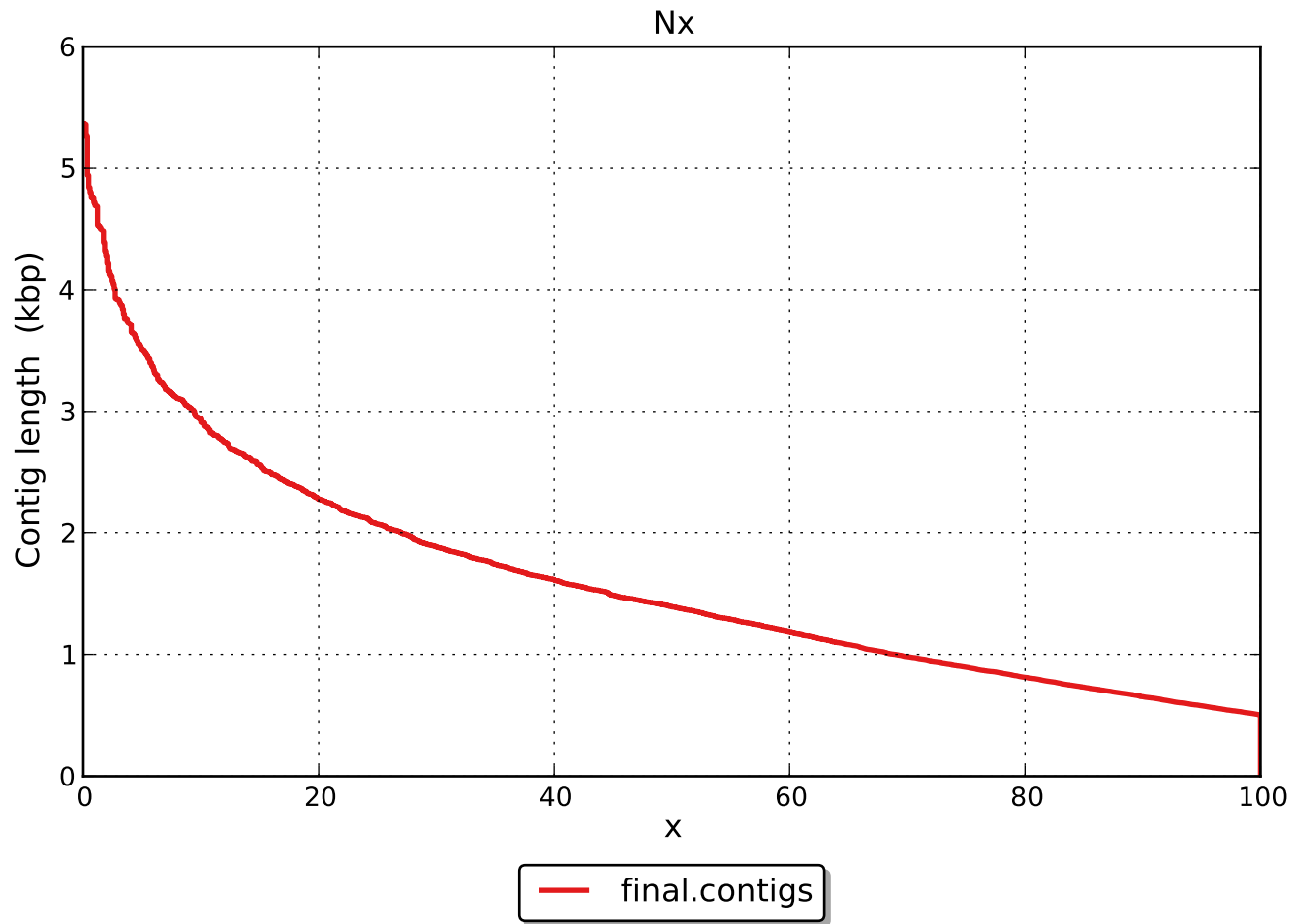
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1369
# indels	0
# short indels	0
# long indels	0
Indels length	0

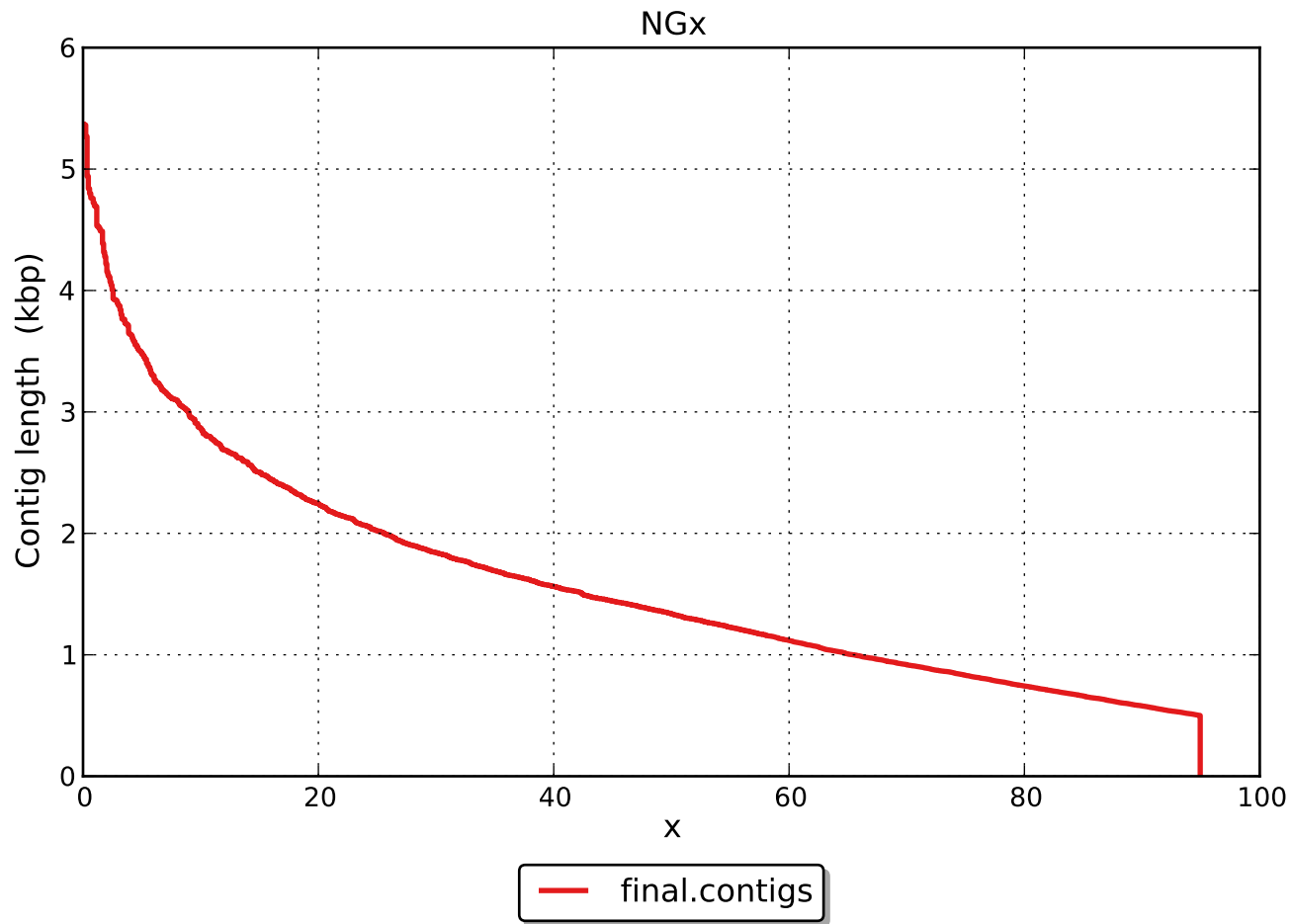
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

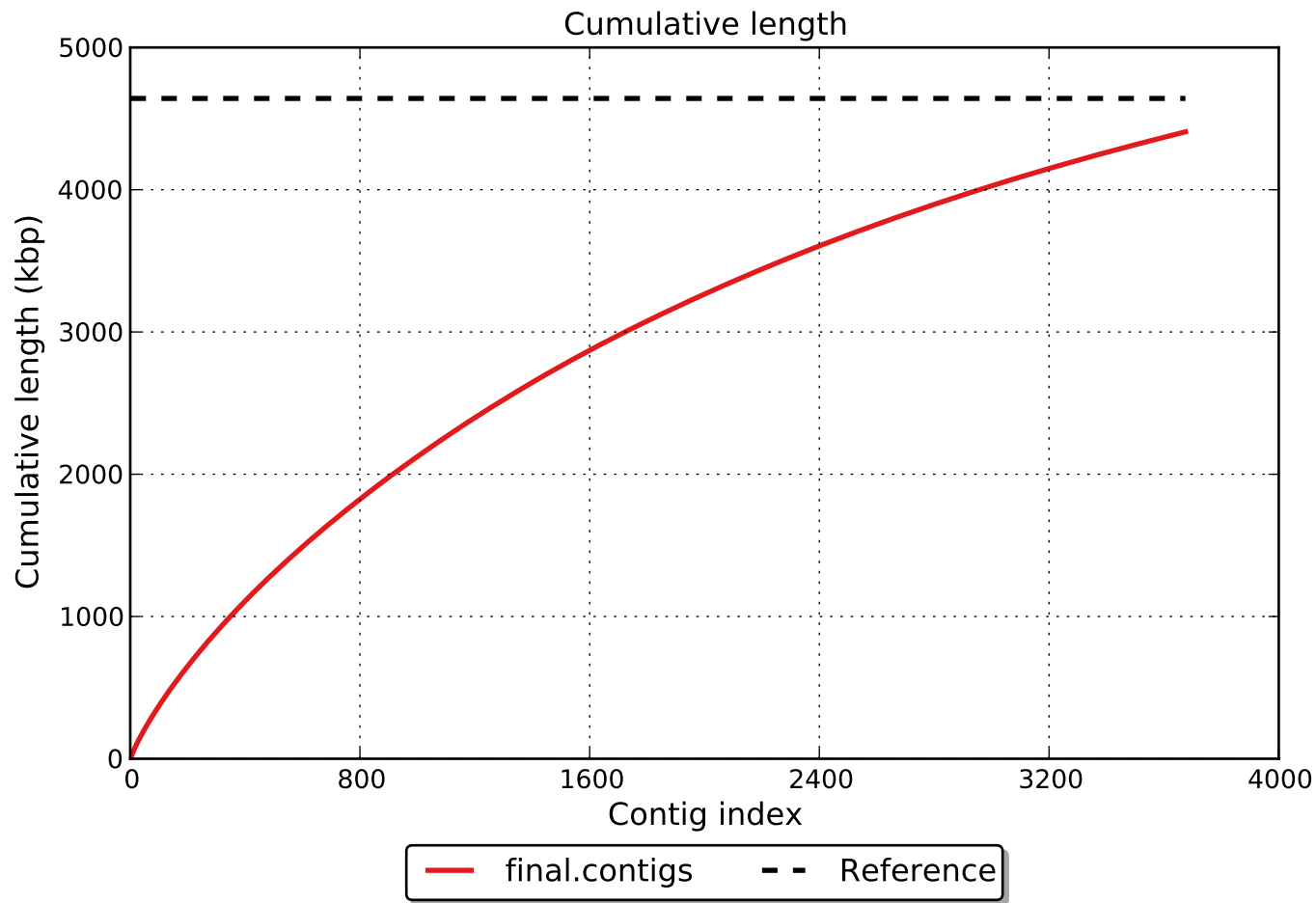
## Unaligned report

	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

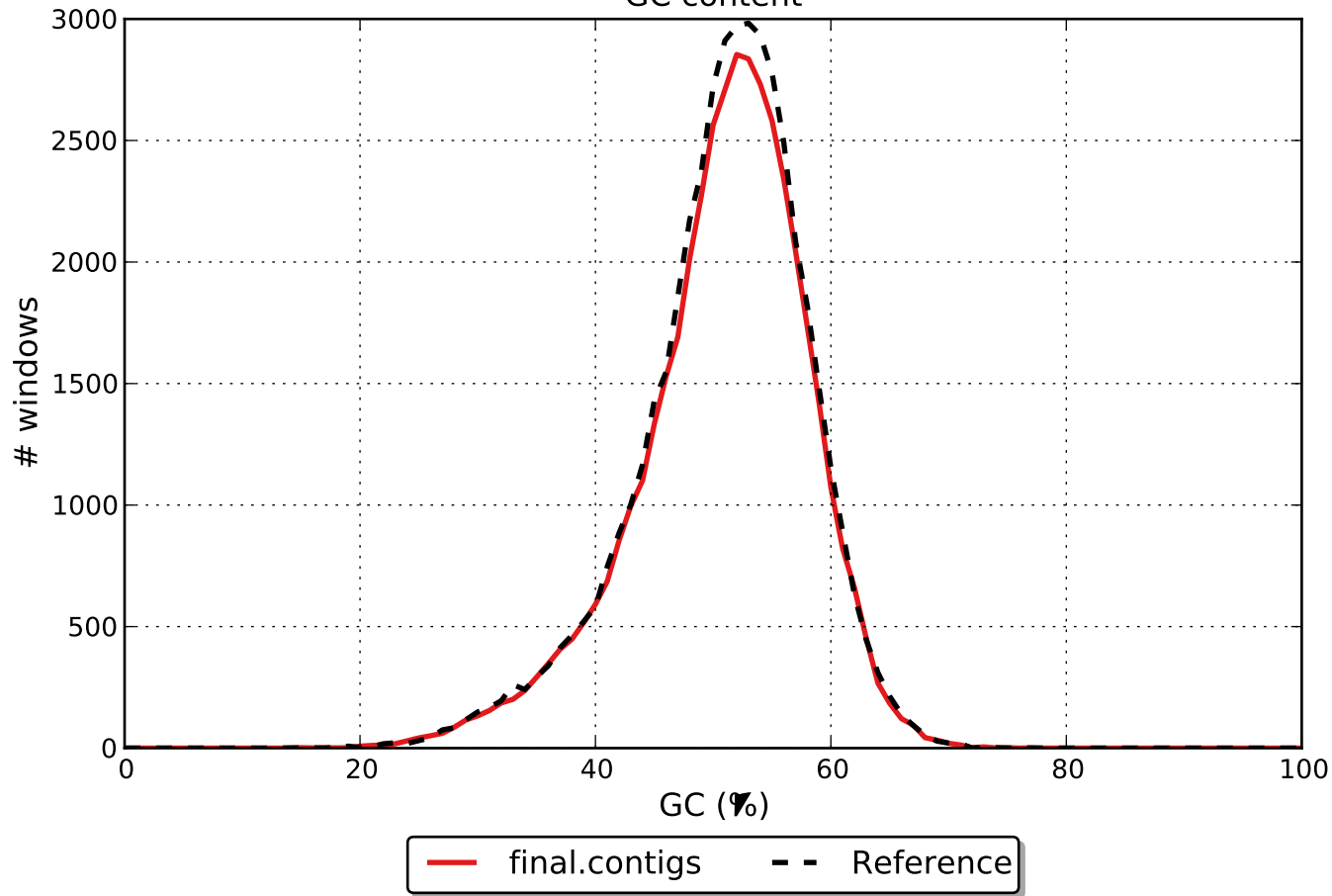
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

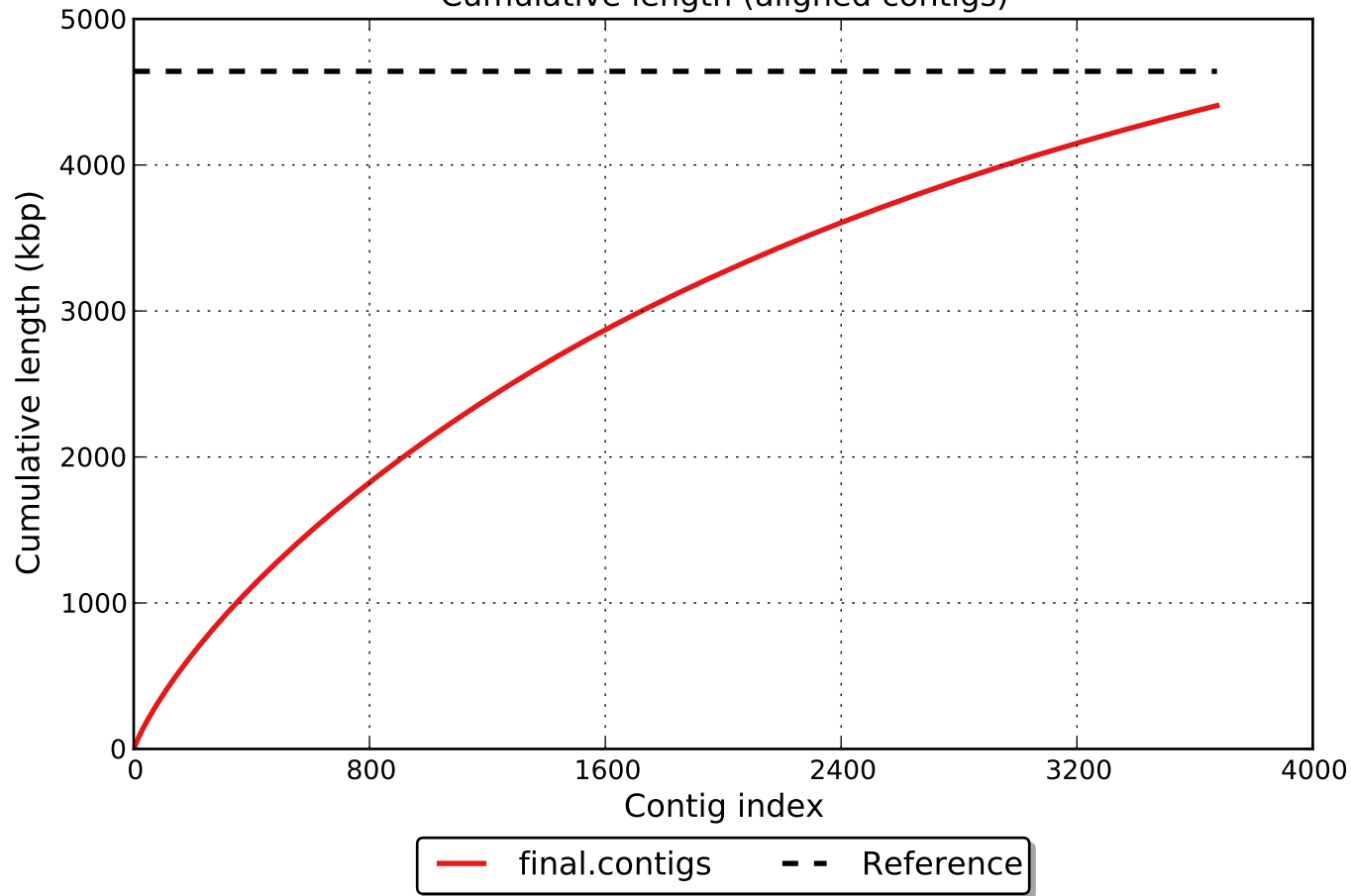


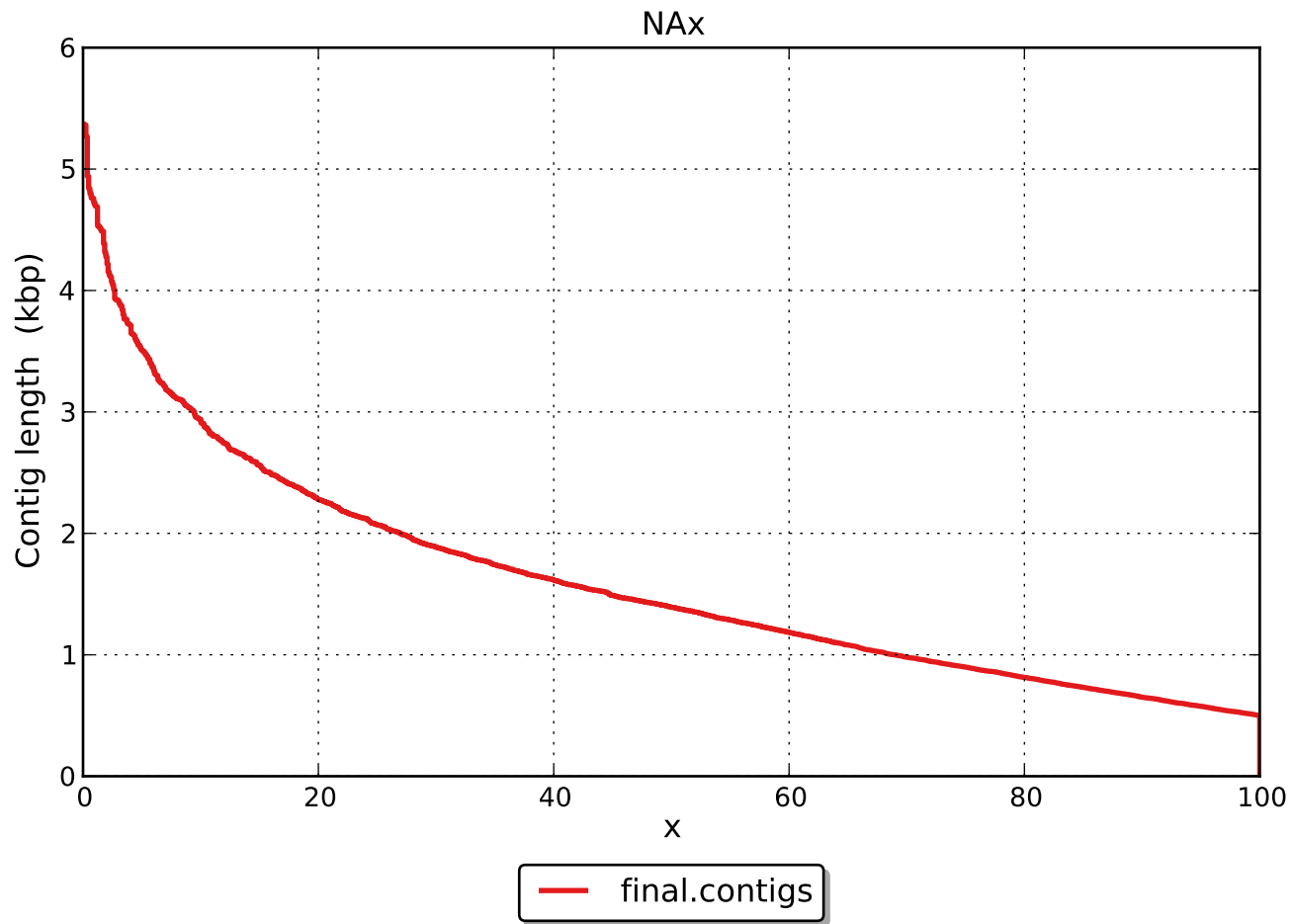
# Misassemblies



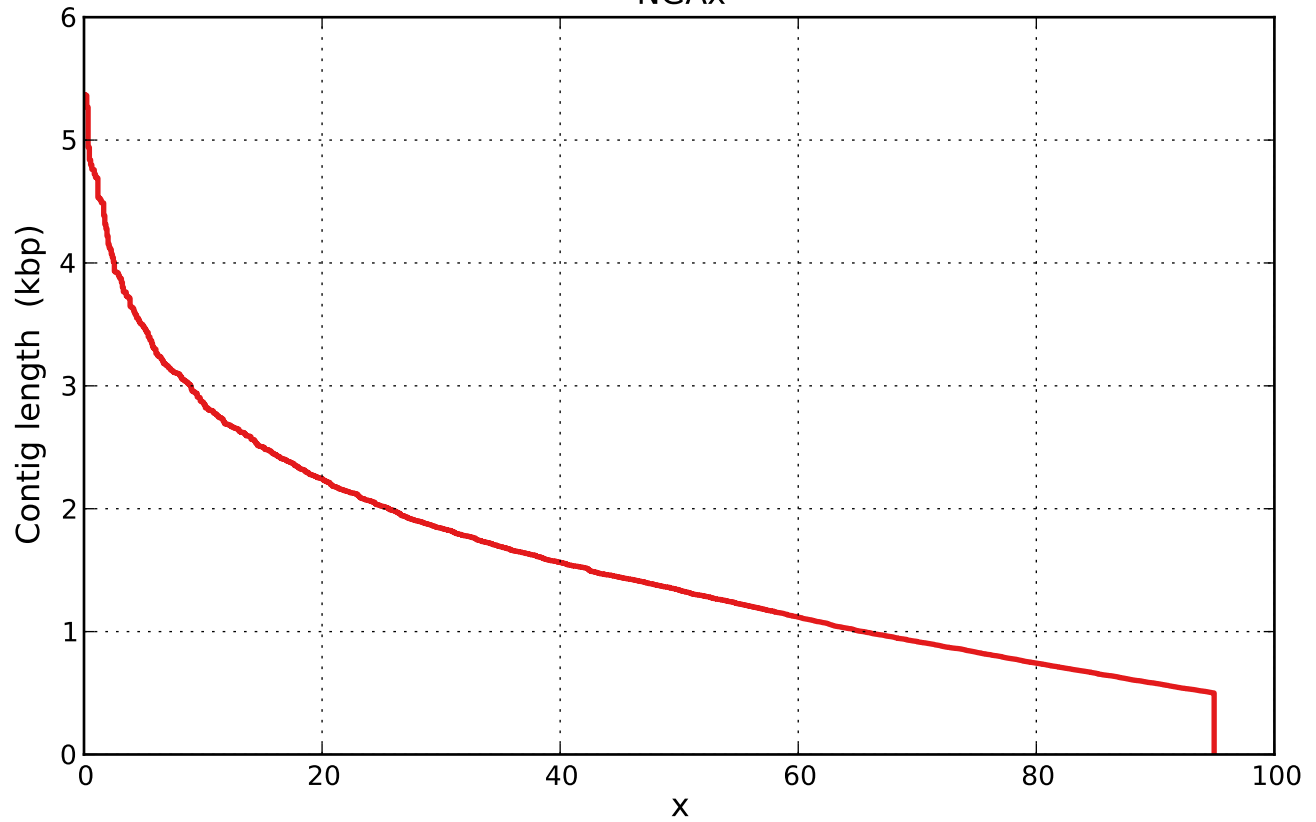


Cumulative length (aligned contigs)





NGAx



— final.contigs