

Report

	final.contigs
# contigs (>= 1000 bp)	1833
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3077814
Total length (>= 5000 bp)	21511
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3894
Largest contig	5692
Total length	4562784
Reference length	4857432
GC (℥)	52.22
Reference GC (℥)	52.22
N50	1315
NG50	1245
N75	878
NG75	807
L50	1135
LG50	1250
L75	2202
LG75	2464
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	89.717
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.40
# indels per 100 kbp	0.09
Largest alignment	5692
NA50	1315
NGA50	1245
NA75	878
NGA75	807
LA50	1135
LGA50	1250
LA75	2202
LGA75	2464

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

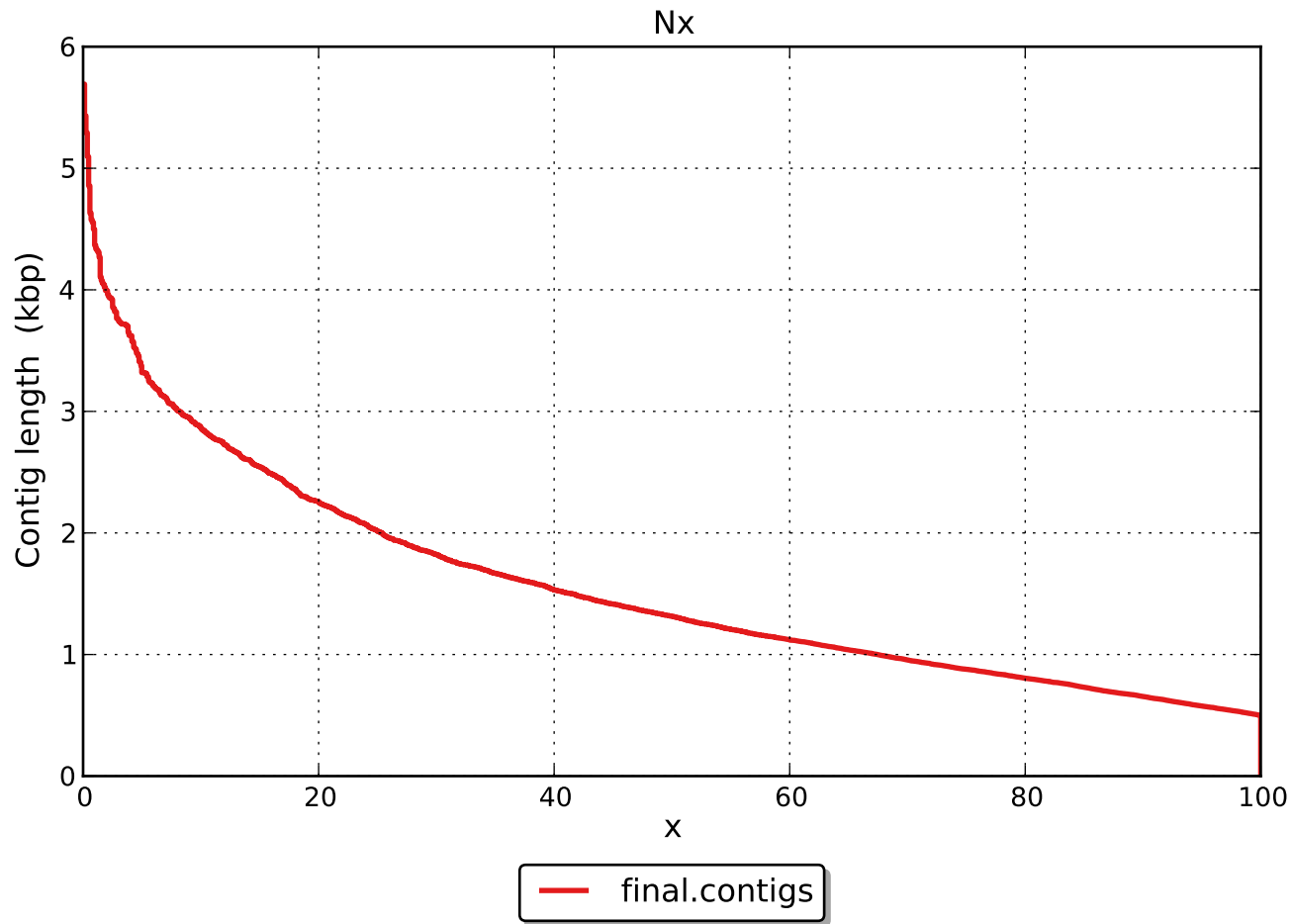
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1717
# indels	4
# short indels	4
# long indels	0
Indels length	4

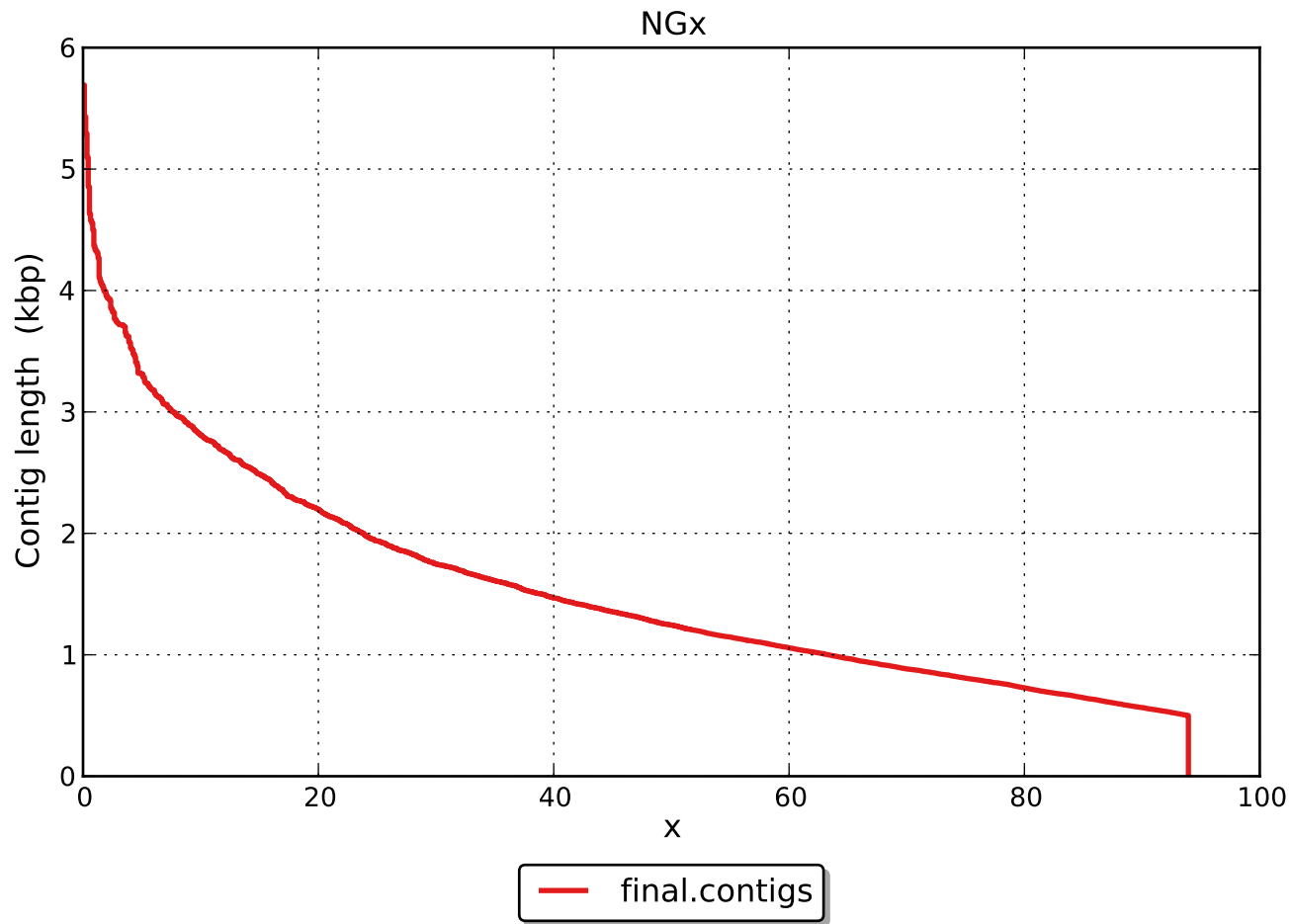
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

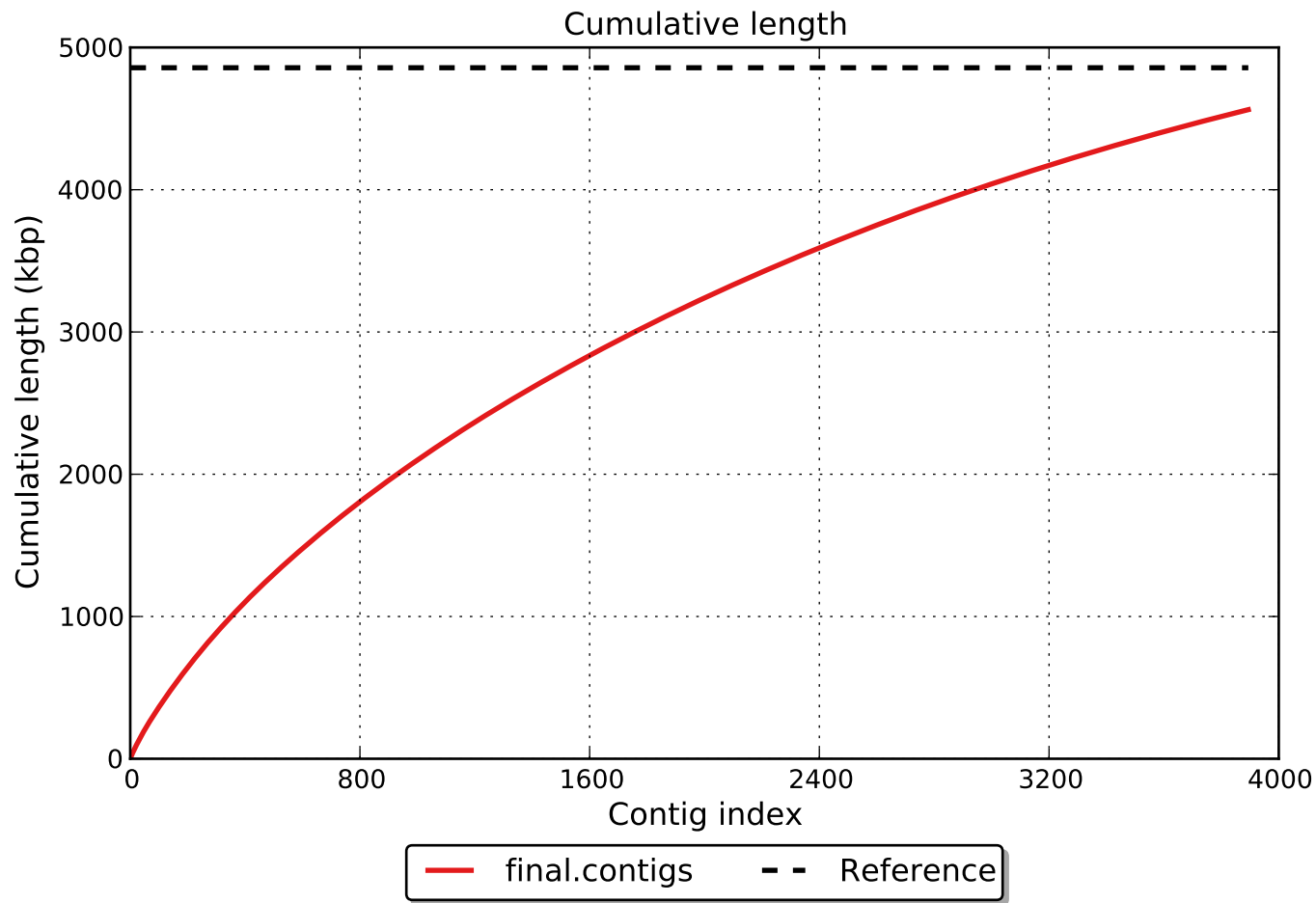
## Unaligned report

	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

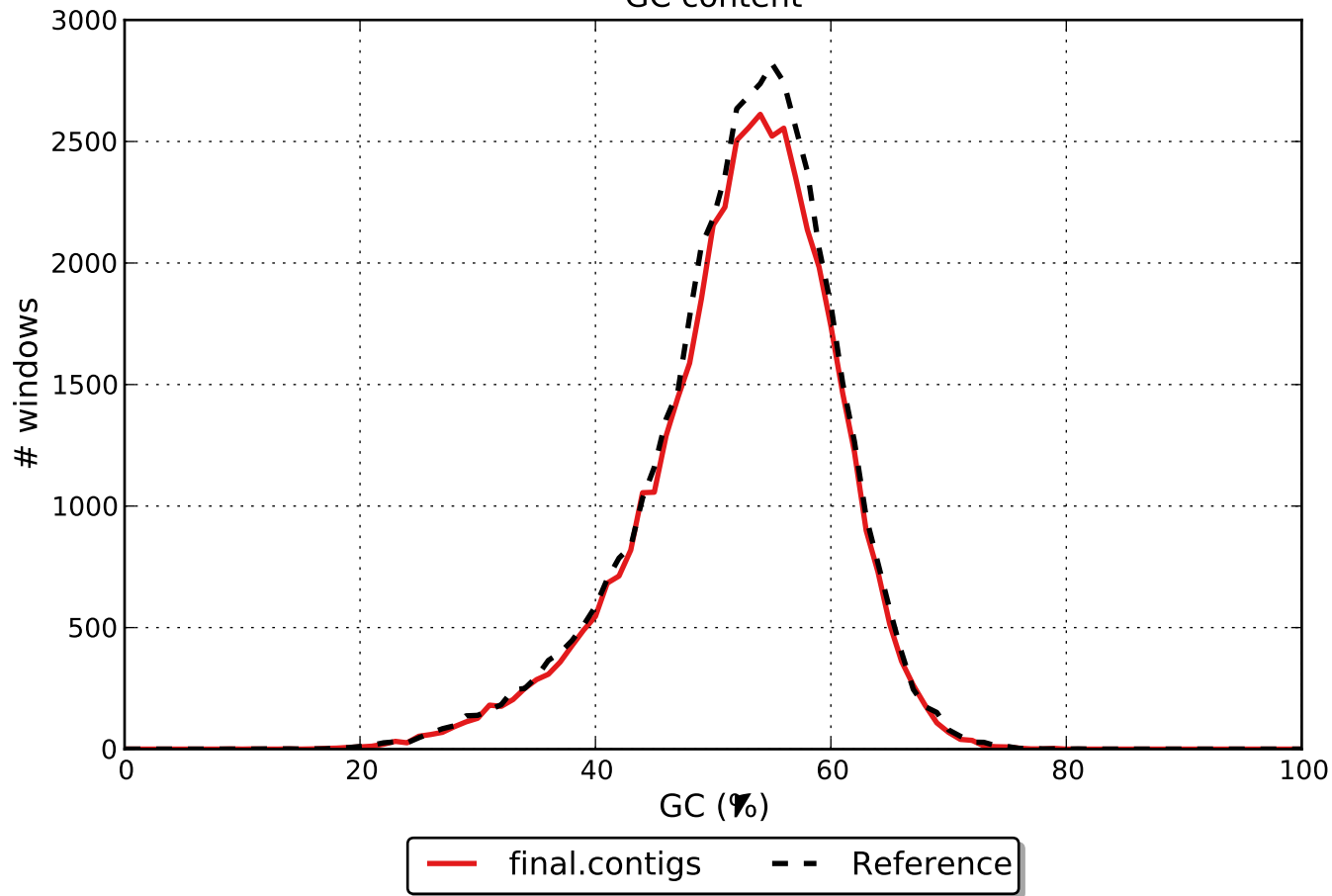
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







GC content

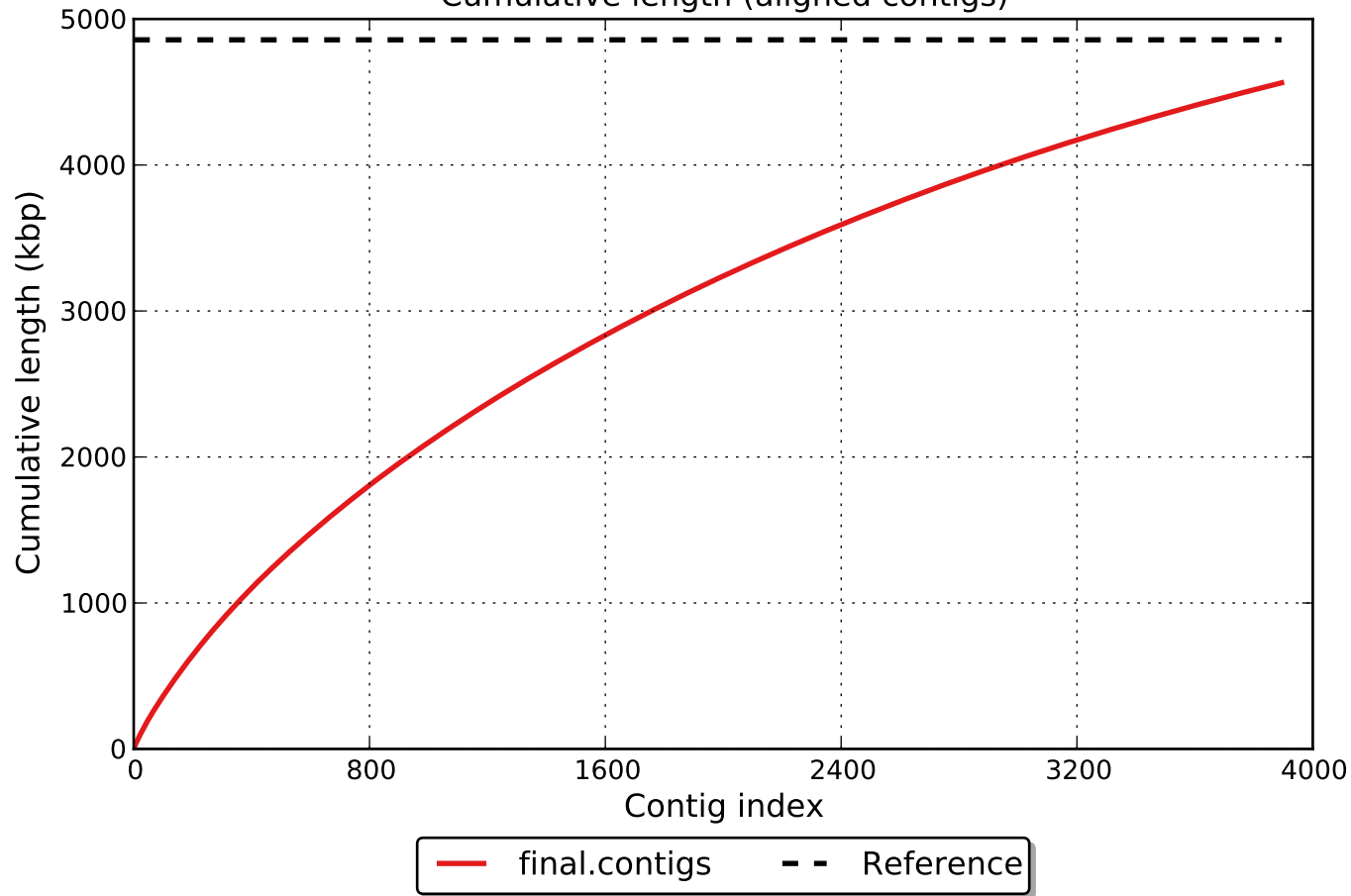


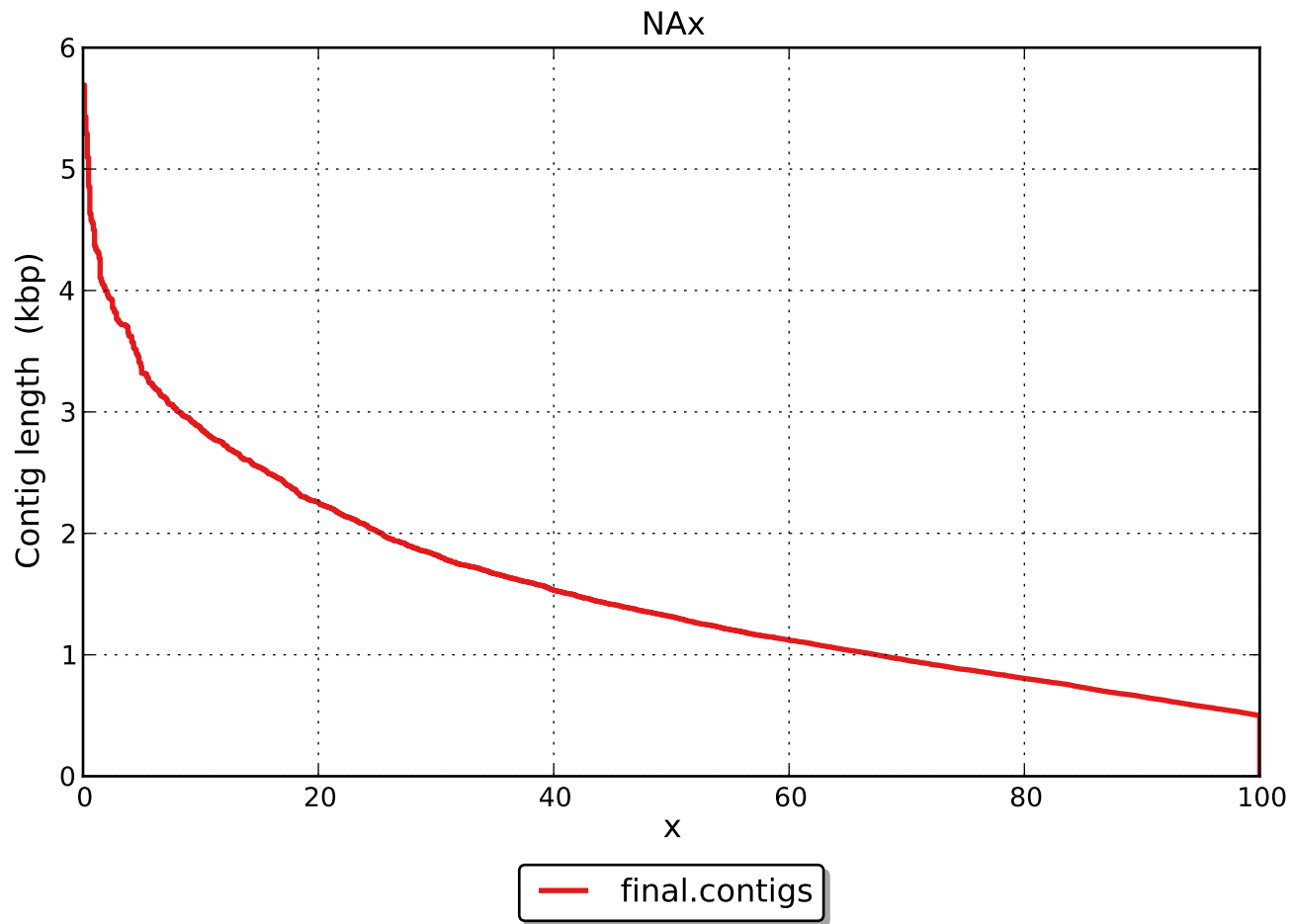
# Misassemblies





Cumulative length (aligned contigs)





NGAx

