

Report

	final.contigs
# contigs (>= 1000 bp)	1669
# contigs (>= 5000 bp)	162
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4490273
Total length (>= 5000 bp)	1036312
Total length (>= 10000 bp)	71875
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2231
Largest contig	15045
Total length	4903745
Reference length	4857432
GC (℥)	52.24
Reference GC (℥)	52.23
N50	2975
NG50	3003
N75	1755
NG75	1787
L50	530
LG50	523
L75	1062
LG75	1043
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.035
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.83
# indels per 100 kbp	0.00
Largest alignment	15045
NA50	2975
NGA50	3003
NA75	1755
NGA75	1787
LA50	530
LGA50	523
LA75	1062
LGA75	1043

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

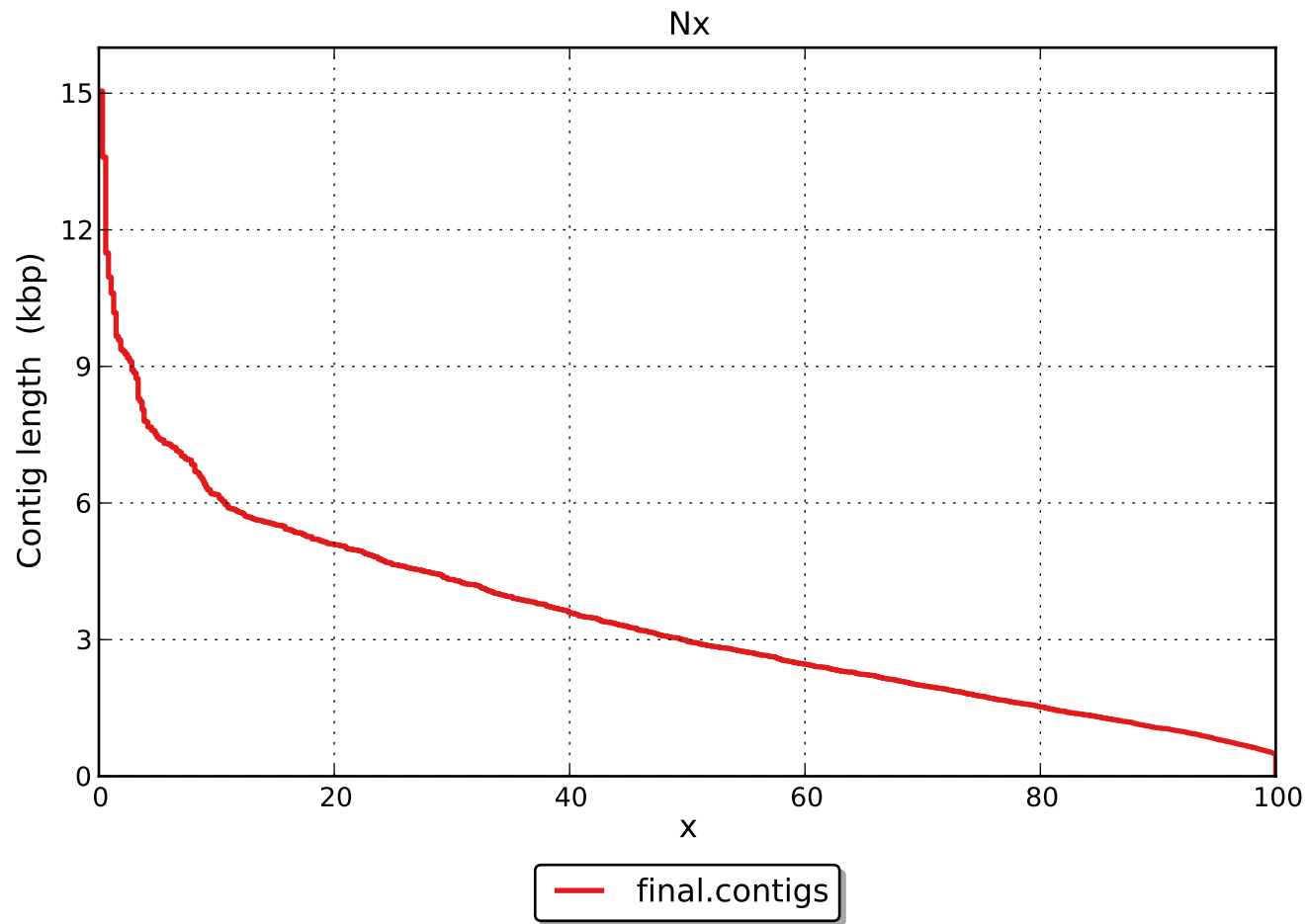
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	87
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

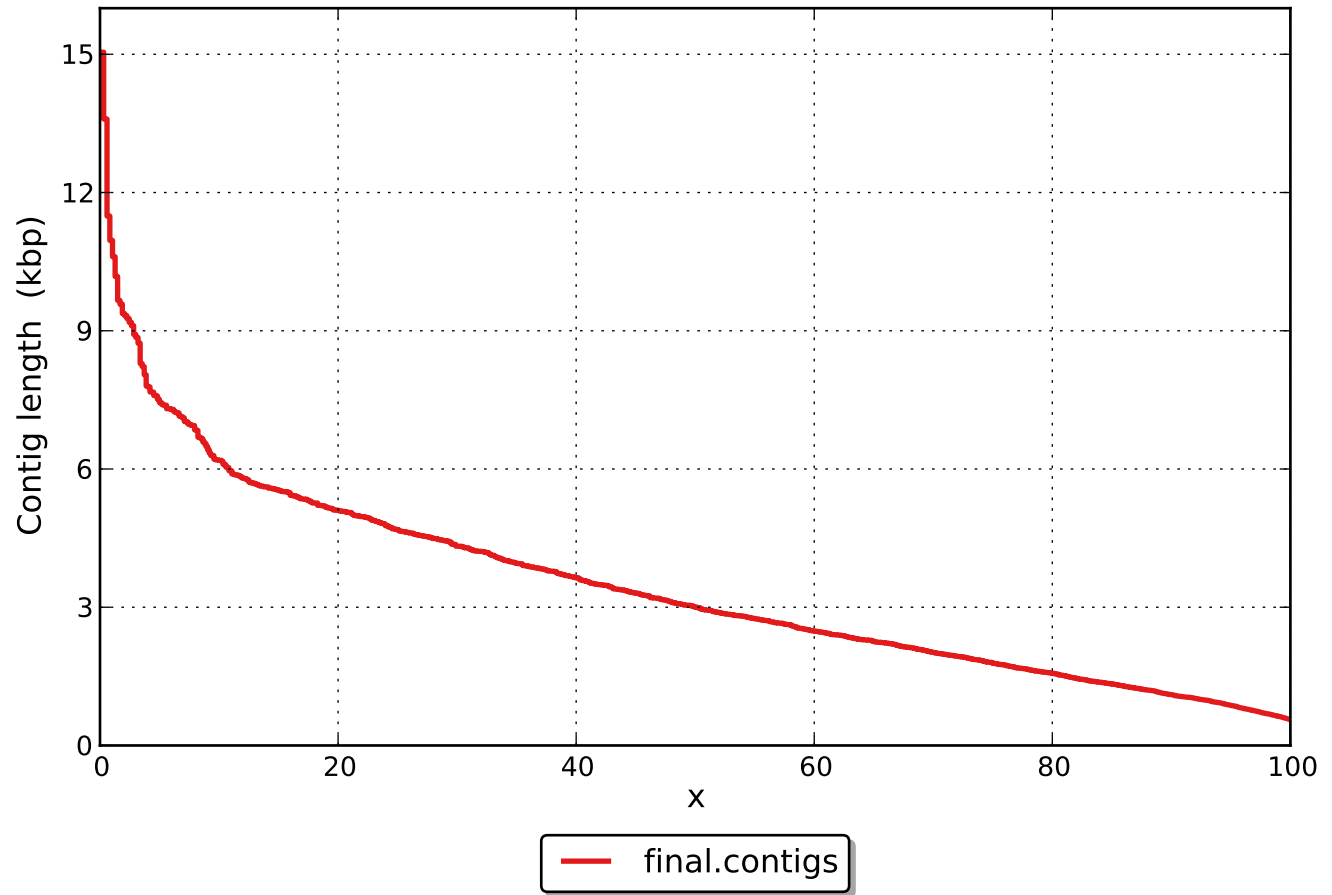
## Unaligned report

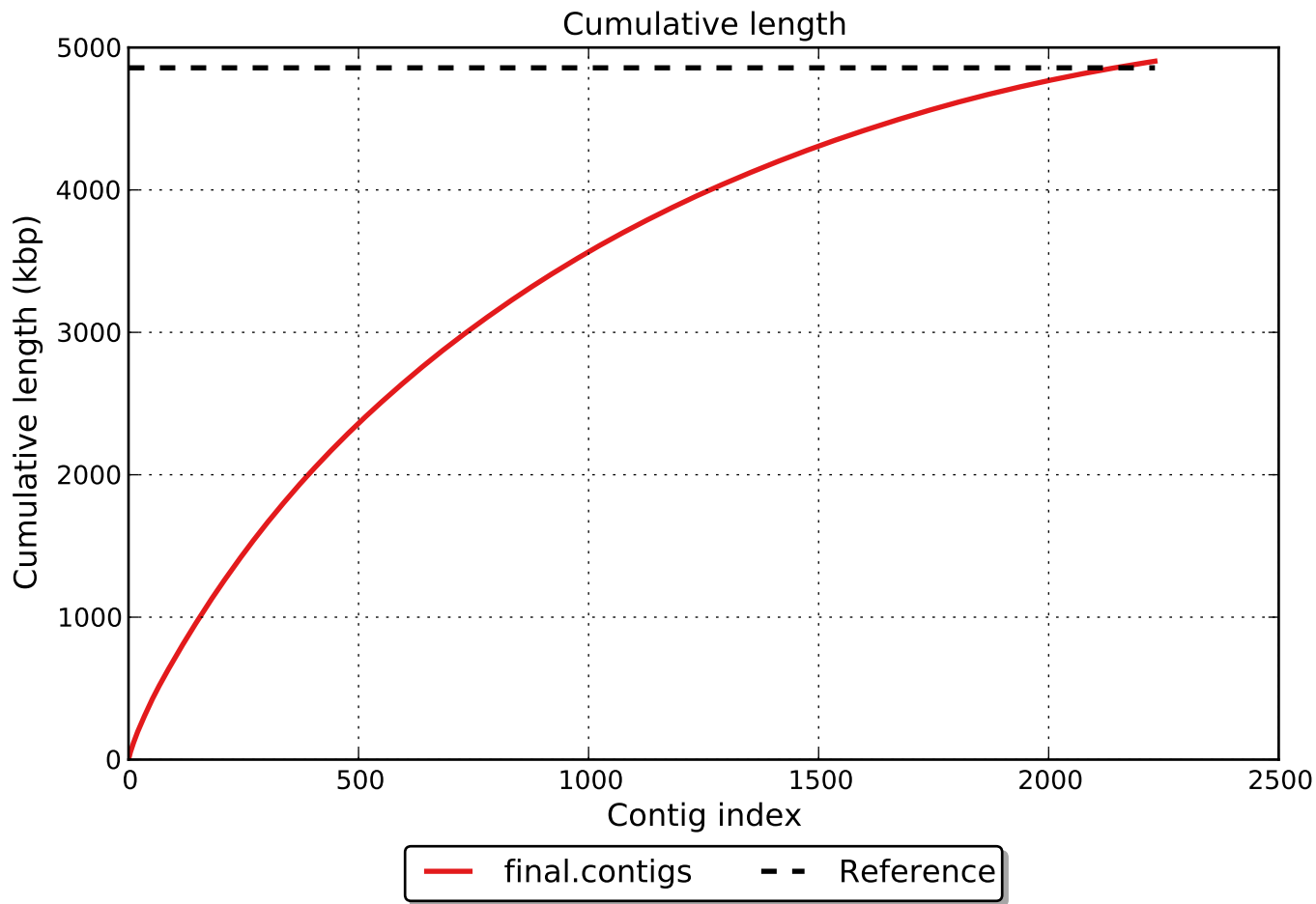
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

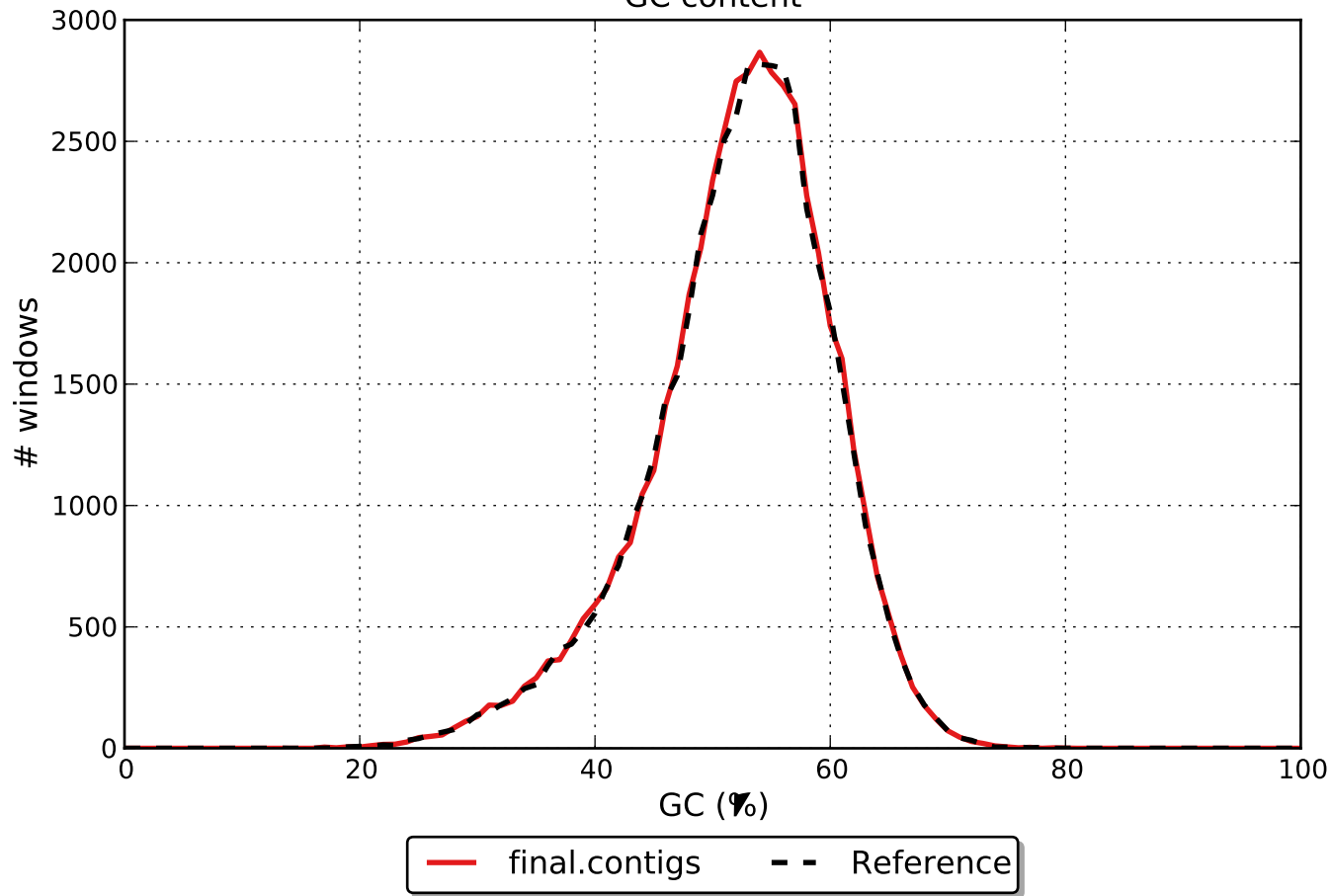


NGx





GC content

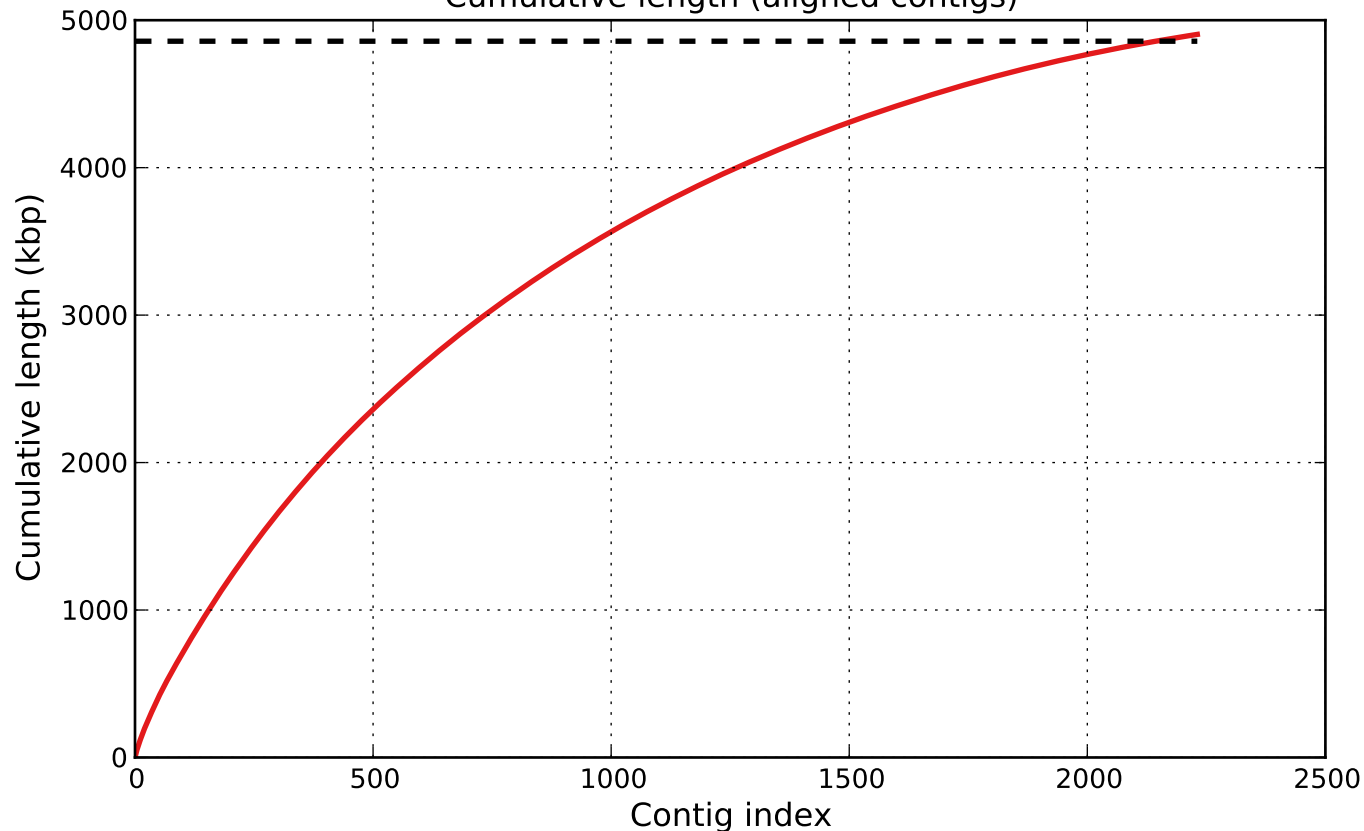


# Misassemblies

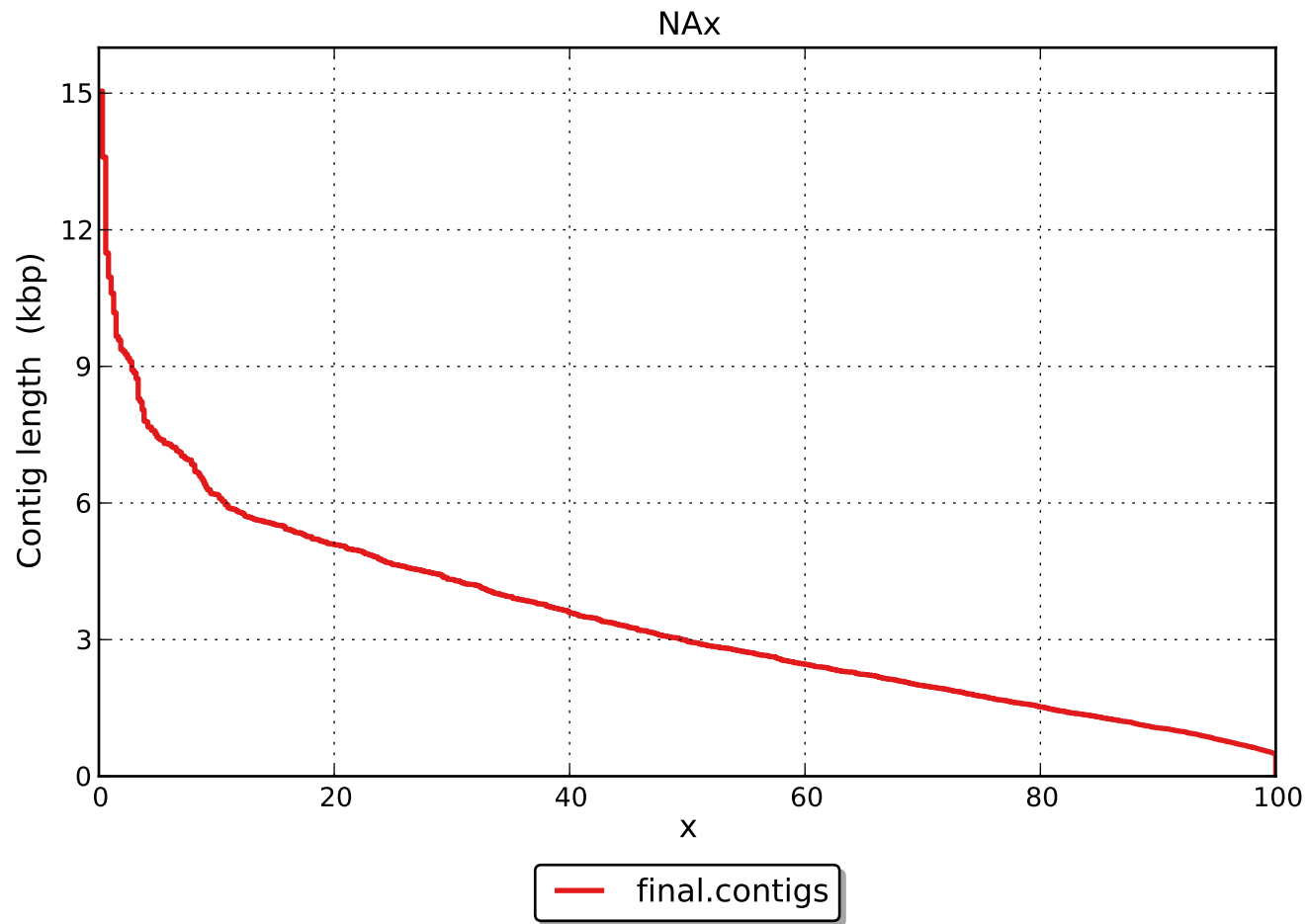




Cumulative length (aligned contigs)



— final.contigs    - - Reference



# NGAx

