

Report

	final.contigs
# contigs (>= 1000 bp)	678
# contigs (>= 5000 bp)	360
# contigs (>= 10000 bp)	153
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4863679
Total length (>= 5000 bp)	3992707
Total length (>= 10000 bp)	2494505
Total length (>= 25000 bp)	445030
Total length (>= 50000 bp)	0
# contigs	736
Largest contig	38916
Total length	4905482
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.22
N50	10064
NG50	10138
N75	6186
NG75	6363
L50	149
LG50	147
L75	303
LG75	298
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.816
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	38916
NA50	10064
NGA50	10138
NA75	6186
NGA75	6363
LA50	149
LGA50	147
LA75	303
LGA75	298

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

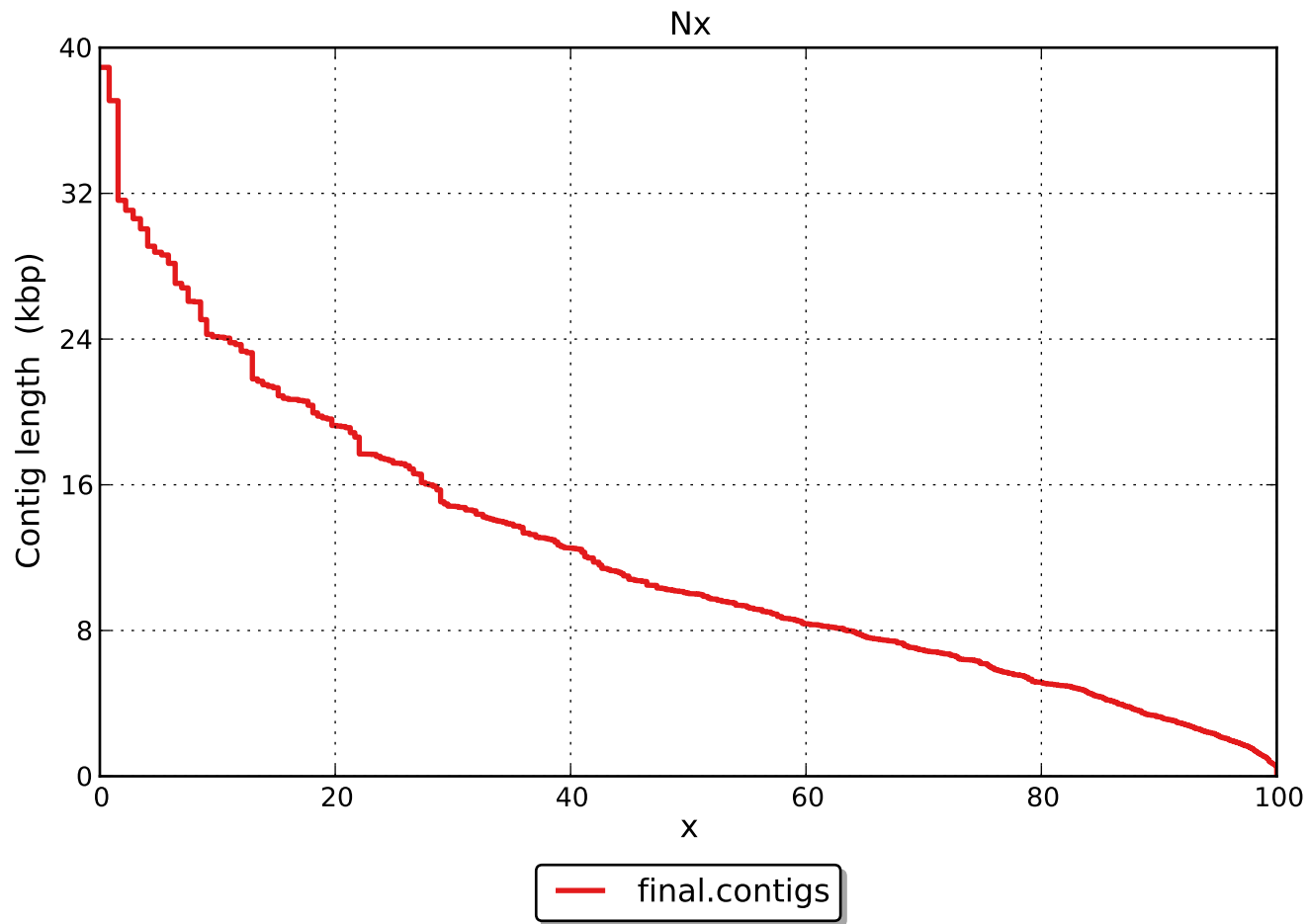
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

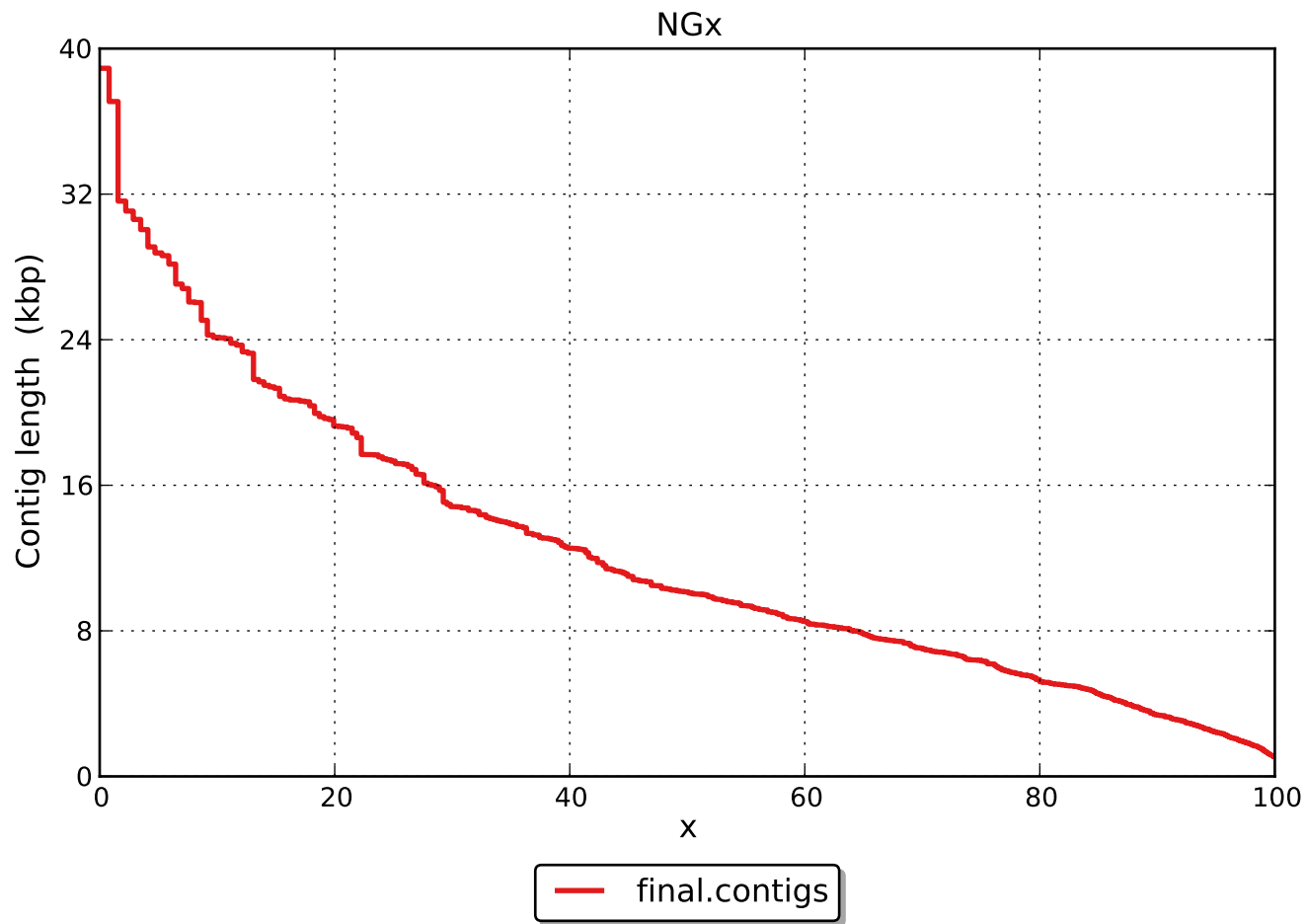
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

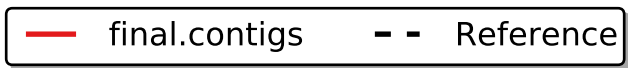
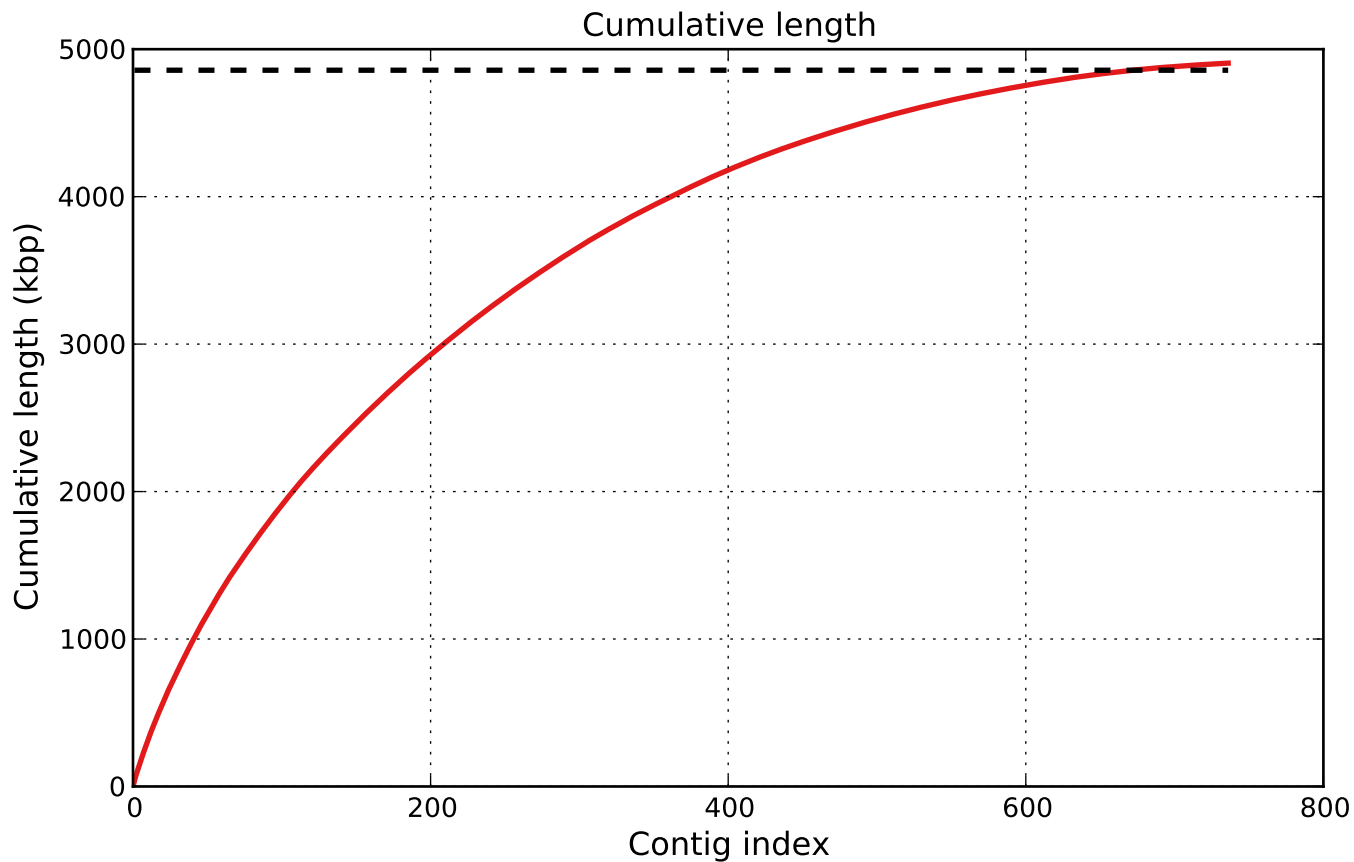
## Unaligned report

	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

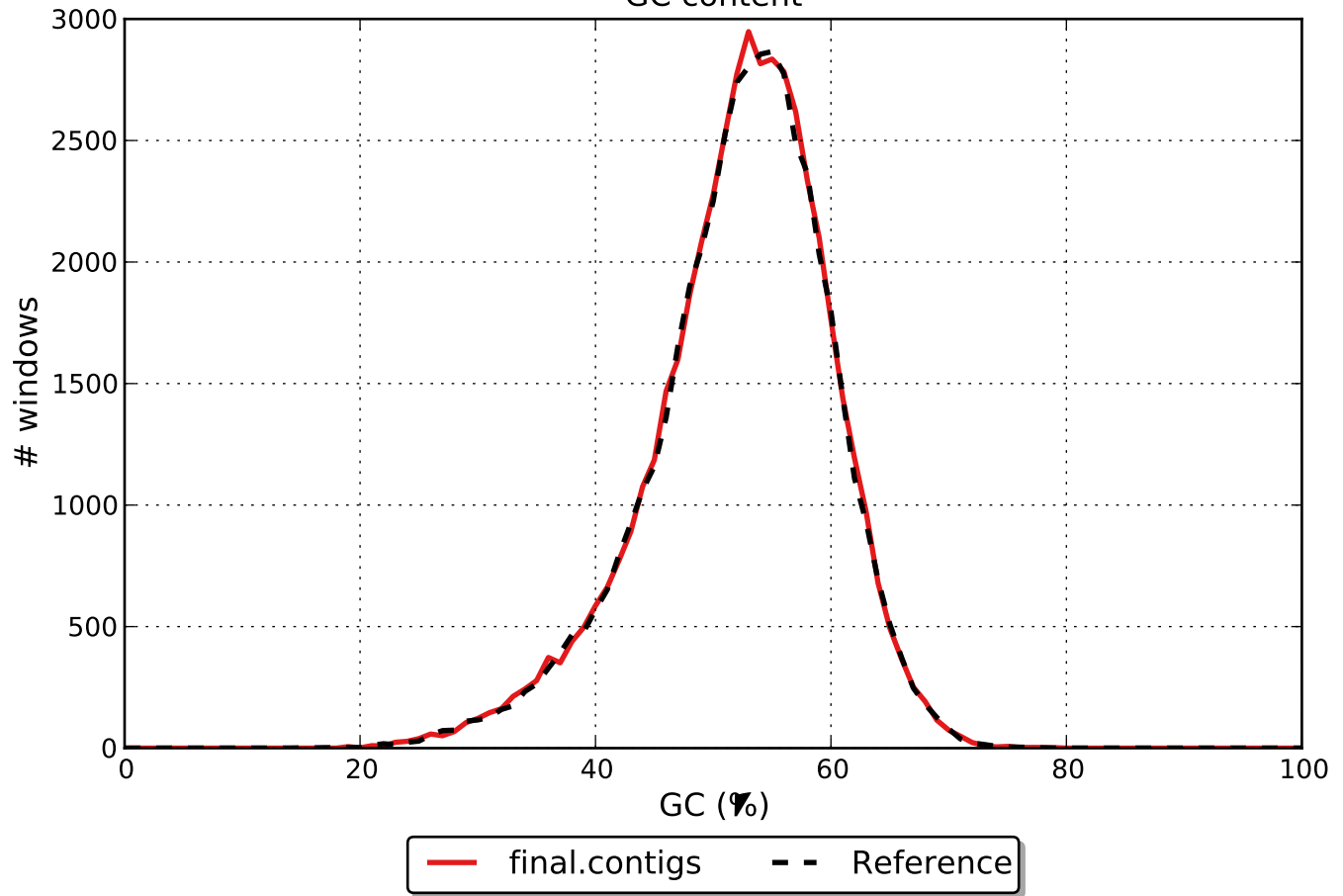
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



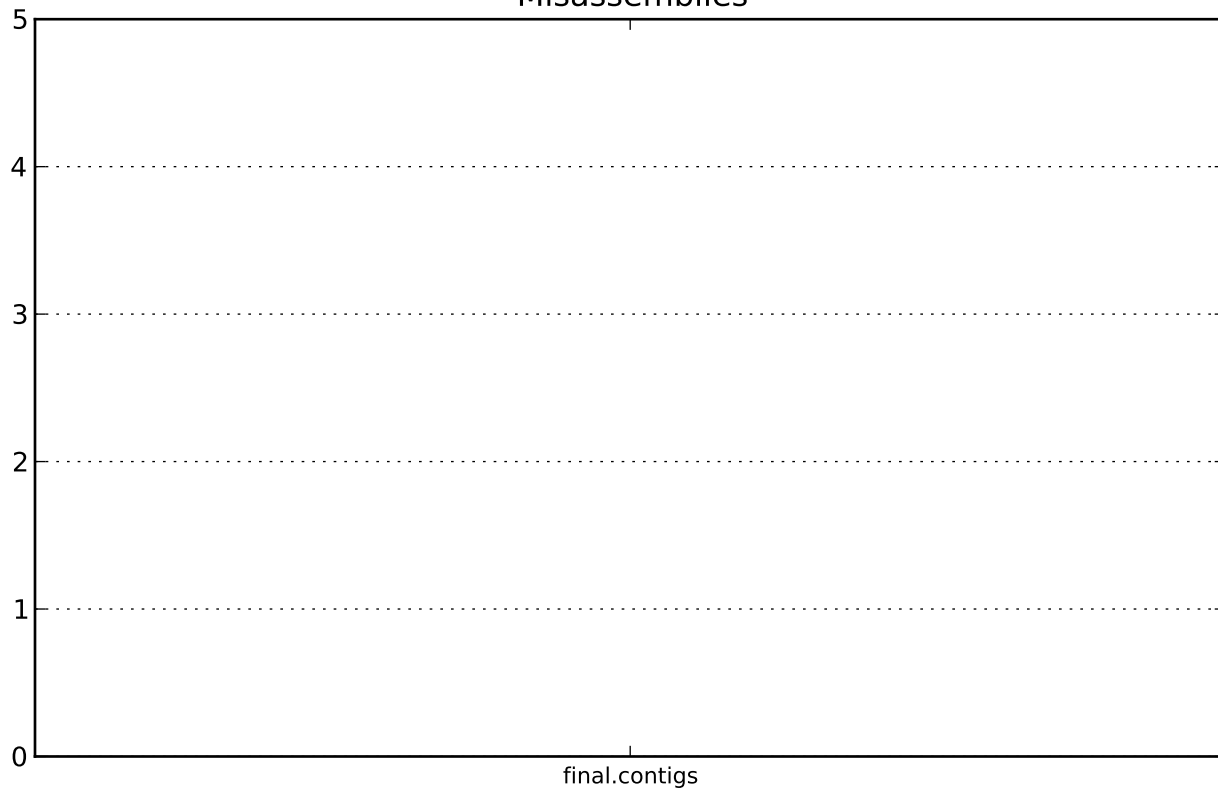




GC content

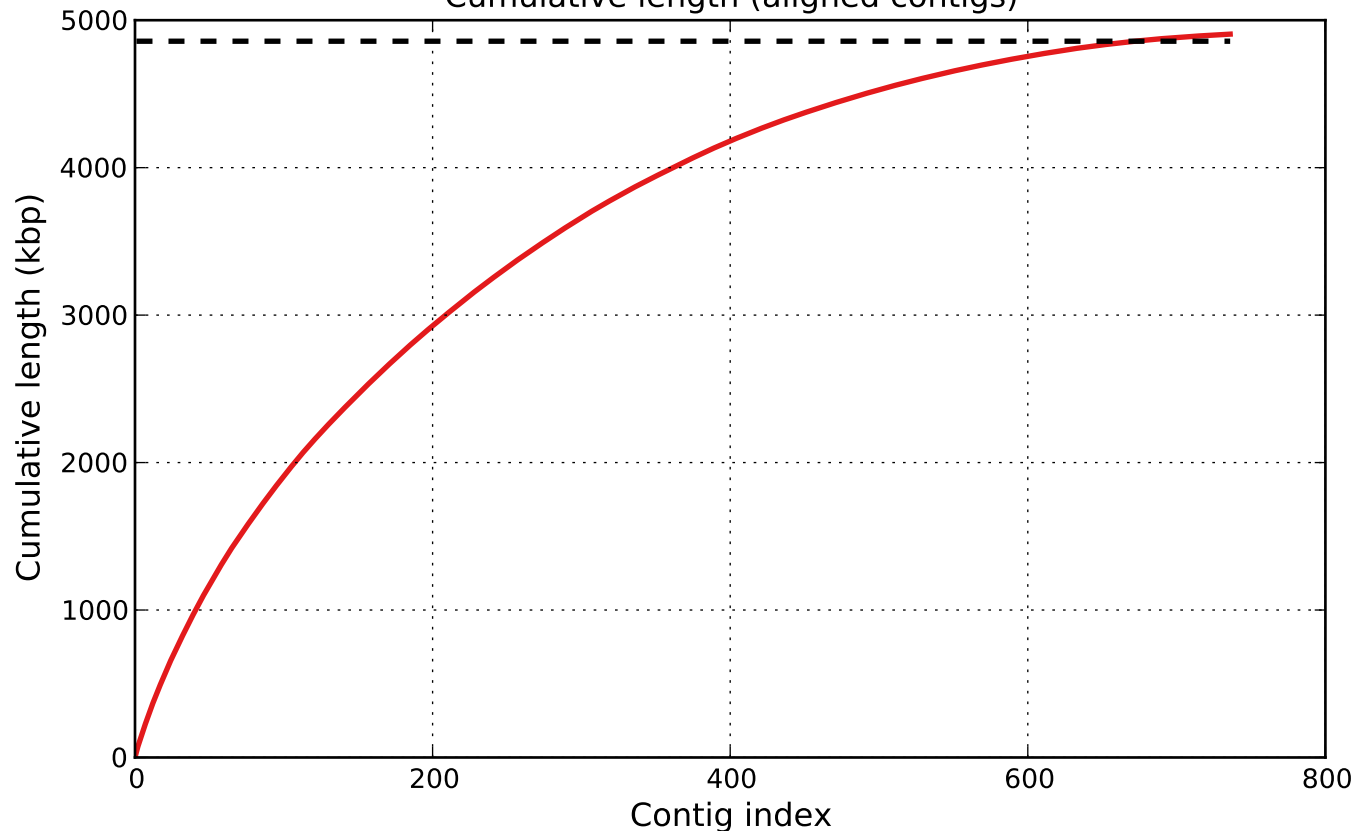


# Misassemblies

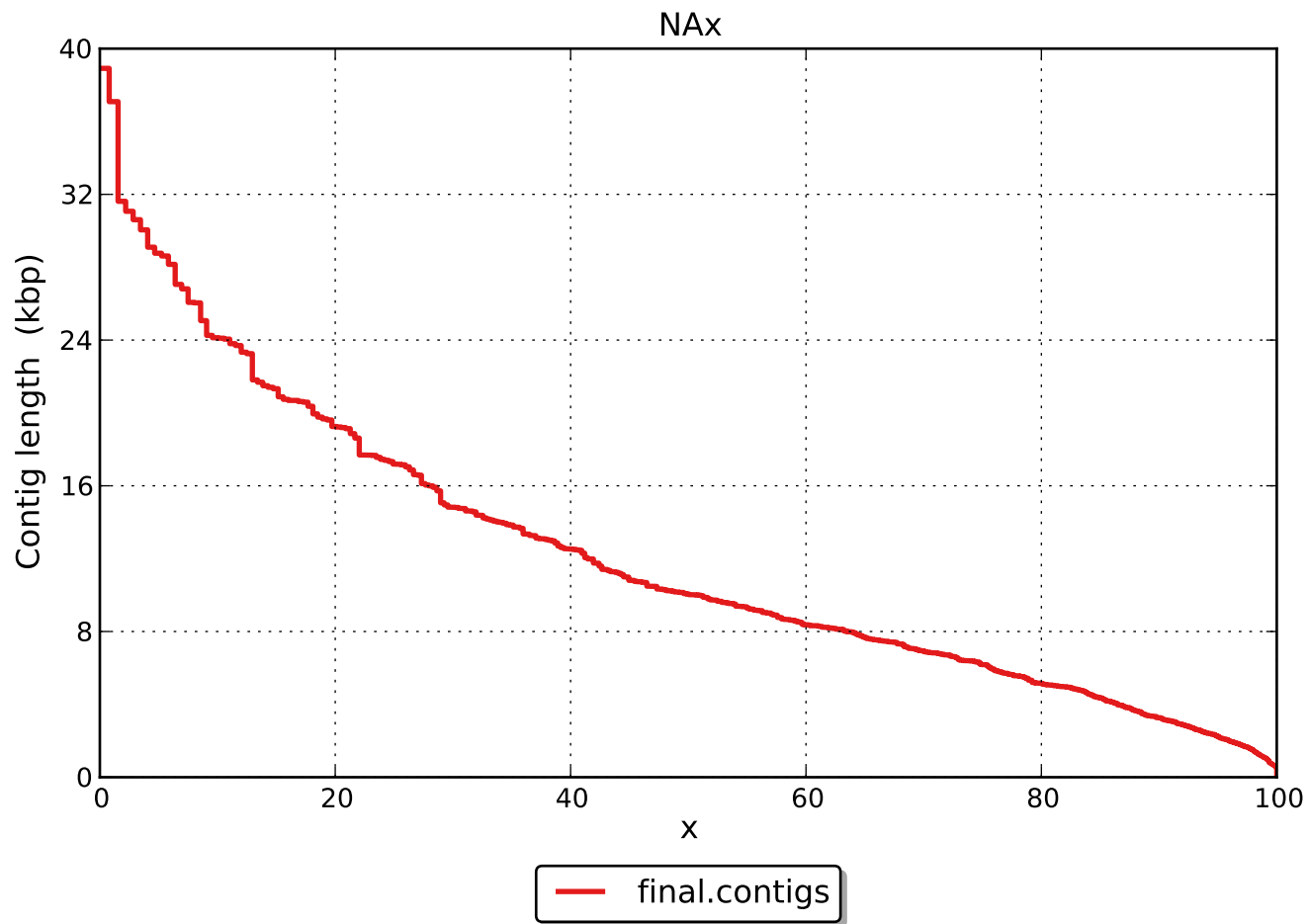




Cumulative length (aligned contigs)



— final.contigs    - - Reference



# NGAx

