

Report

	final.contigs
# contigs (>= 1000 bp)	542
# contigs (>= 5000 bp)	310
# contigs (>= 10000 bp)	164
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4538535
Total length (>= 5000 bp)	3878820
Total length (>= 10000 bp)	2831064
Total length (>= 25000 bp)	727737
Total length (>= 50000 bp)	0
# contigs	613
Largest contig	38551
Total length	4594289
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	12344
NG50	12252
N75	6895
NG75	6748
L50	116
LG50	118
L75	238
LG75	243
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.045
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.35
# indels per 100 kbp	0.00
Largest alignment	38551
NA50	12344
NGA50	12252
NA75	6887
NGA75	6722
LA50	116
LGA50	118
LA75	238
LGA75	243

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

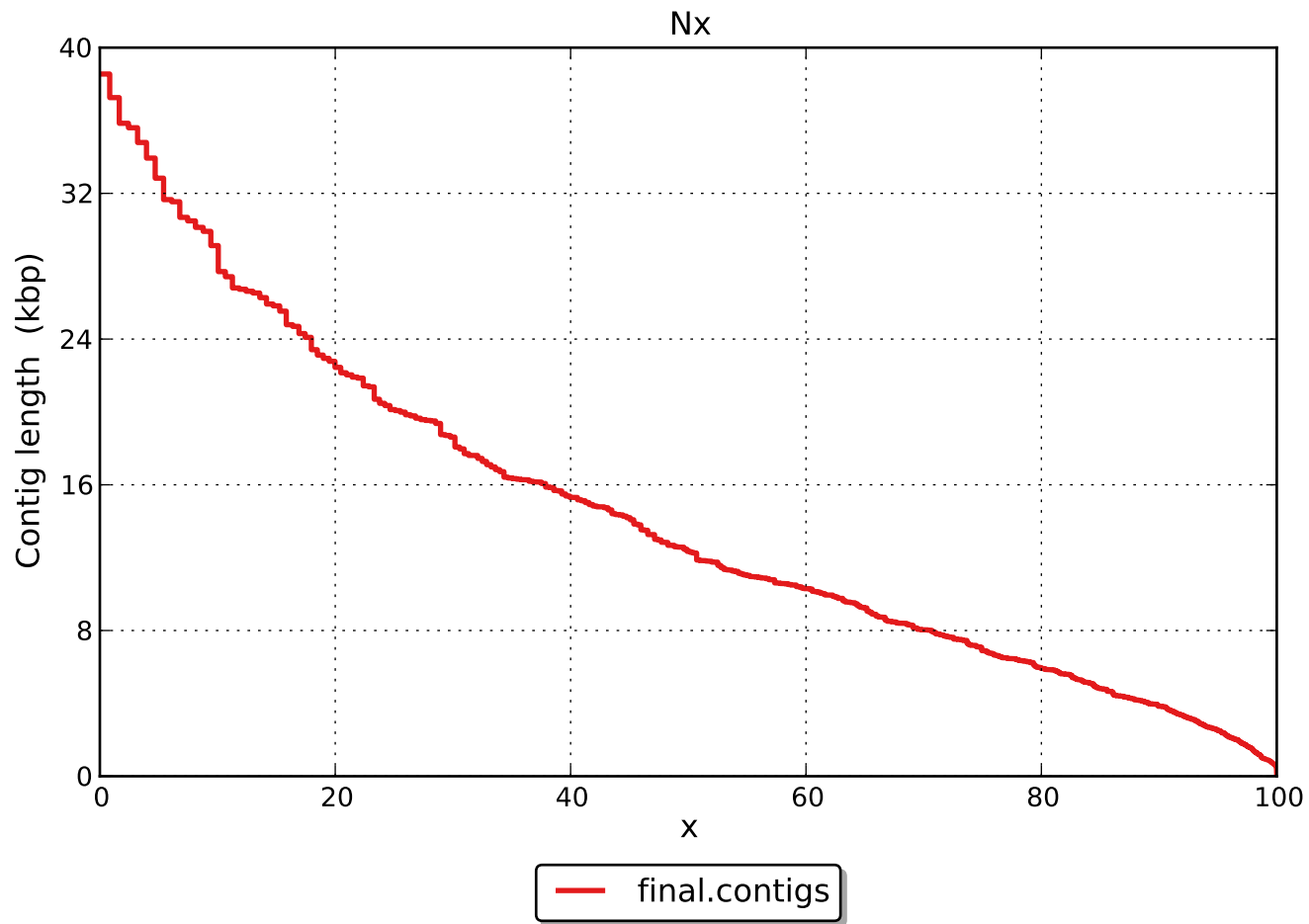
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	7679
# local misassemblies	0
# mismatches	16
# indels	0
# short indels	0
# long indels	0
Indels length	0

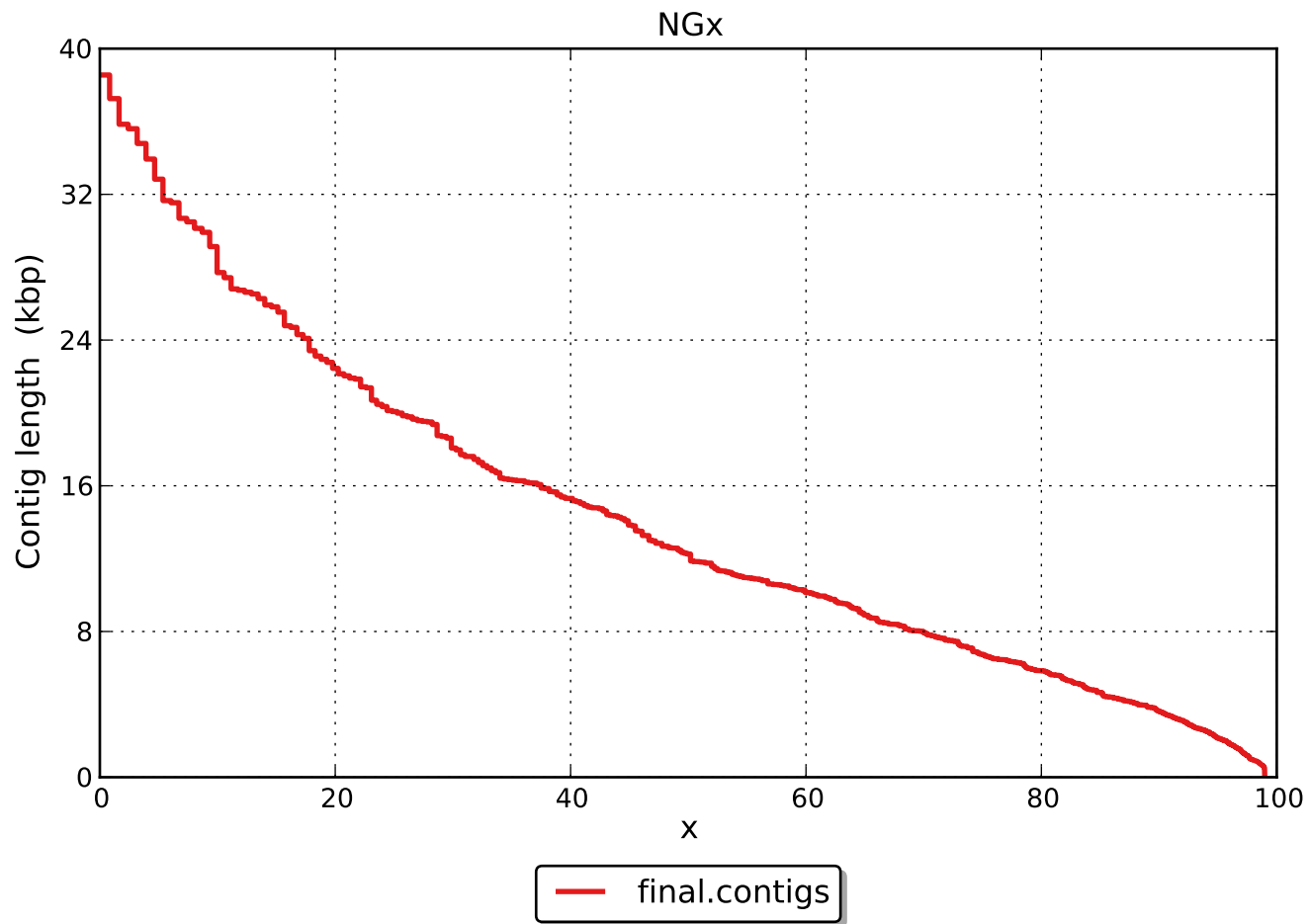
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

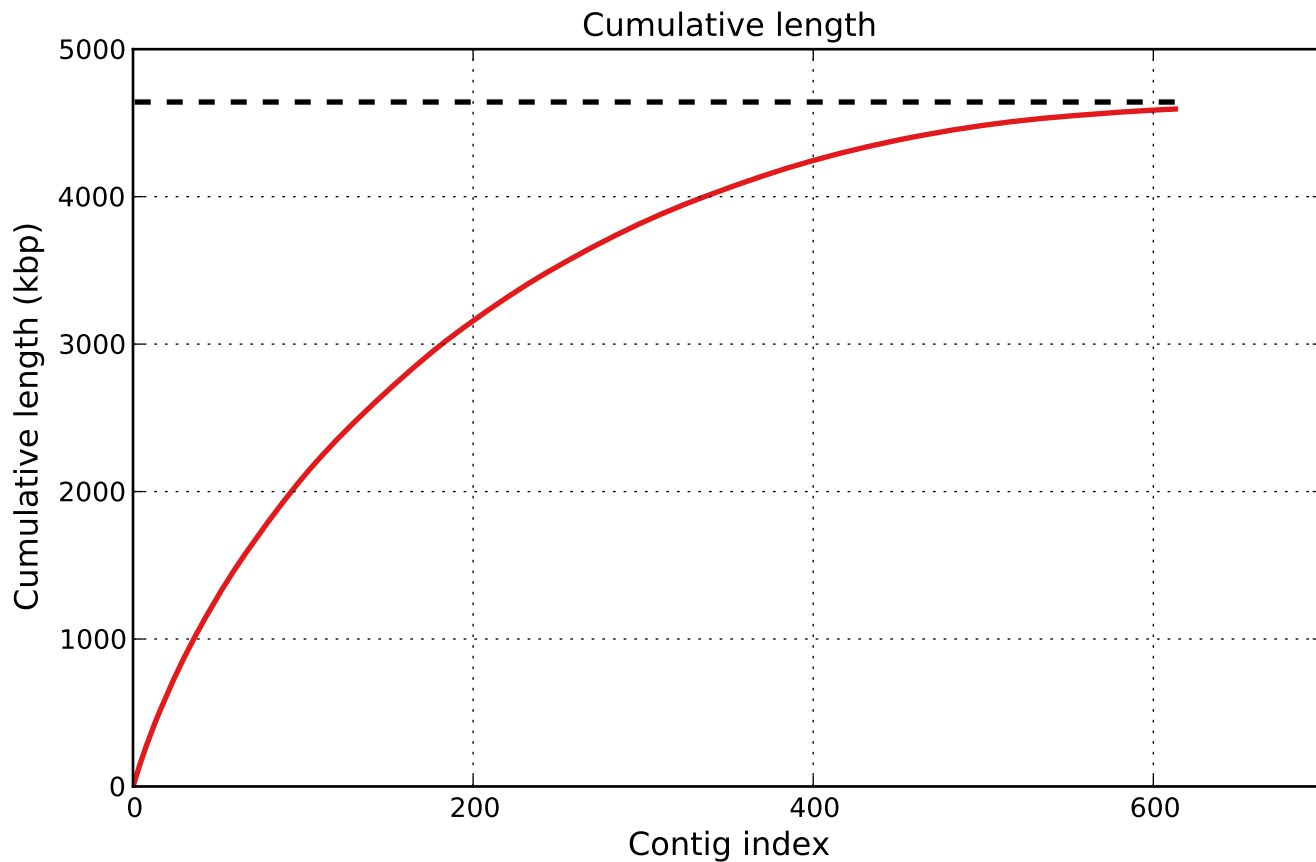
## Unaligned report

	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

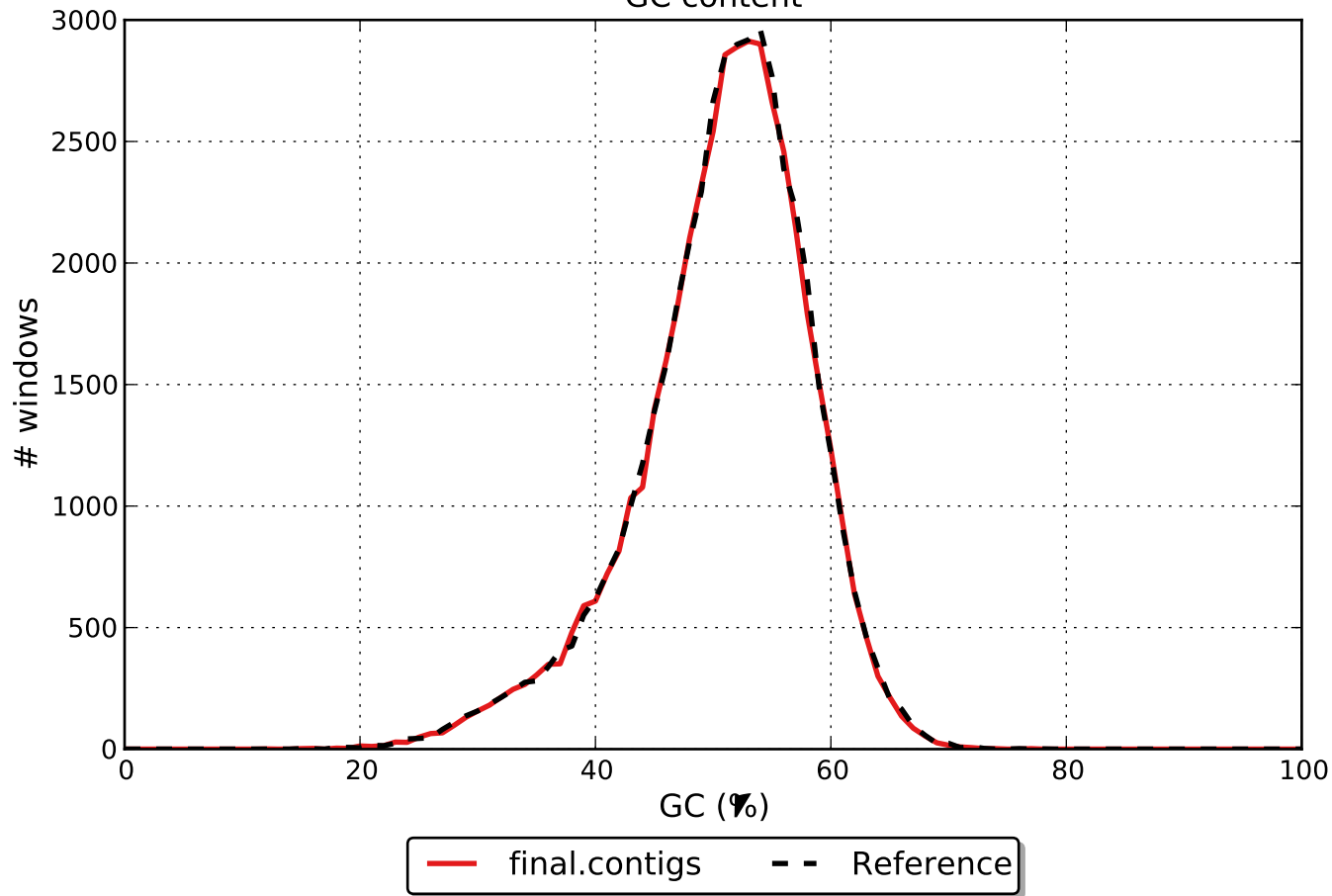
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).







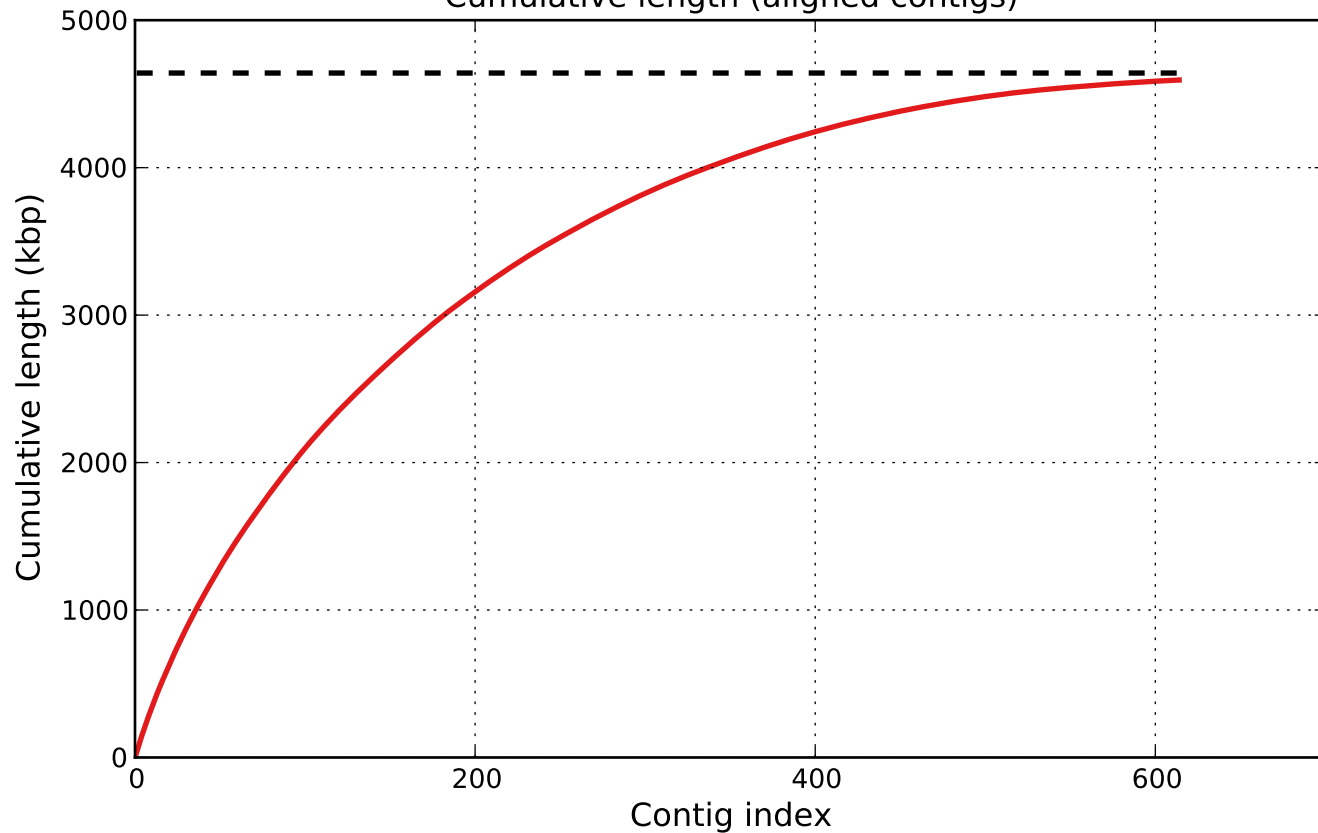
GC content



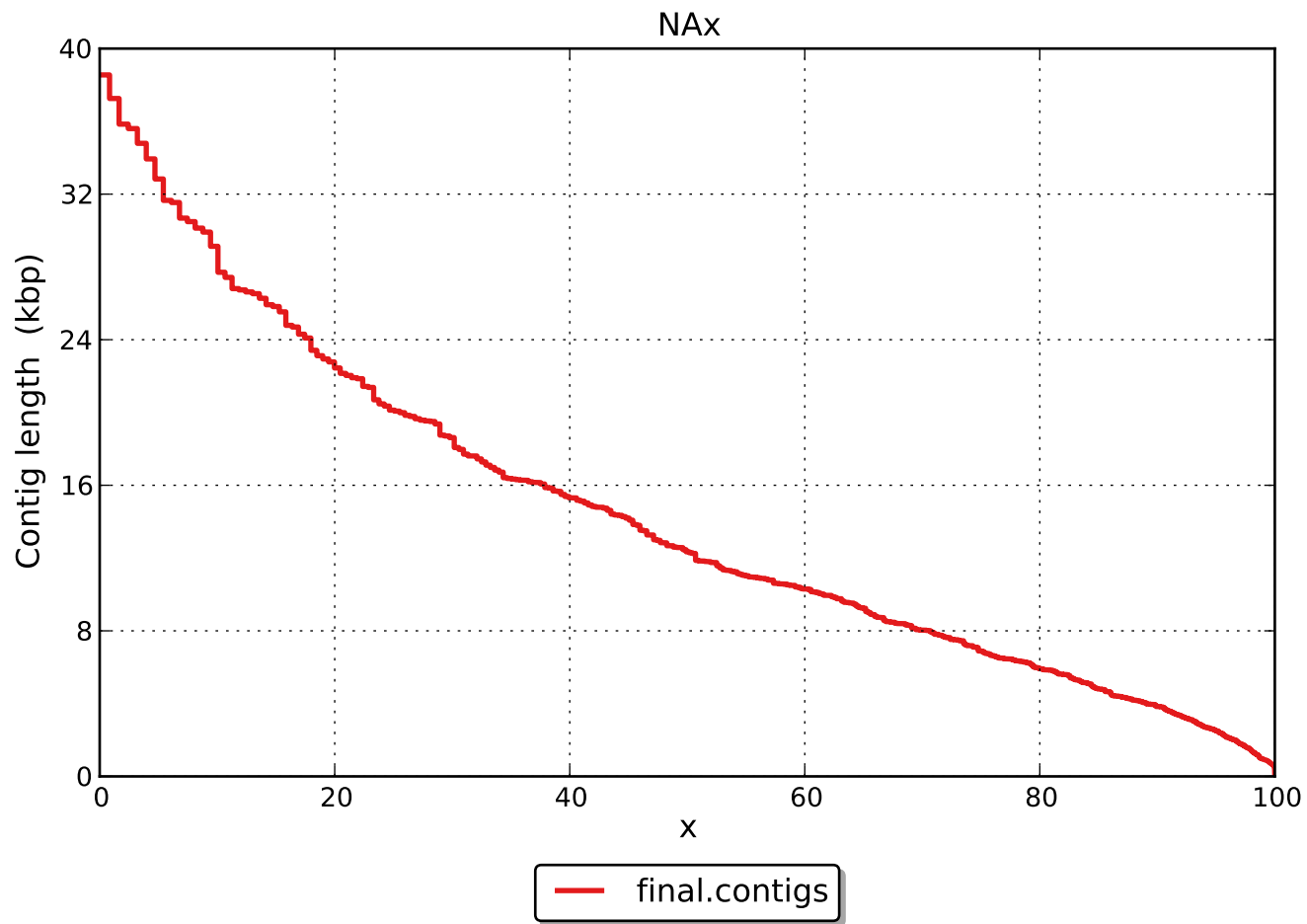




Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx

