

## Report

	final.contigs
# contigs (>= 0 bp)	738
# contigs (>= 1000 bp)	593
Total length (>= 0 bp)	3756986
Total length (>= 1000 bp)	3689909
# contigs	638
Largest contig	37555
Total length	3726052
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.26
N50	9000
NG50	8978
N75	4921
NG75	4882
L50	127
LG50	130
L75	266
LG75	275
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.042
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.48
# indels per 100 kbp	0.00
Largest alignment	37555
NA50	9000
NGA50	8978
NA75	4921
NGA75	4882
LA50	127
LGA50	130
LA75	266
LGA75	275

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

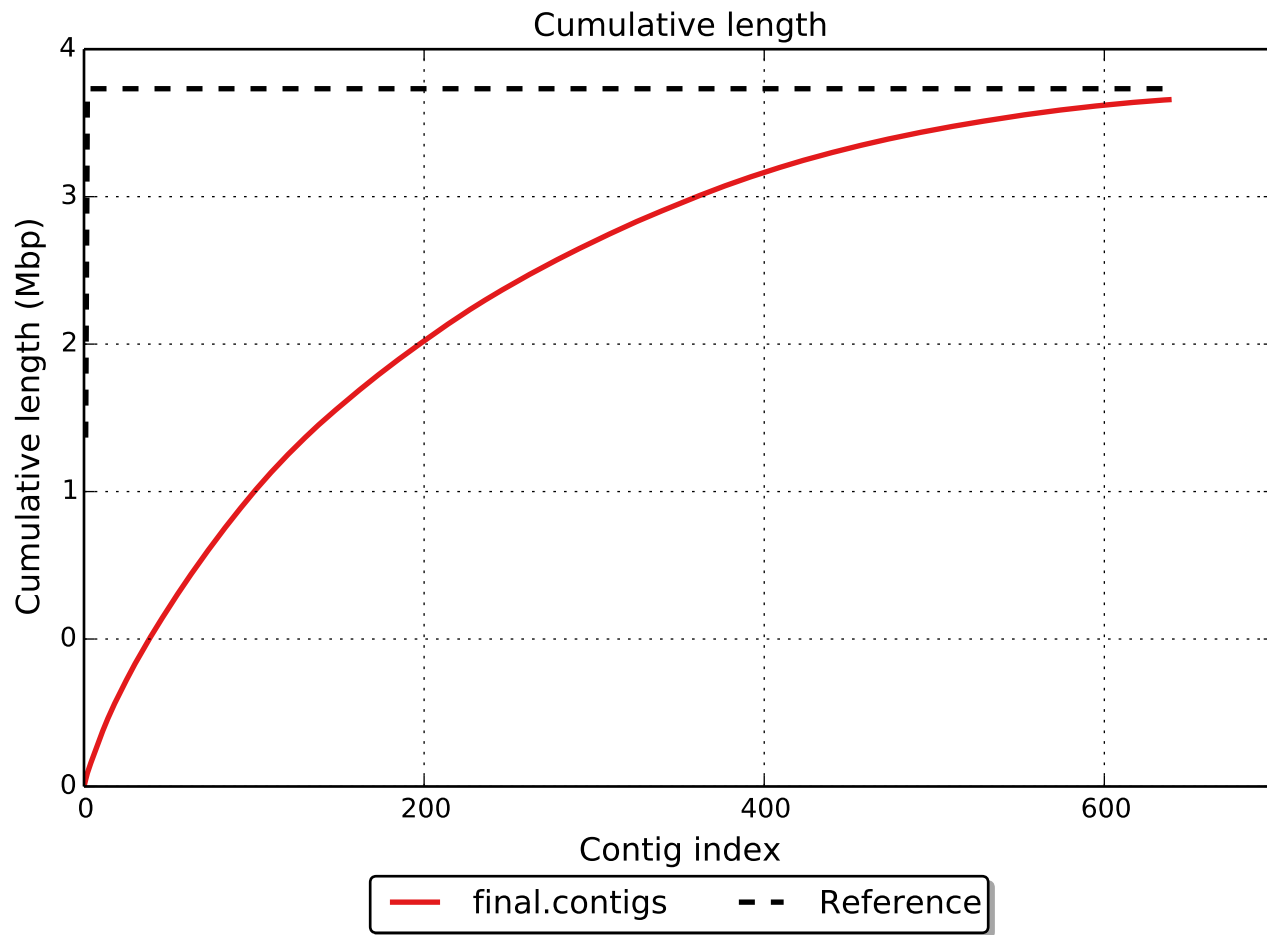
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	389
# indels	0
# short indels	0
# long indels	0
Indels length	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).

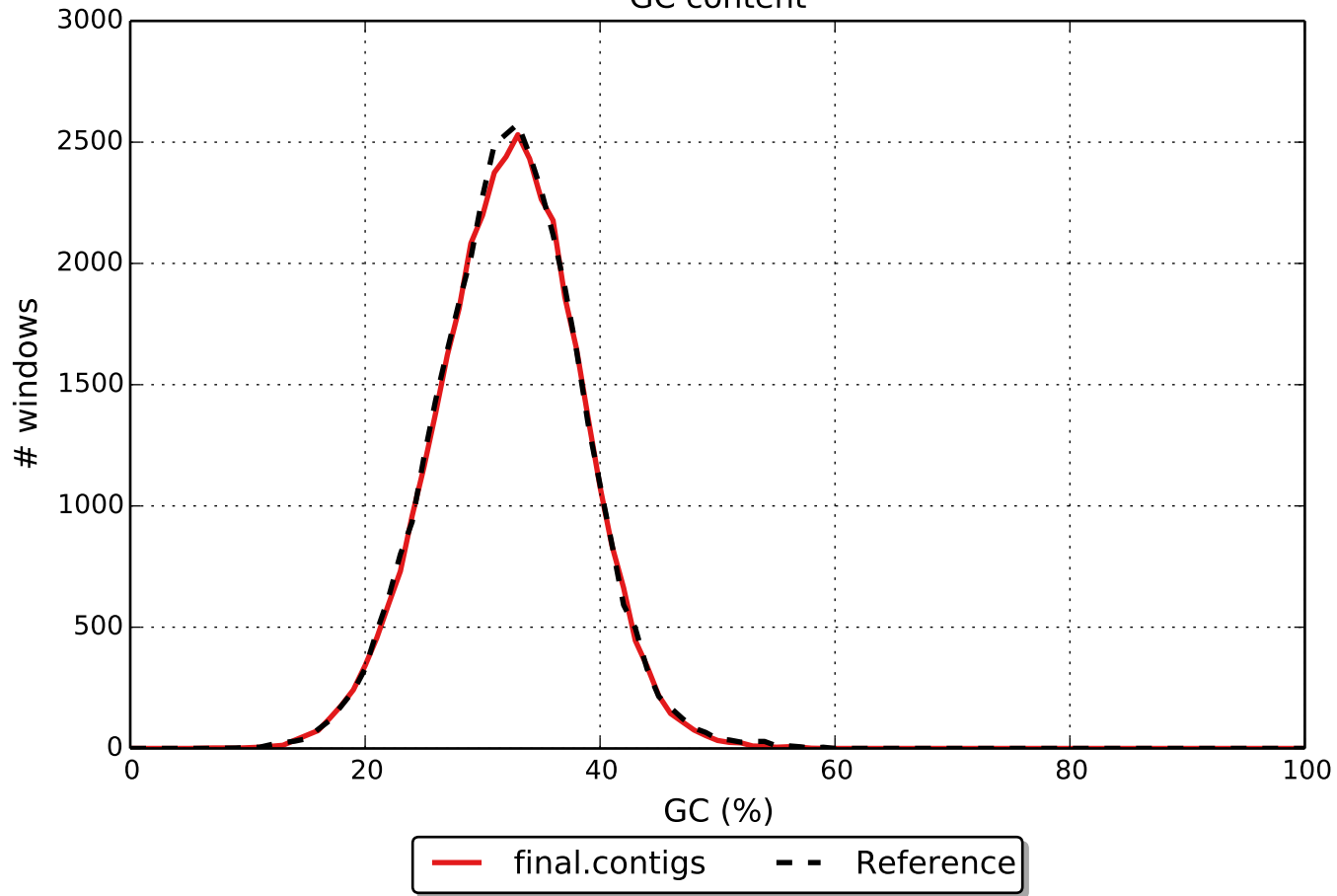
## Unaligned report

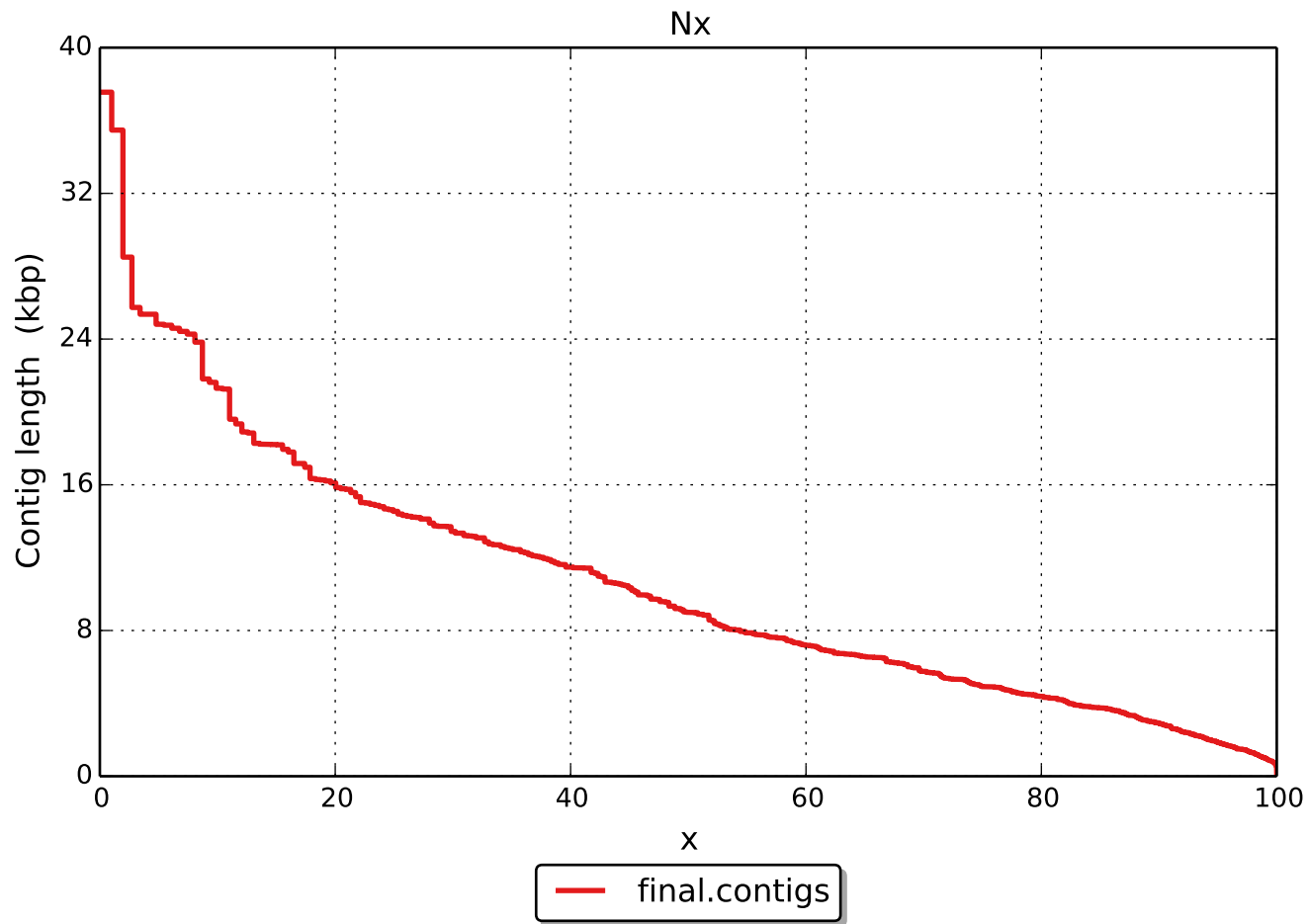
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

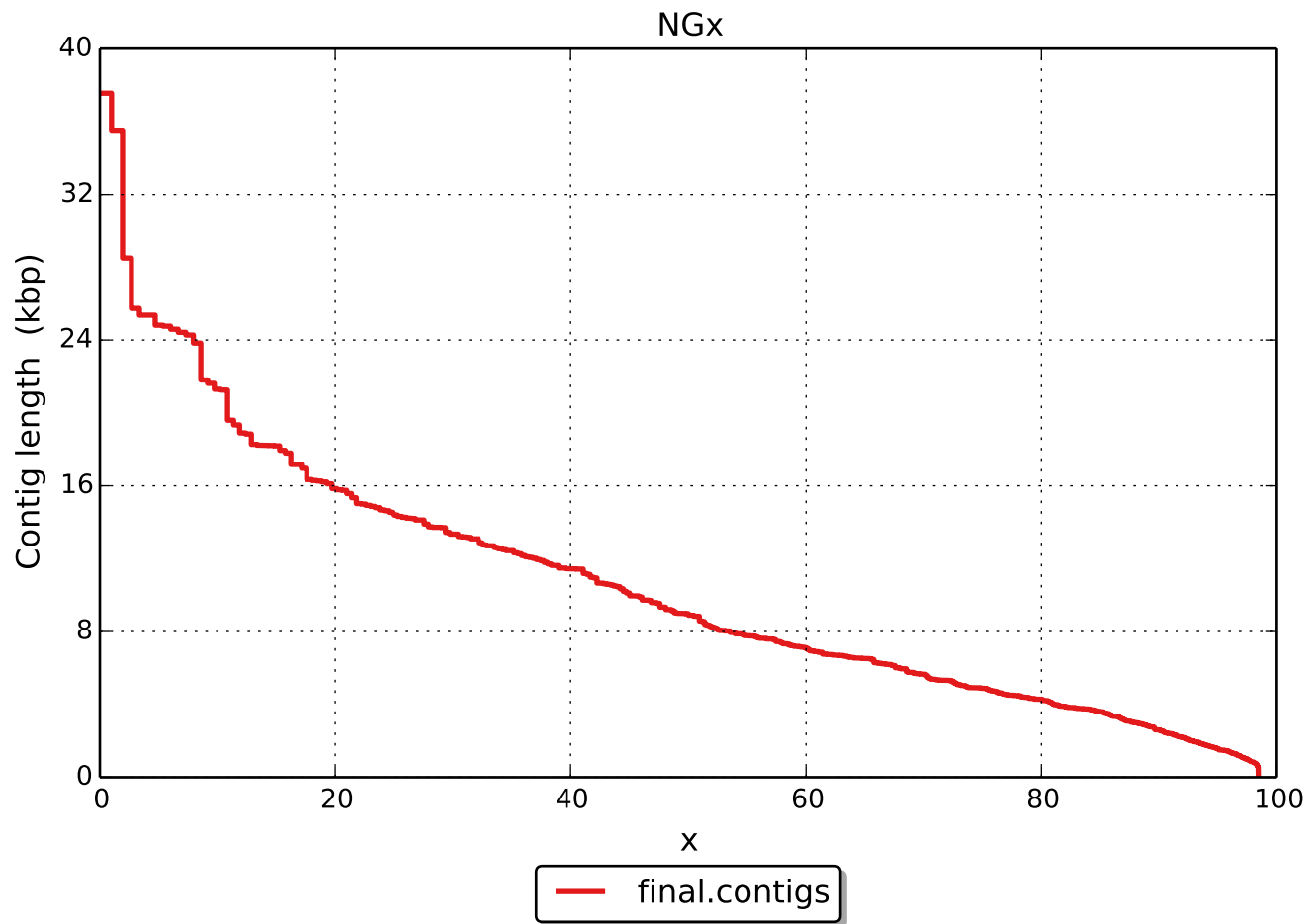
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



GC content



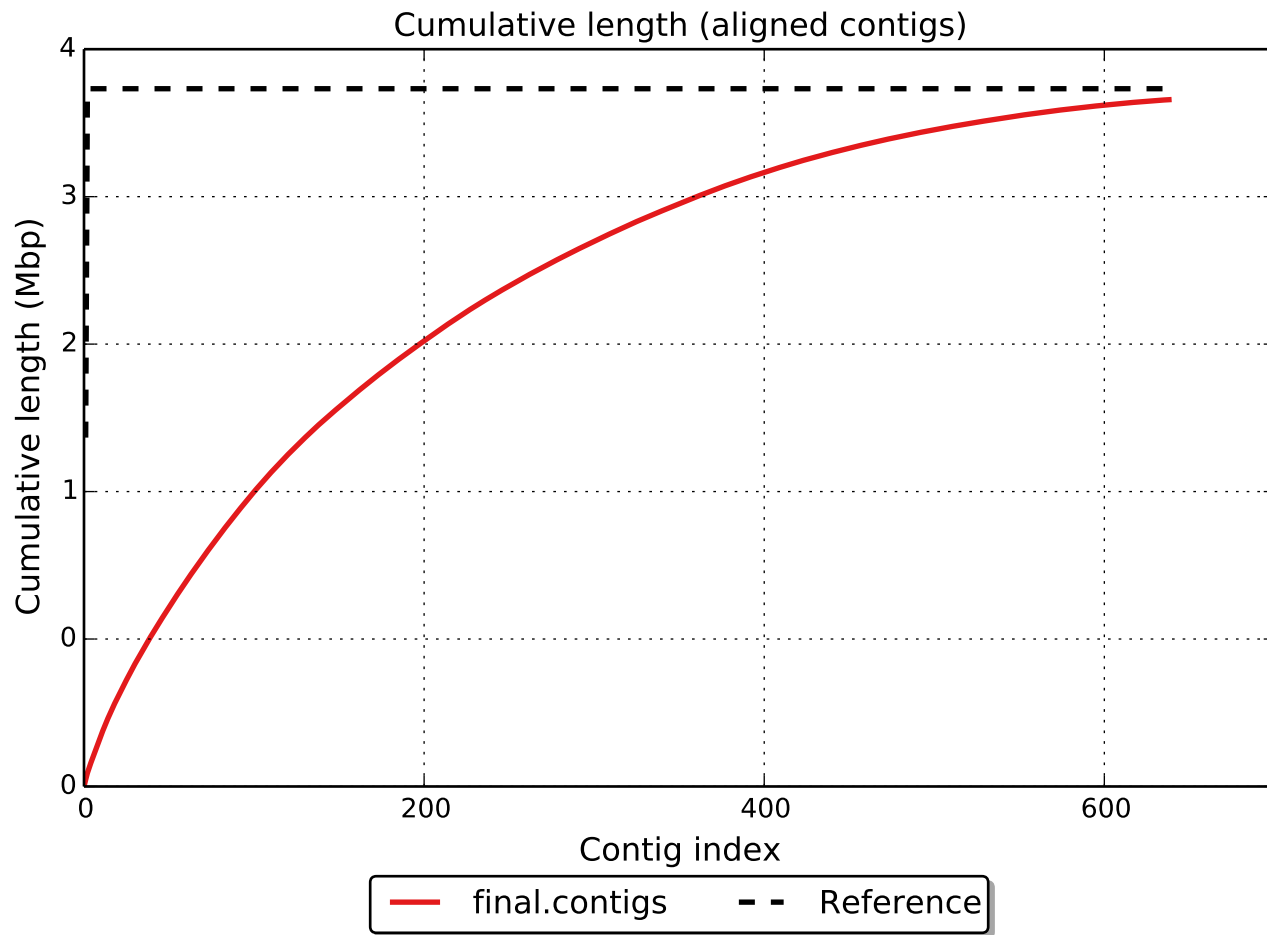


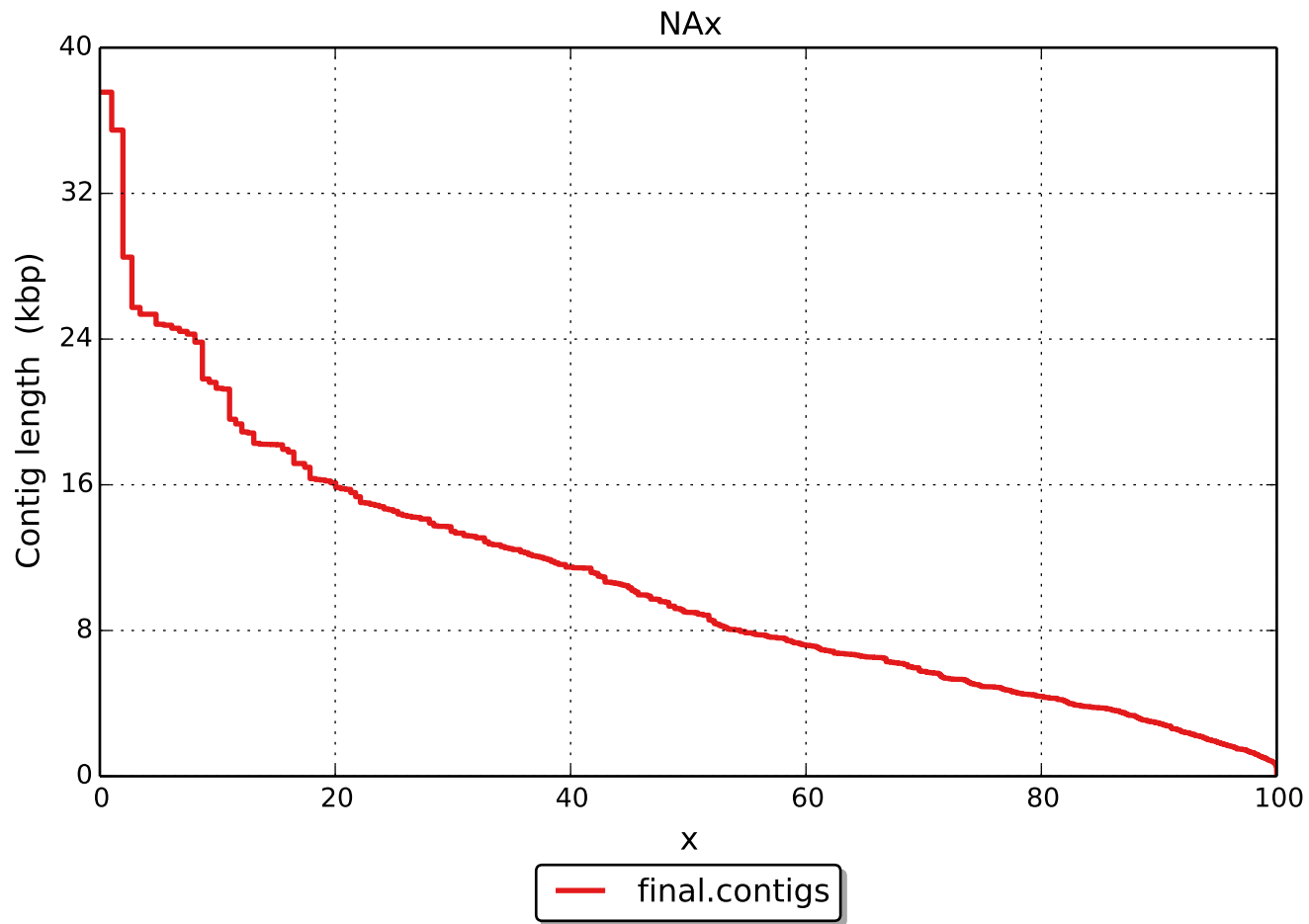


# Misassemblies









# NGAx

