

# Report

	final.contigs
# contigs (>= 0 bp)	638
# contigs (>= 1000 bp)	593
Total length (>= 0 bp)	3726052
Total length (>= 1000 bp)	3689909
# contigs	638
Largest contig	37555
Total length	3726052
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.26
N50	9000
NG50	14395
N75	4921
NG75	11893
L50	127
LG50	49
L75	266
LG75	85
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	7029
# local misassemblies	0
# unaligned contigs	216 + 85 part
Unaligned length	1719215
Genome fraction (%)	99.884
Duplication ratio	1.061
# N's per 100 kbp	0.00
# mismatches per 100 kbp	87.59
# indels per 100 kbp	0.00
Largest alignment	35473
NA50	1941
NGA50	9959
NGA75	5753
LA50	246
LGA50	61
LGA75	124

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

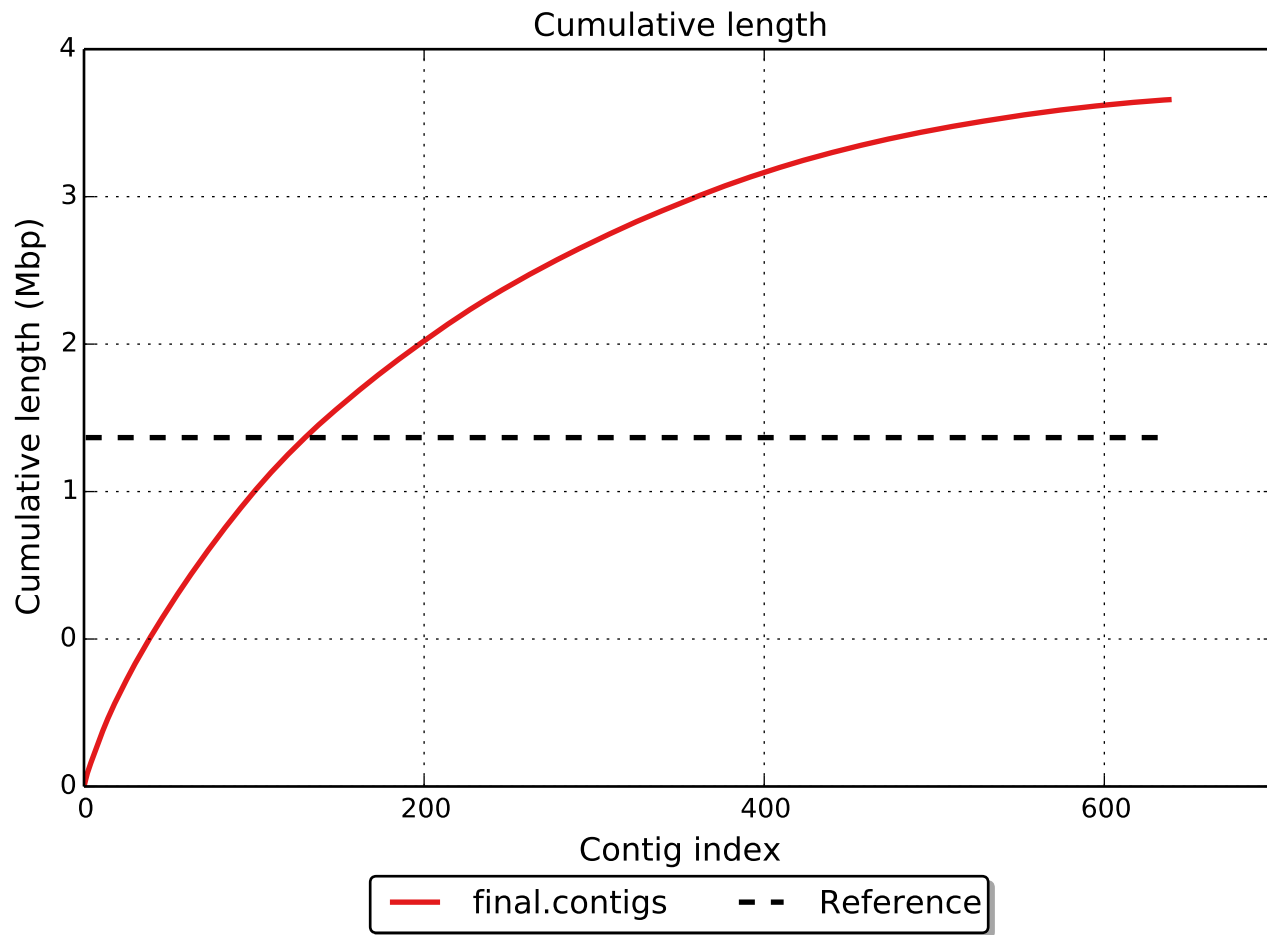
	final.contigs
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# possibly misassembled contigs	15
# misassembled contigs	4
Misassembled contigs length	7029
# local misassemblies	0
# mismatches	1656
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

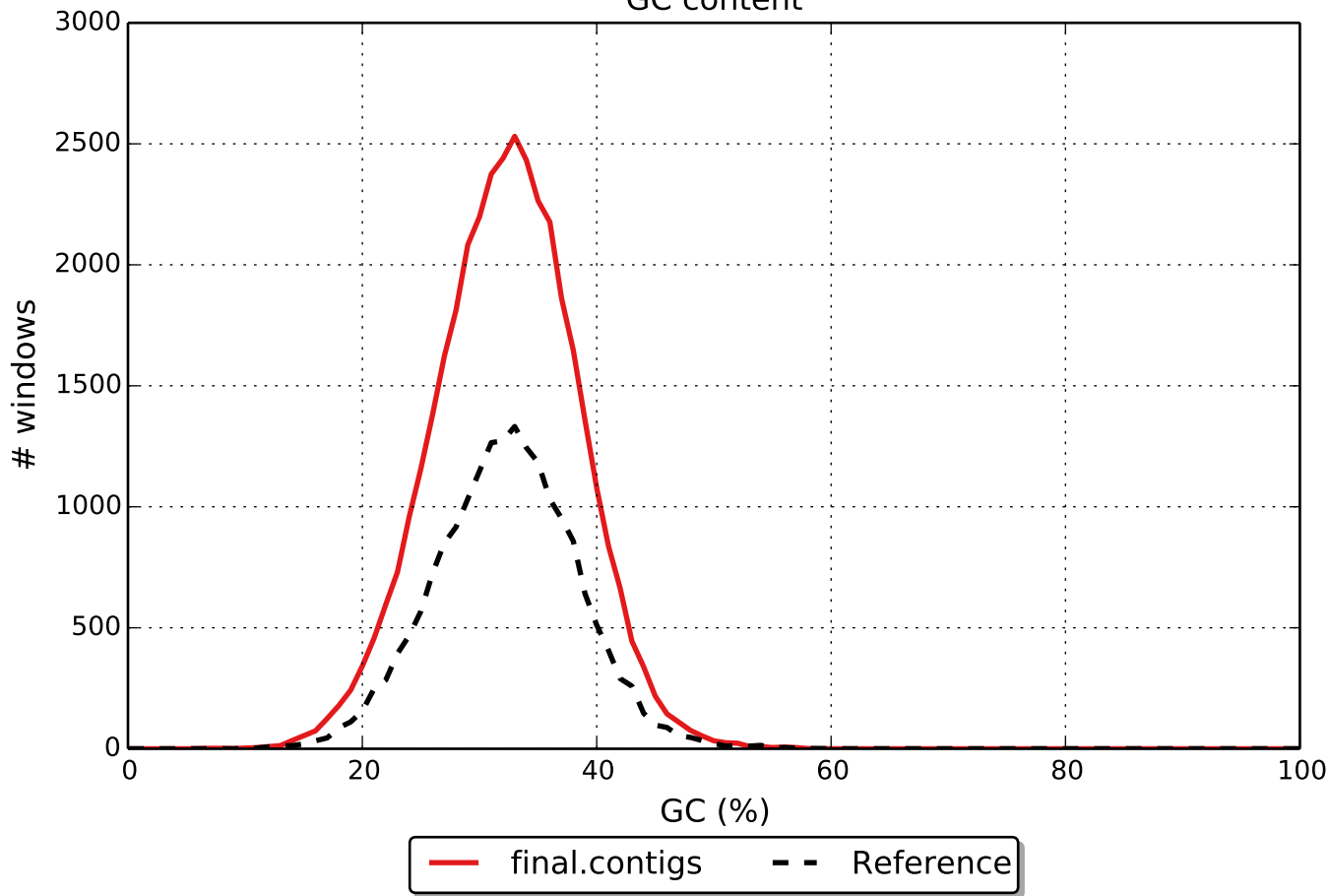
## Unaligned report

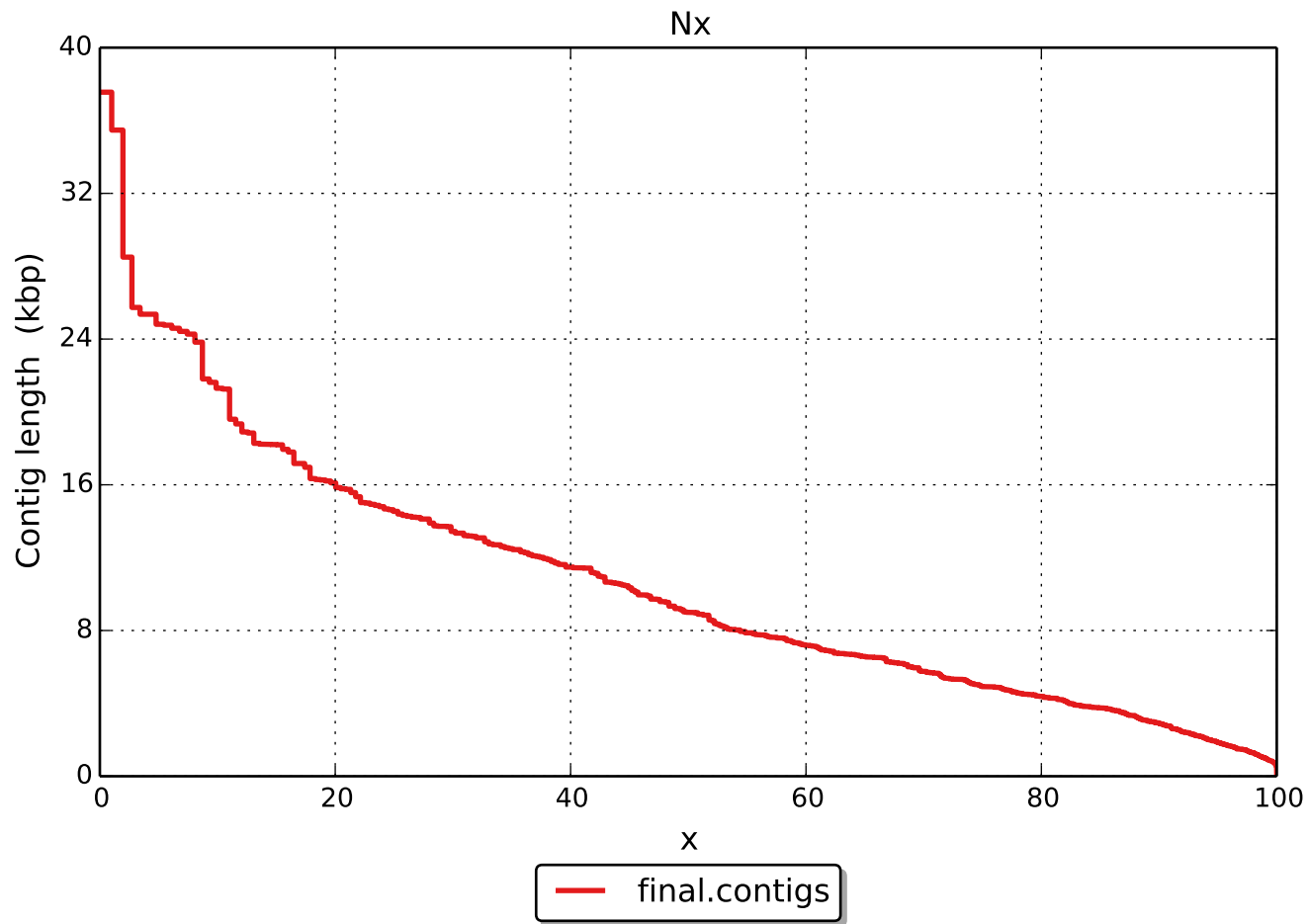
	final.contigs
# fully unaligned contigs	216
Fully unaligned length	1180356
# partially unaligned contigs	85
# with misassembly	7
# both parts are significant	14
Partially unaligned length	538859
# N's	0

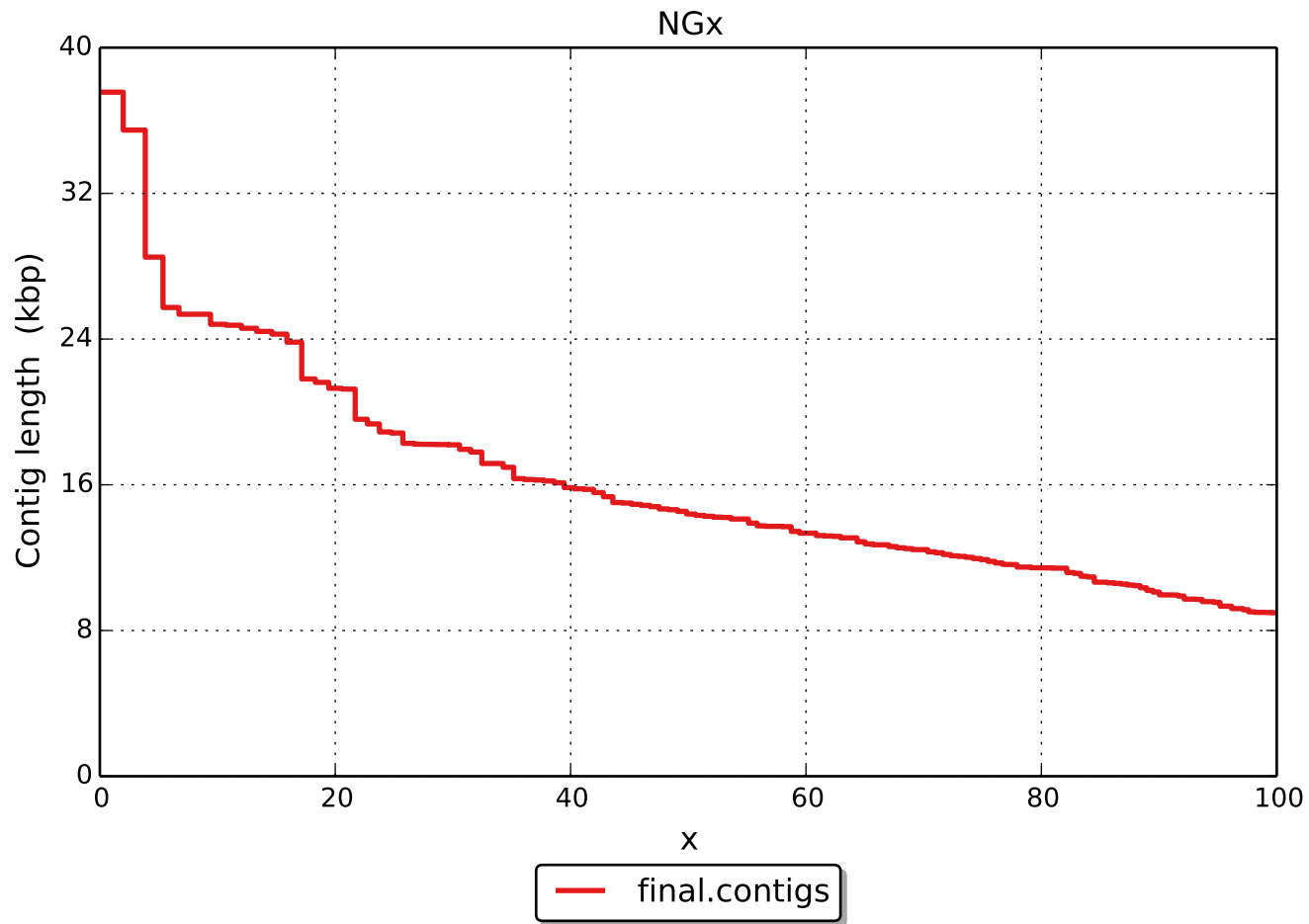
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

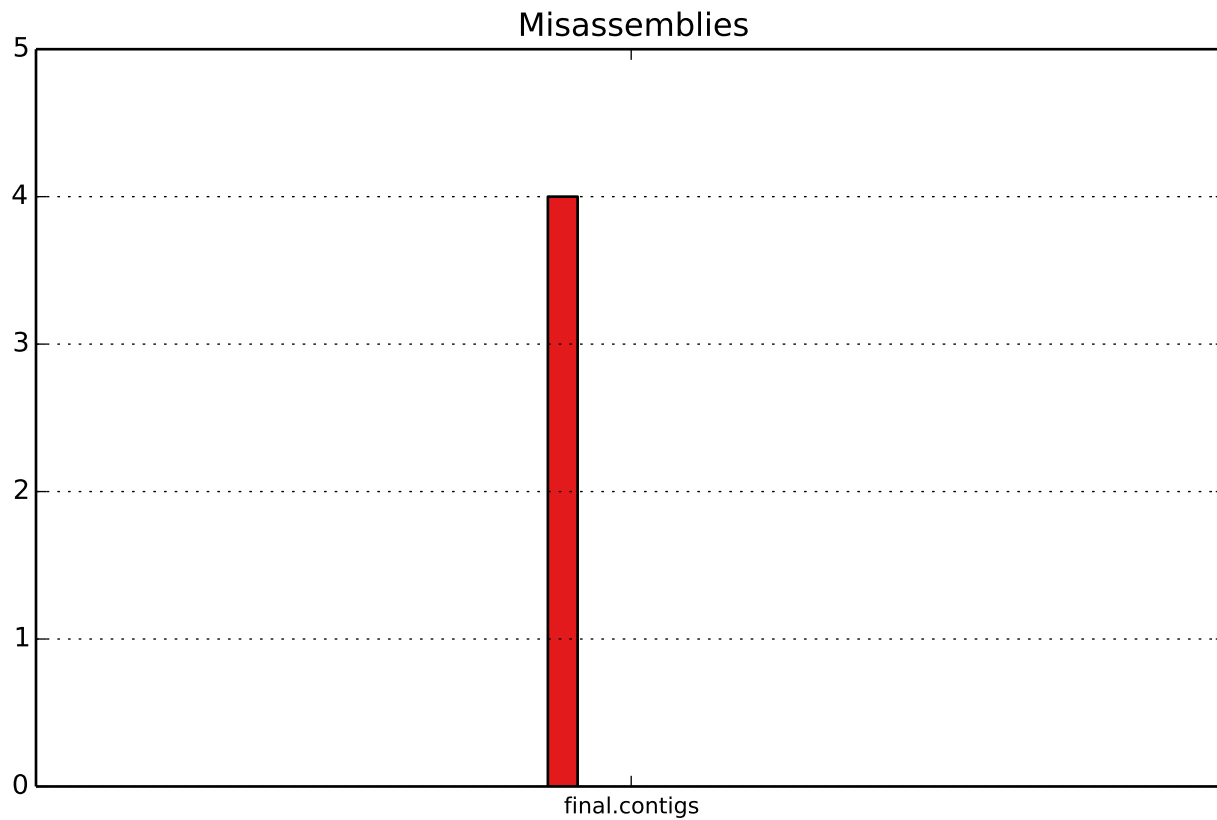


# GC content



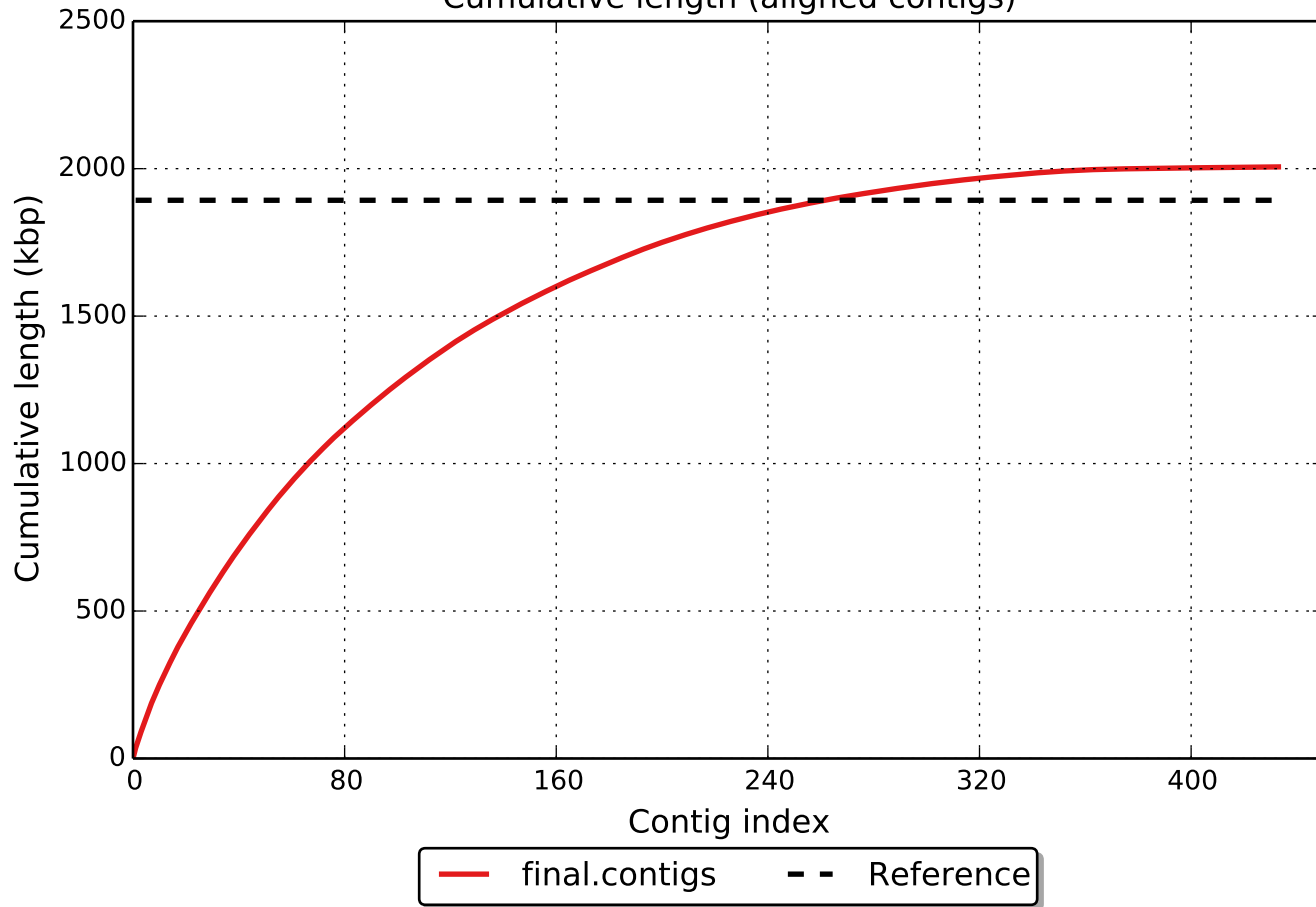


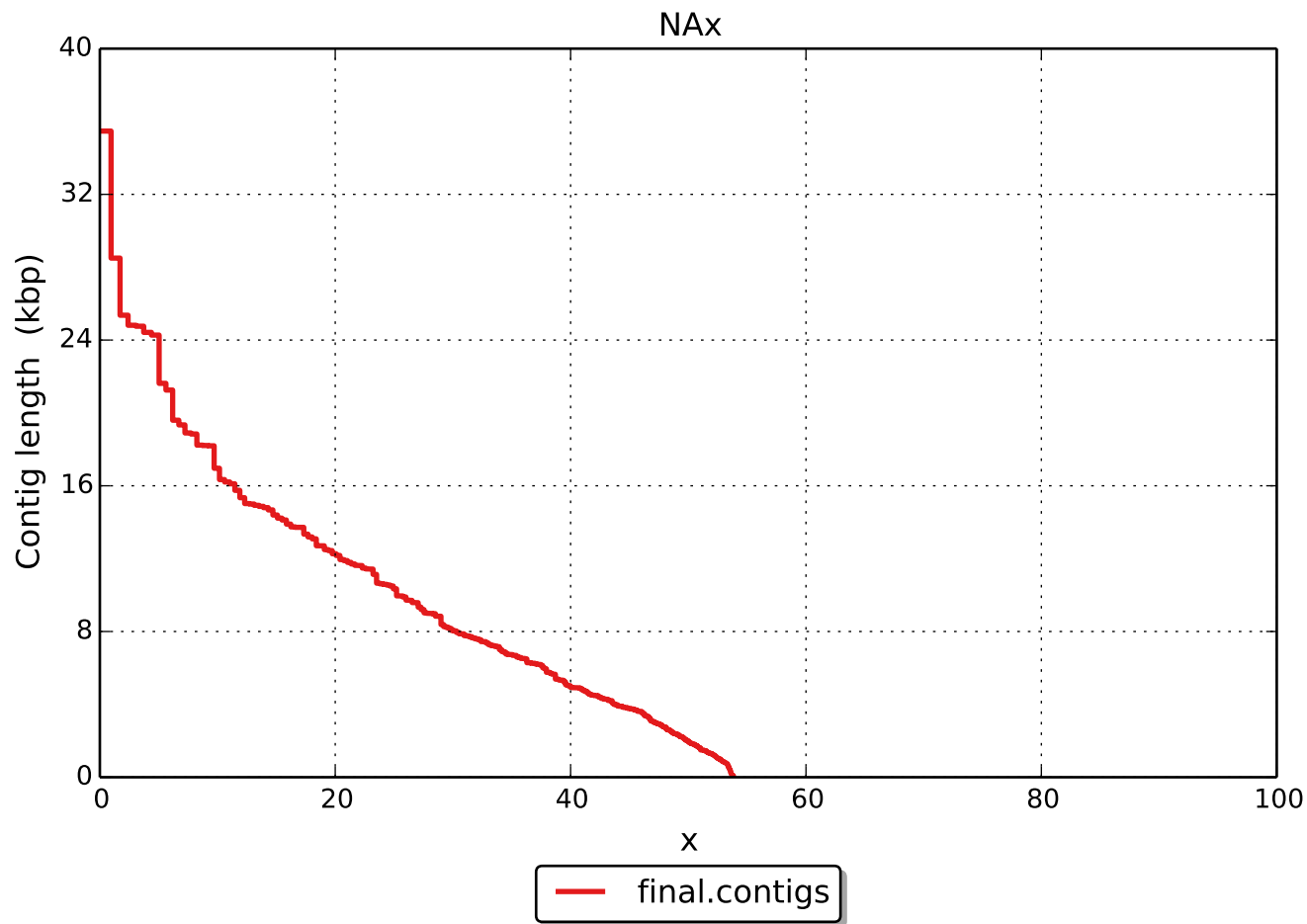






Cumulative length (aligned contigs)





# NGAx

