

## Report

	final.contigs
# contigs (>= 0 bp)	115
# contigs (>= 1000 bp)	107
Total length (>= 0 bp)	1292526
Total length (>= 1000 bp)	1289546
# contigs	107
Largest contig	53647
Total length	1289546
Reference length	1283598
GC (%)	26.31
Reference GC (%)	26.31
N50	18788
NG50	18788
N75	11480
NG75	11480
L50	23
LG50	23
L75	46
LG75	45
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	25473
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.718
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	102.35
# indels per 100 kbp	0.47
Largest alignment	53647
NA50	18788
NGA50	18788
NA75	11480
NGA75	11480
LA50	23
LGA50	23
LA75	46
LGA75	45

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	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	25473
# local misassemblies	0
# mismatches	1310
# indels	6
# short indels	6
# long indels	0
Indels length	6

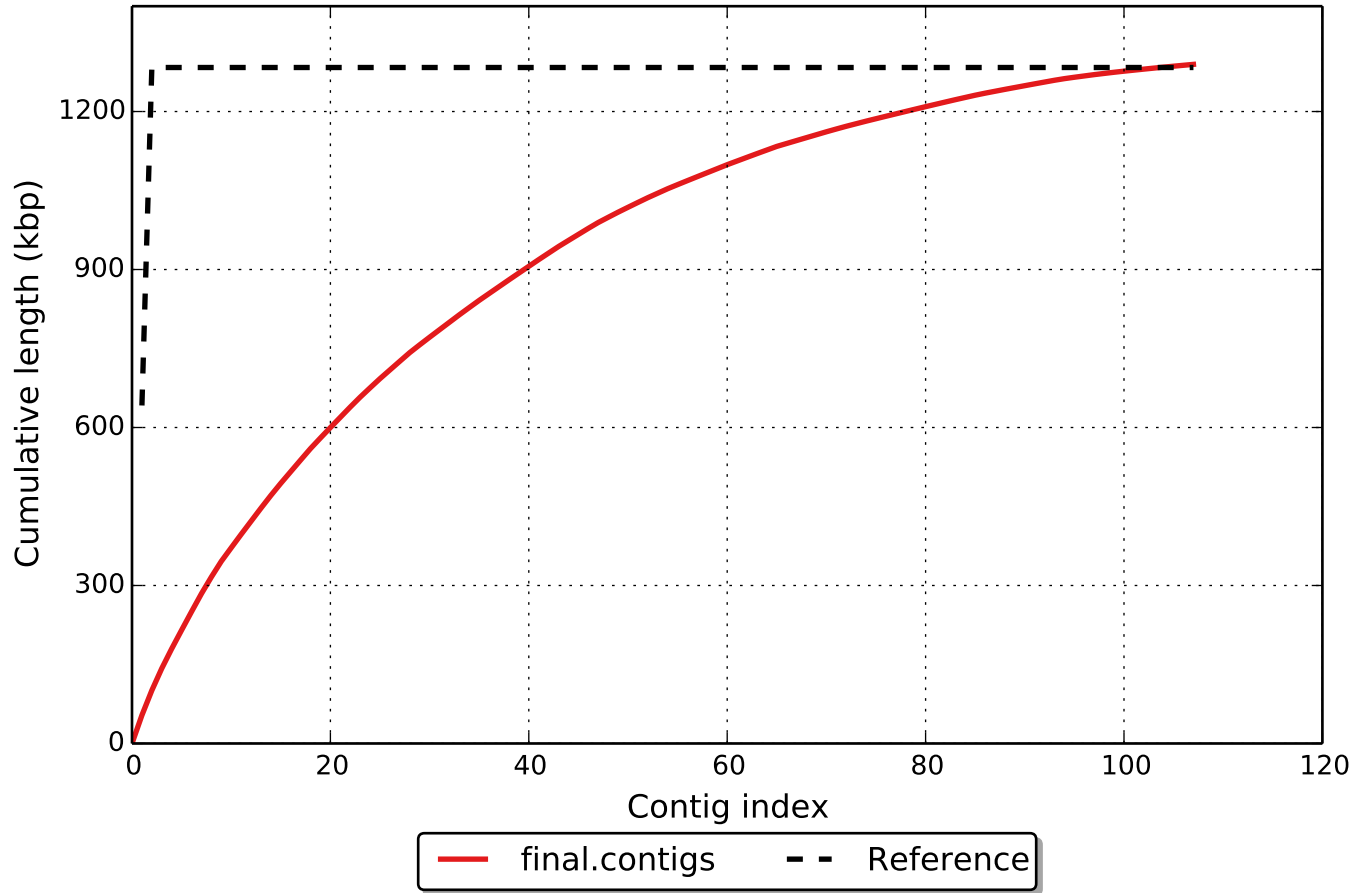
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

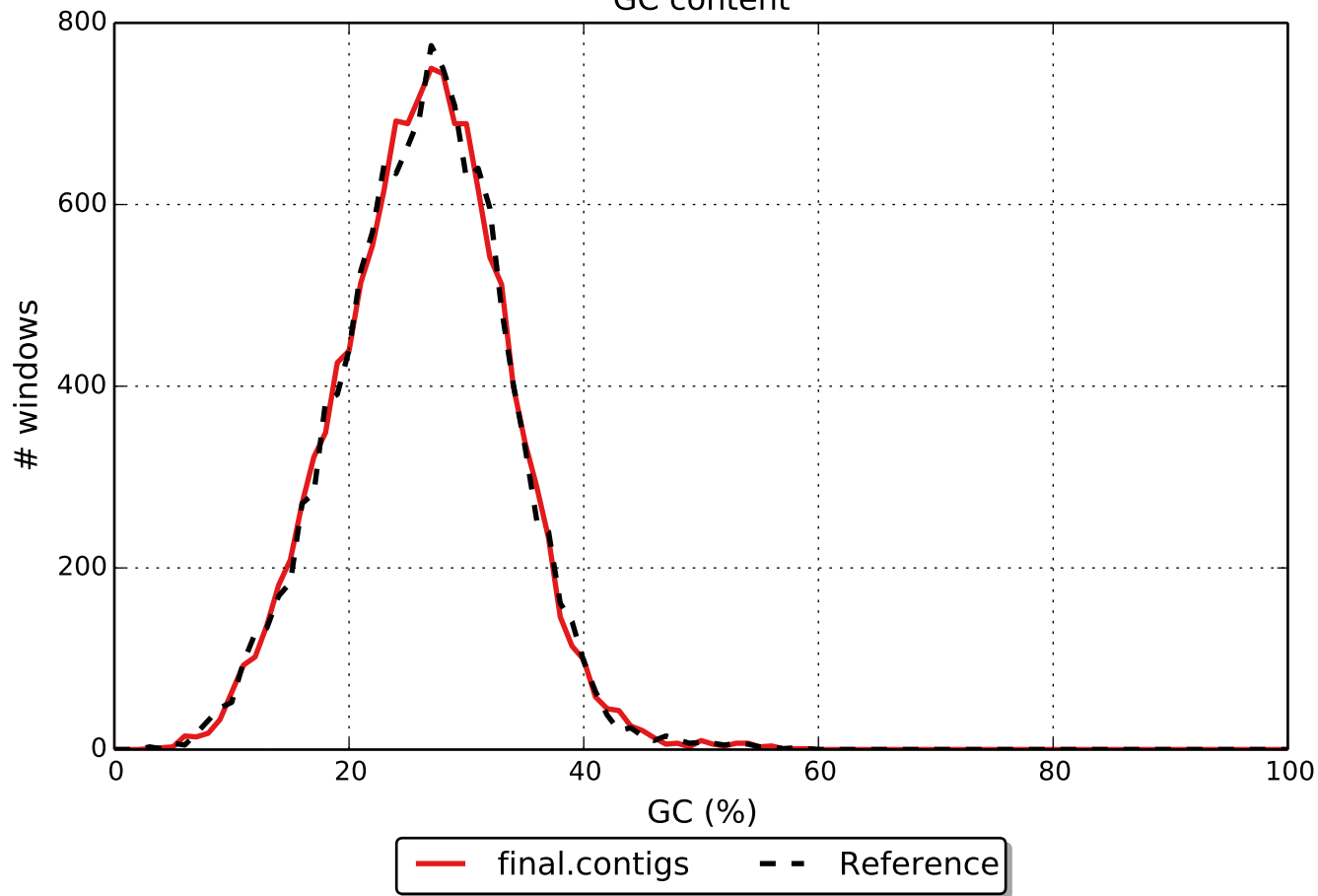
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

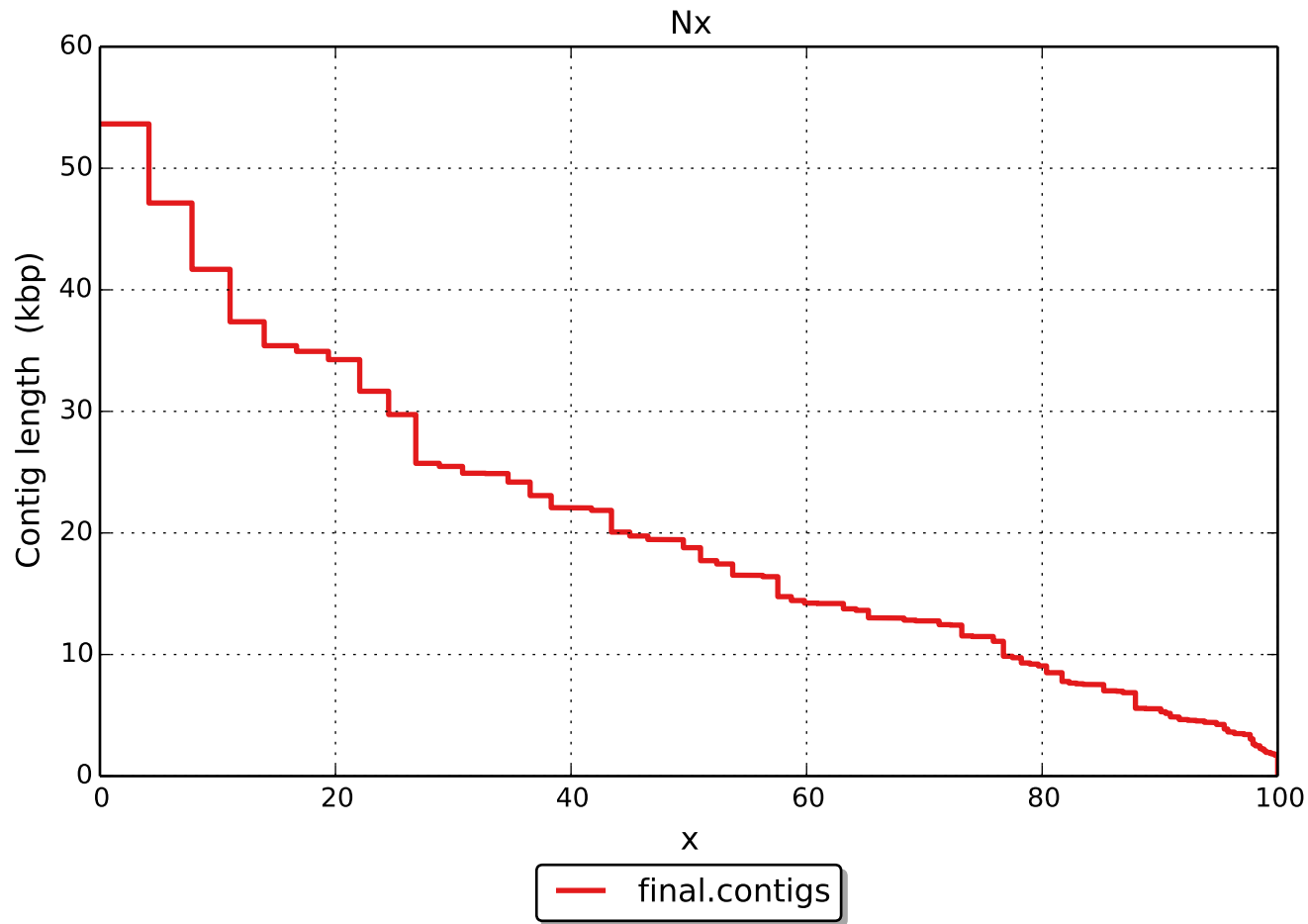
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

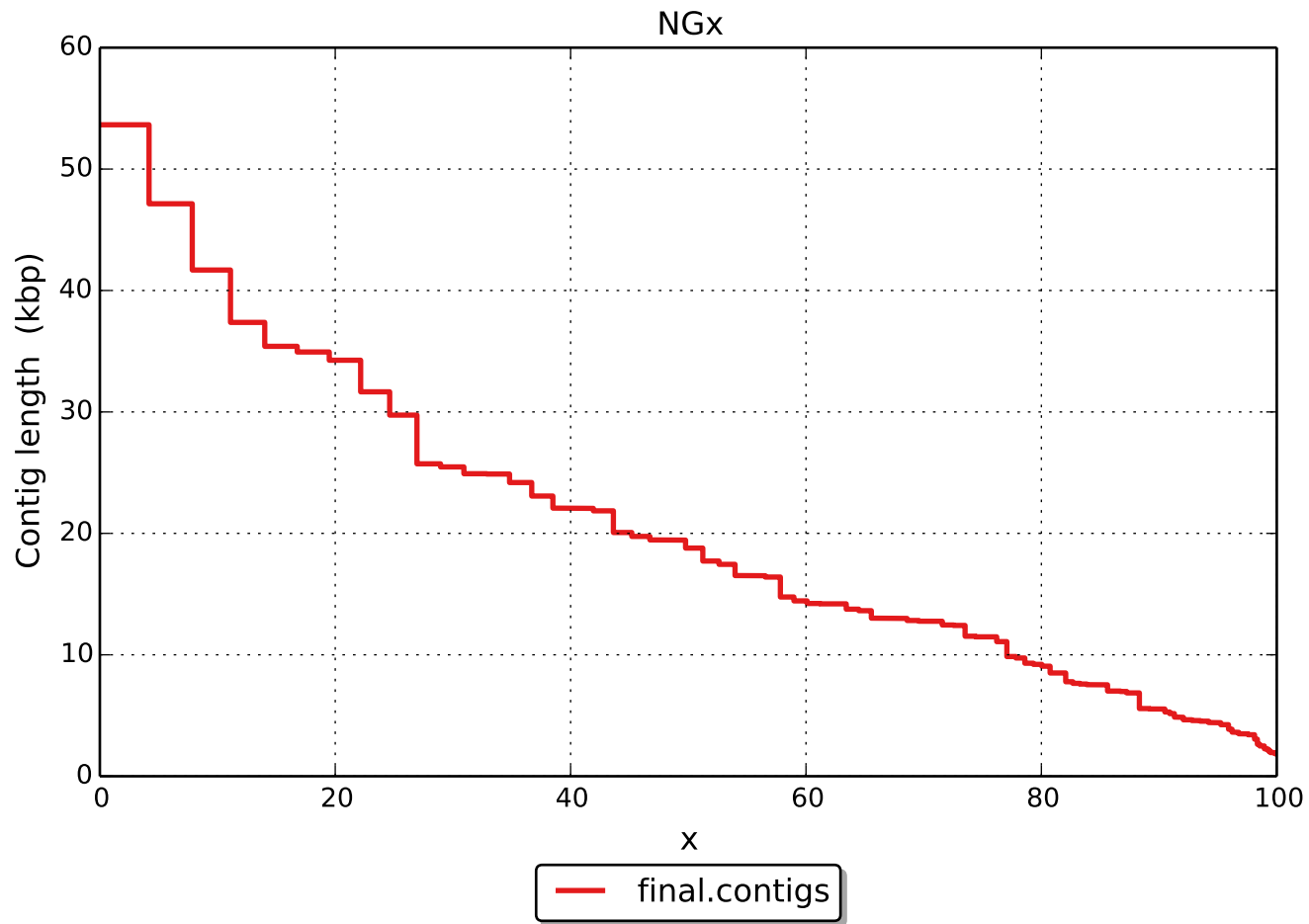
Cumulative length

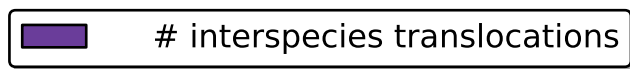
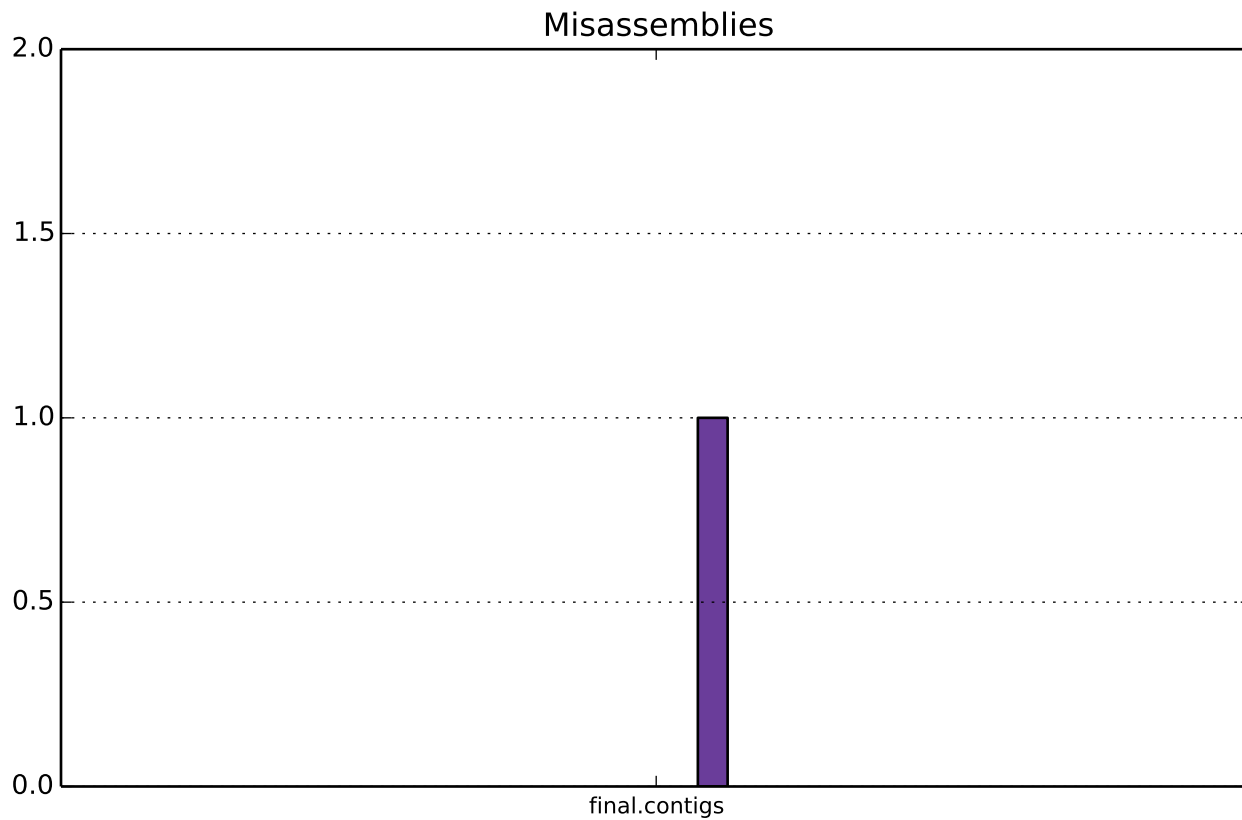


GC content



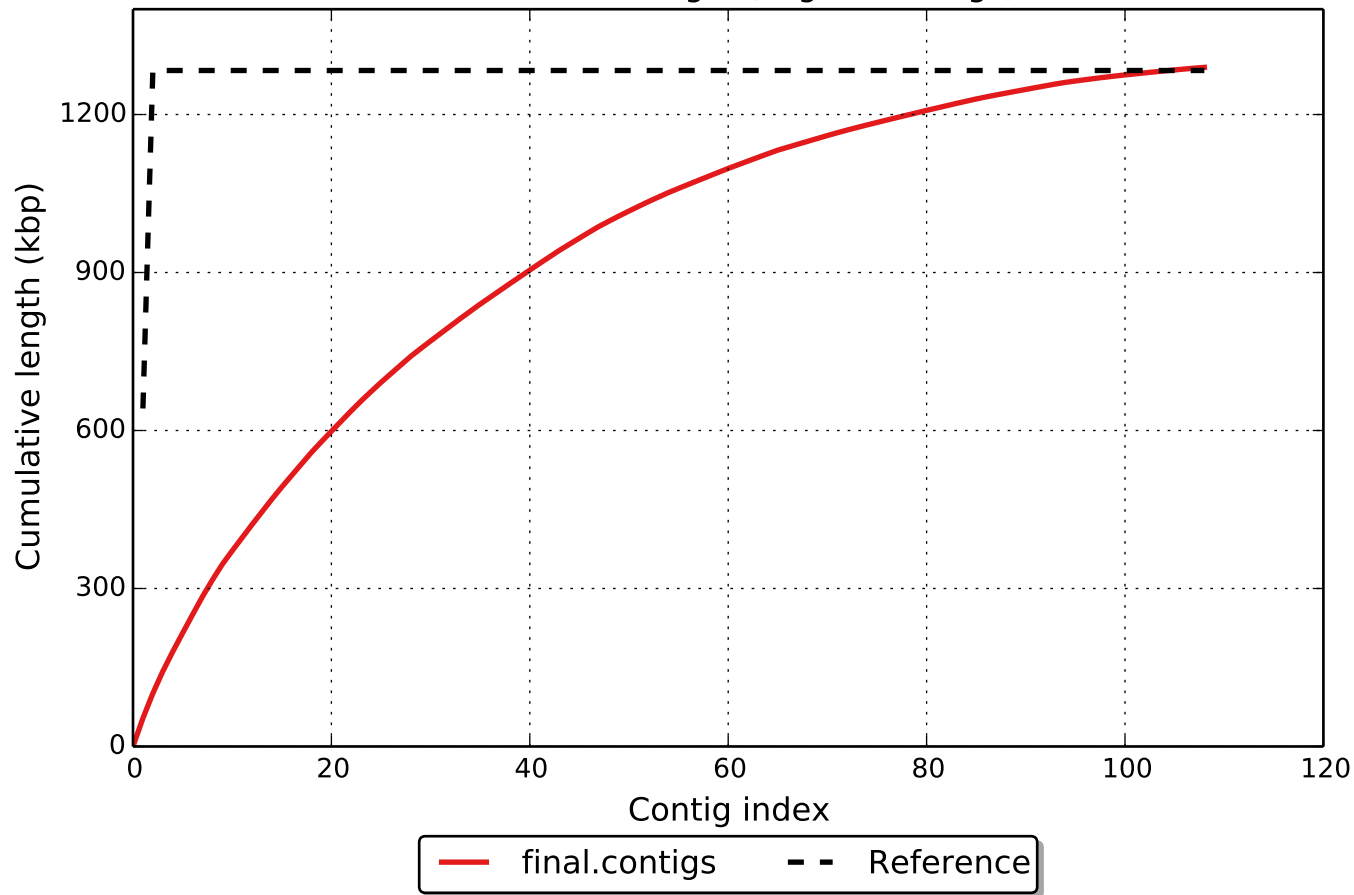


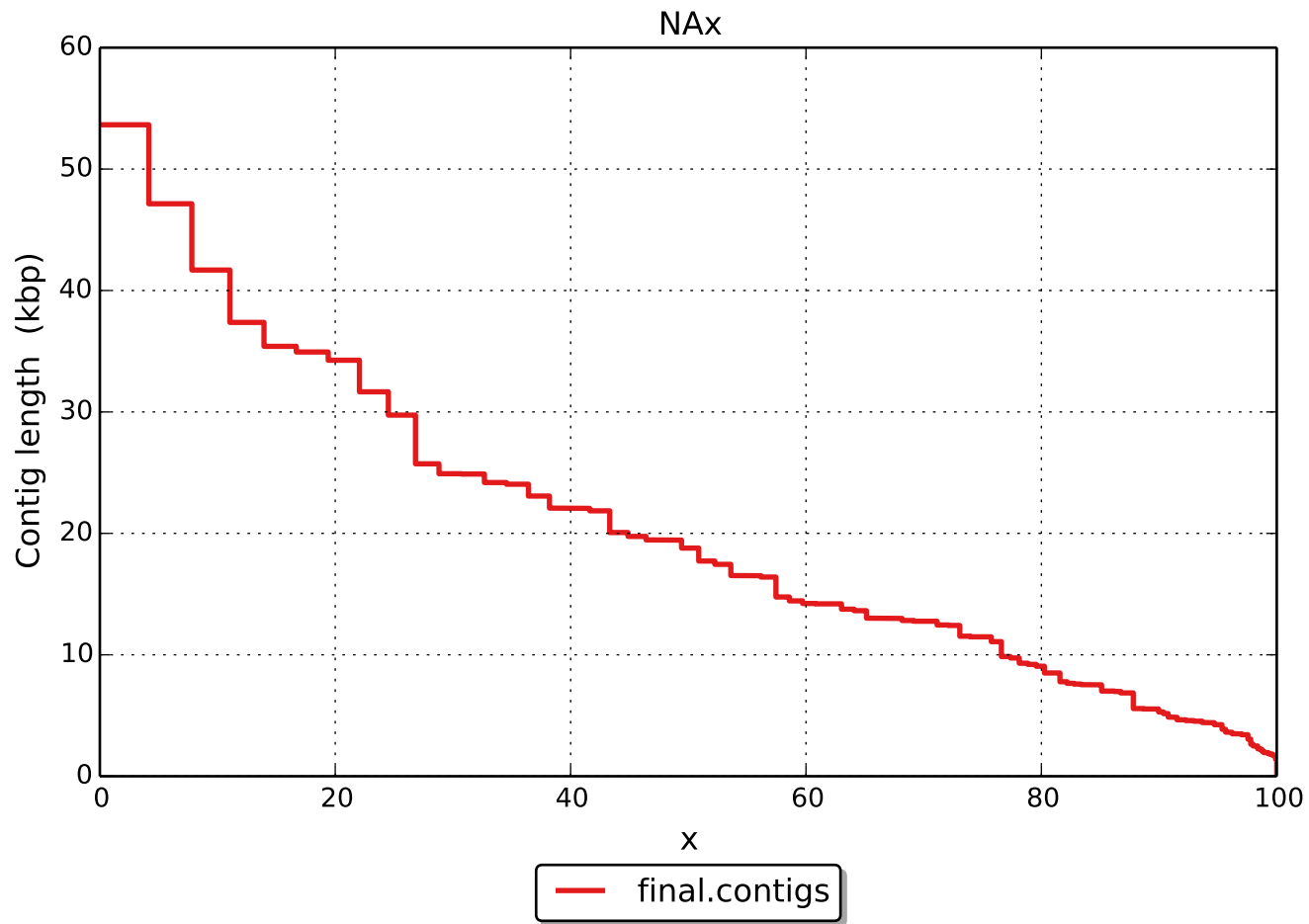






Cumulative length (aligned contigs)





NGAx

