

## Report

	final.contigs
# contigs (>= 0 bp)	245
# contigs (>= 1000 bp)	146
Total length (>= 0 bp)	641029
Total length (>= 1000 bp)	575096
# contigs	245
Largest contig	15816
Total length	641029
Reference length	615980
GC (%)	25.36
Reference GC (%)	25.34
N50	4661
NG50	4800
N75	2314
NG75	2523
L50	42
LG50	39
L75	91
LG75	83
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	4545
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.456
Duplication ratio	1.068
# N's per 100 kbp	0.00
# mismatches per 100 kbp	658.16
# indels per 100 kbp	0.00
Largest alignment	15816
NA50	4661
NGA50	4800
NA75	2314
NGA75	2523
LA50	42
LGA50	39
LA75	91
LGA75	83

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

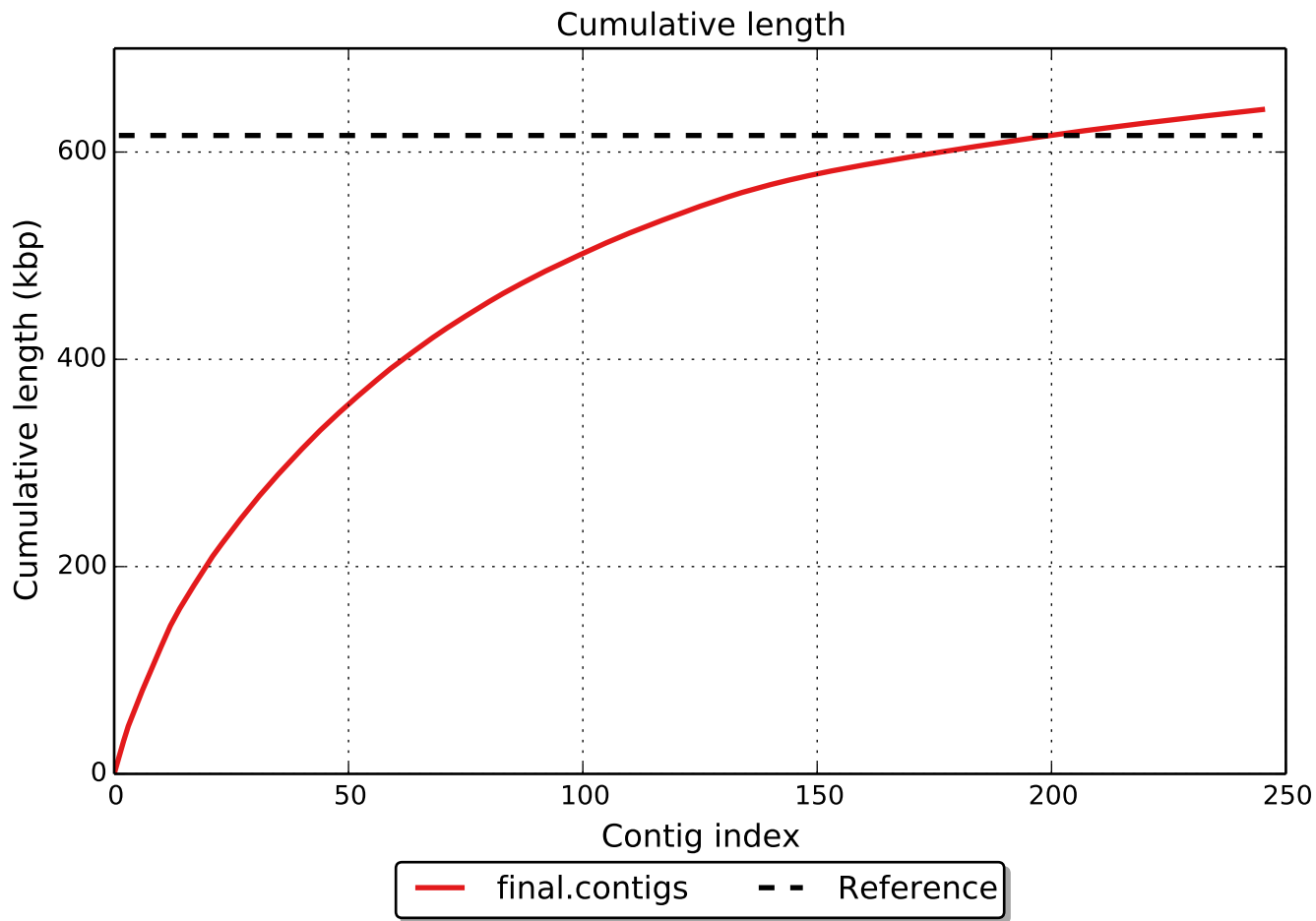
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	4545
# local misassemblies	0
# mismatches	3951
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

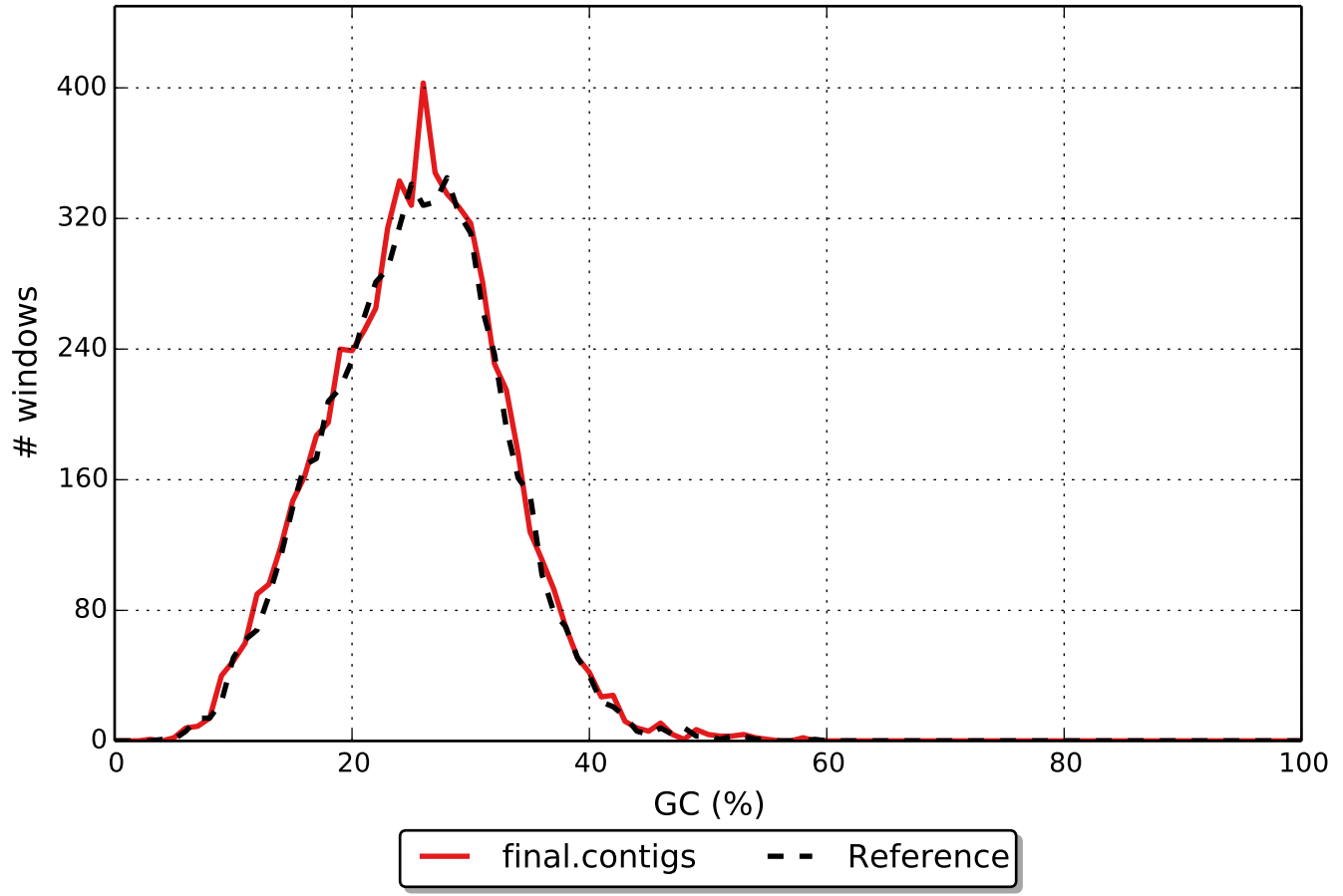
## Unaligned report

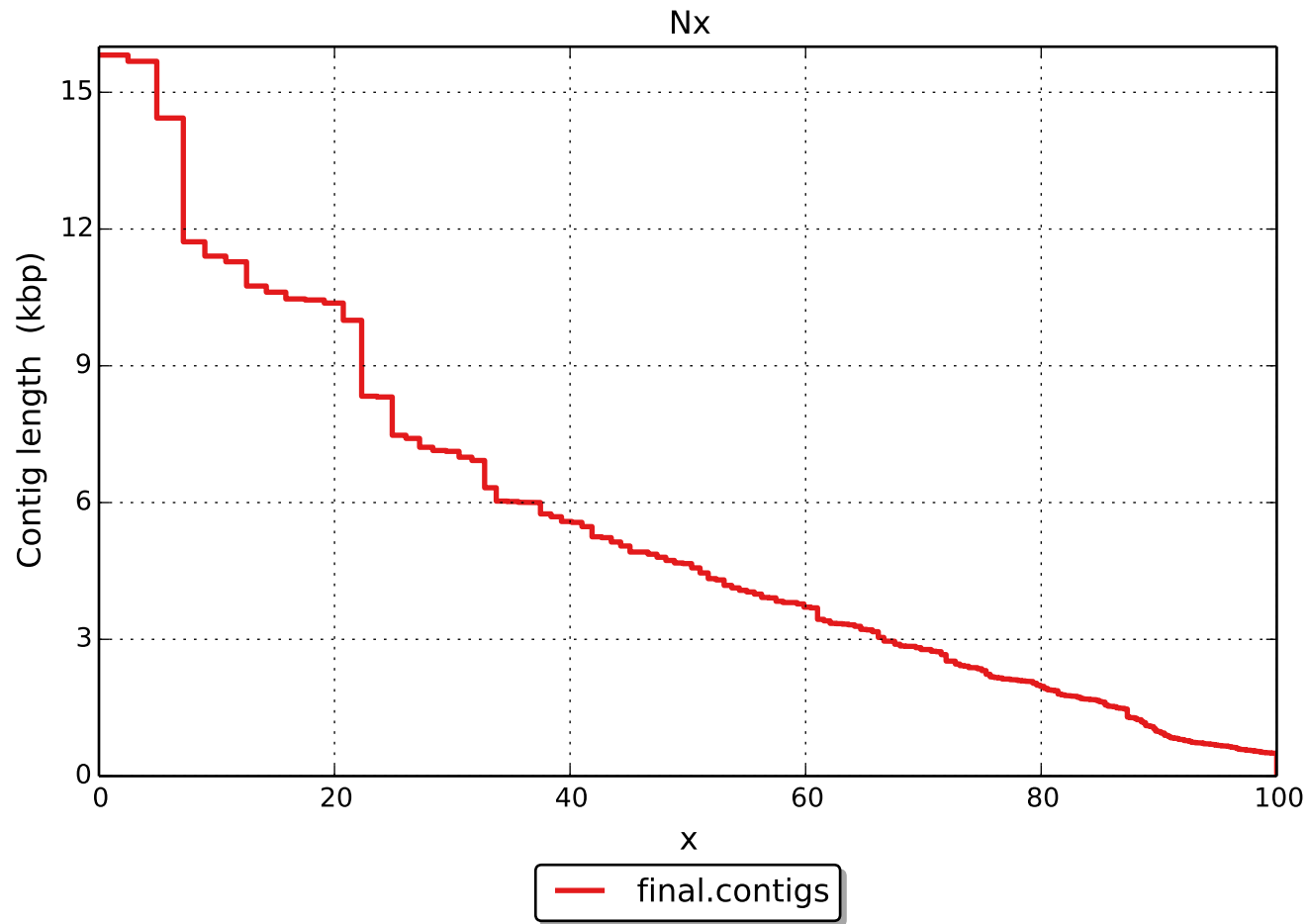
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

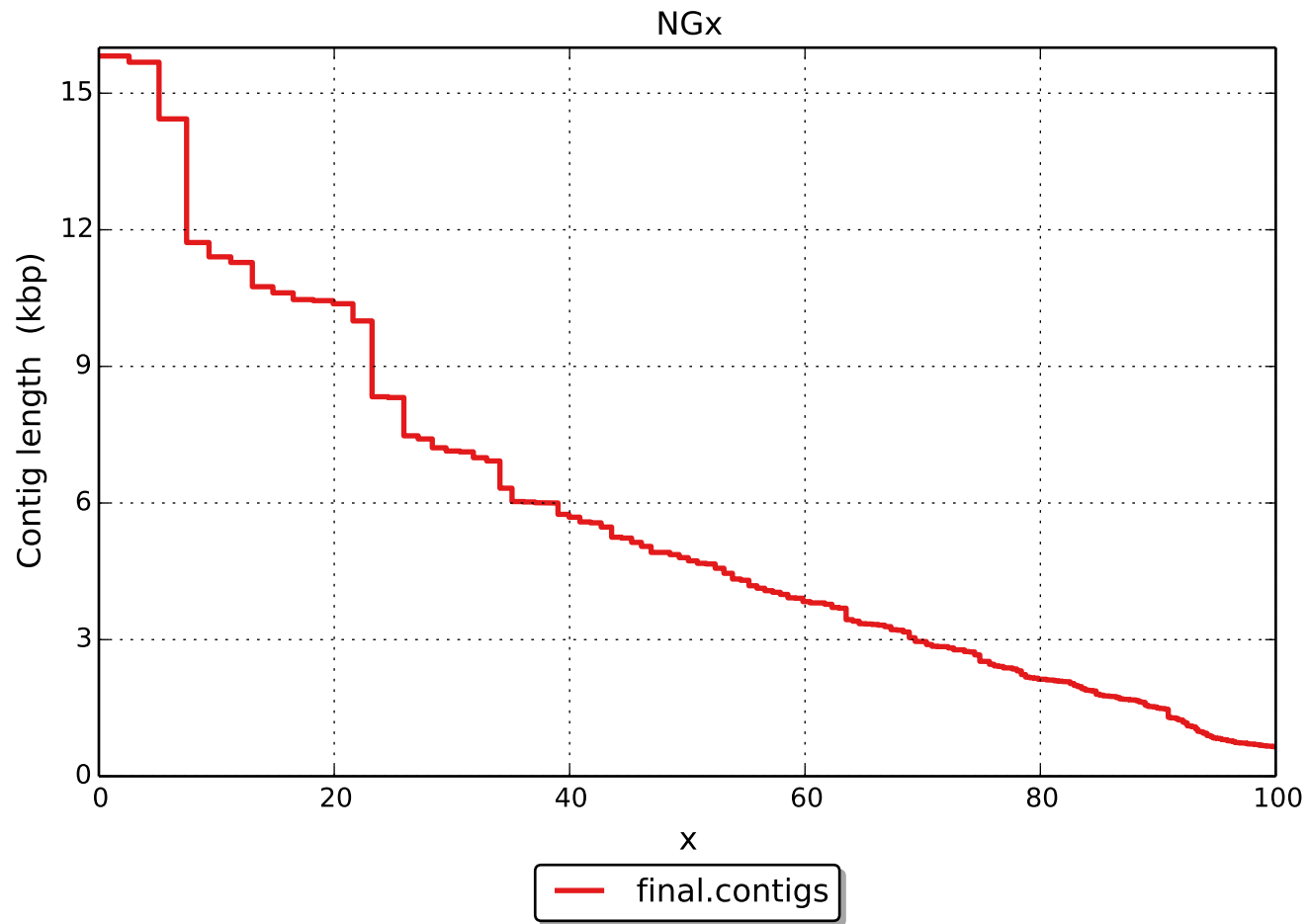
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

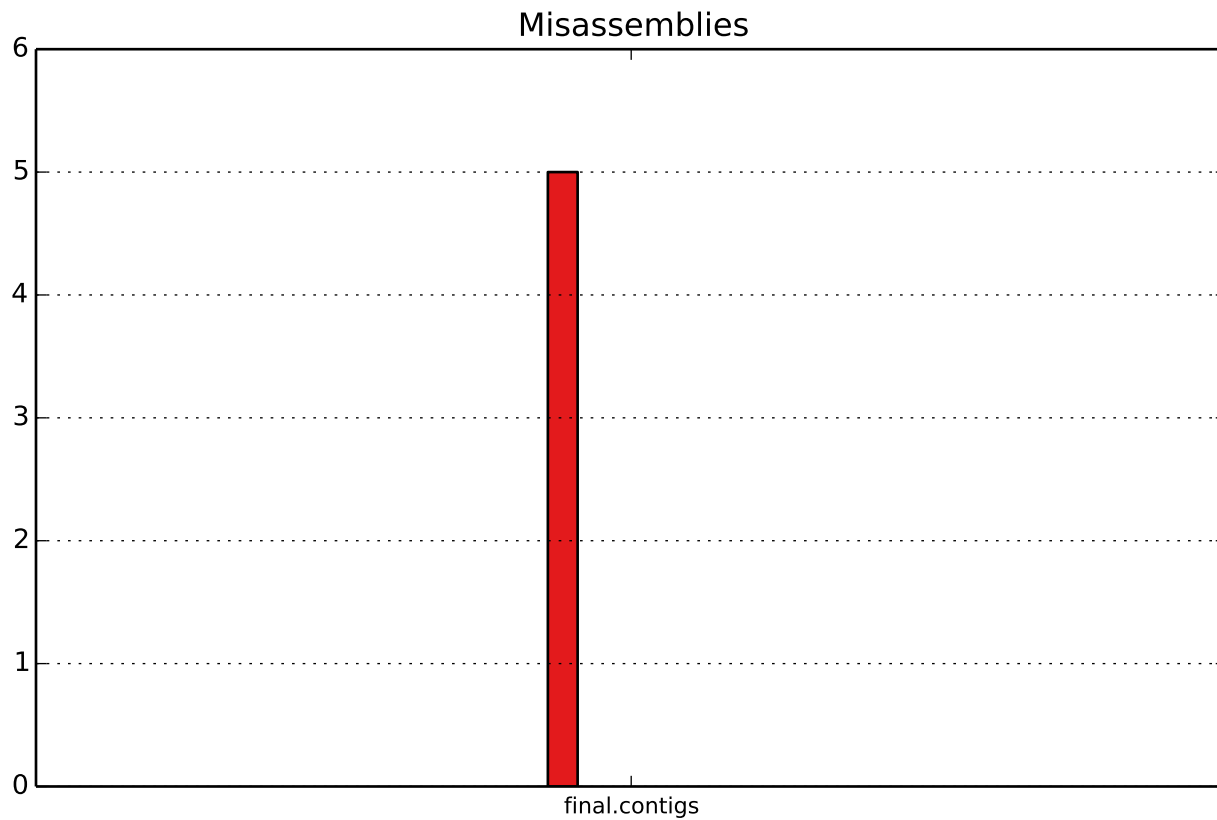


GC content

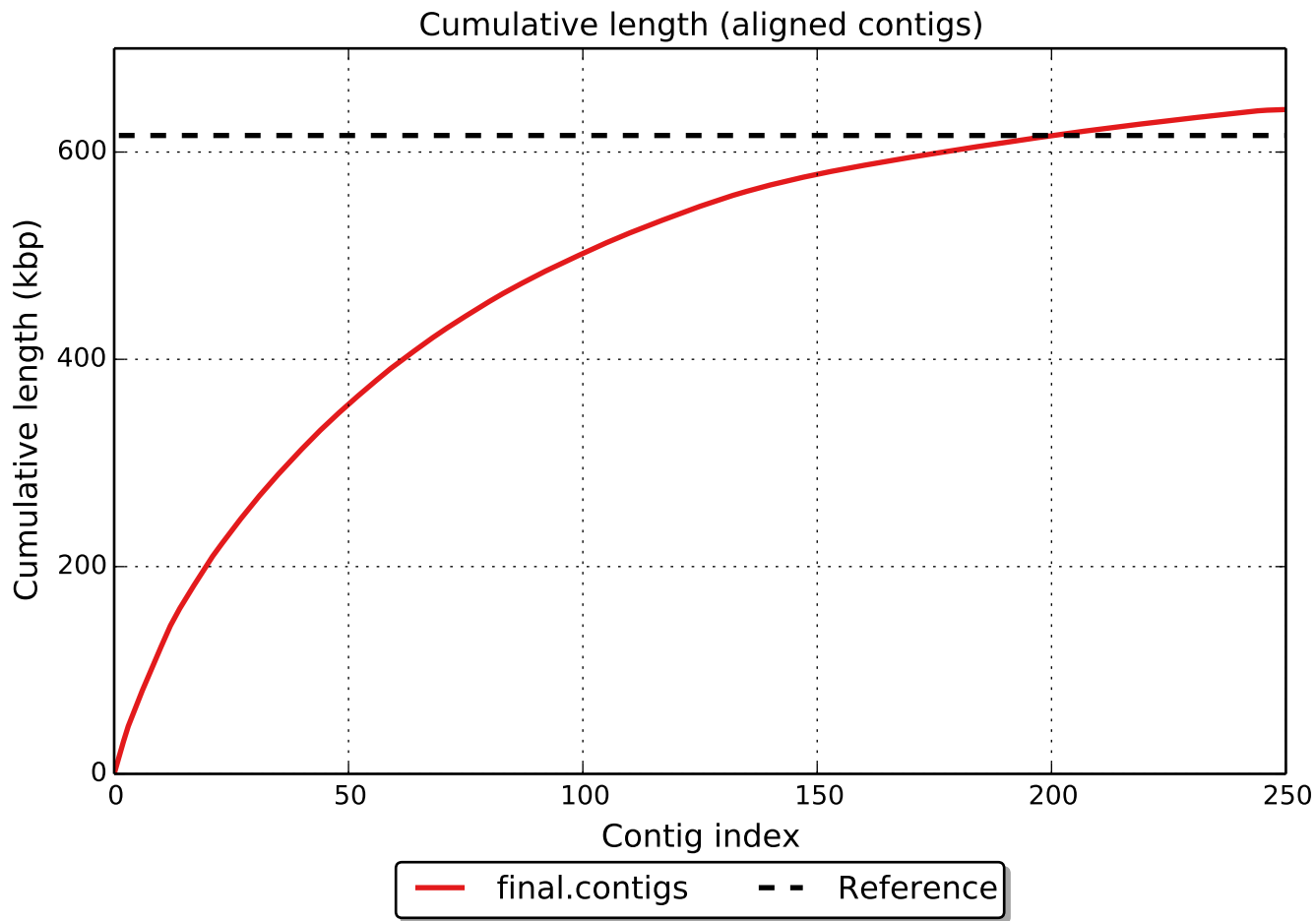


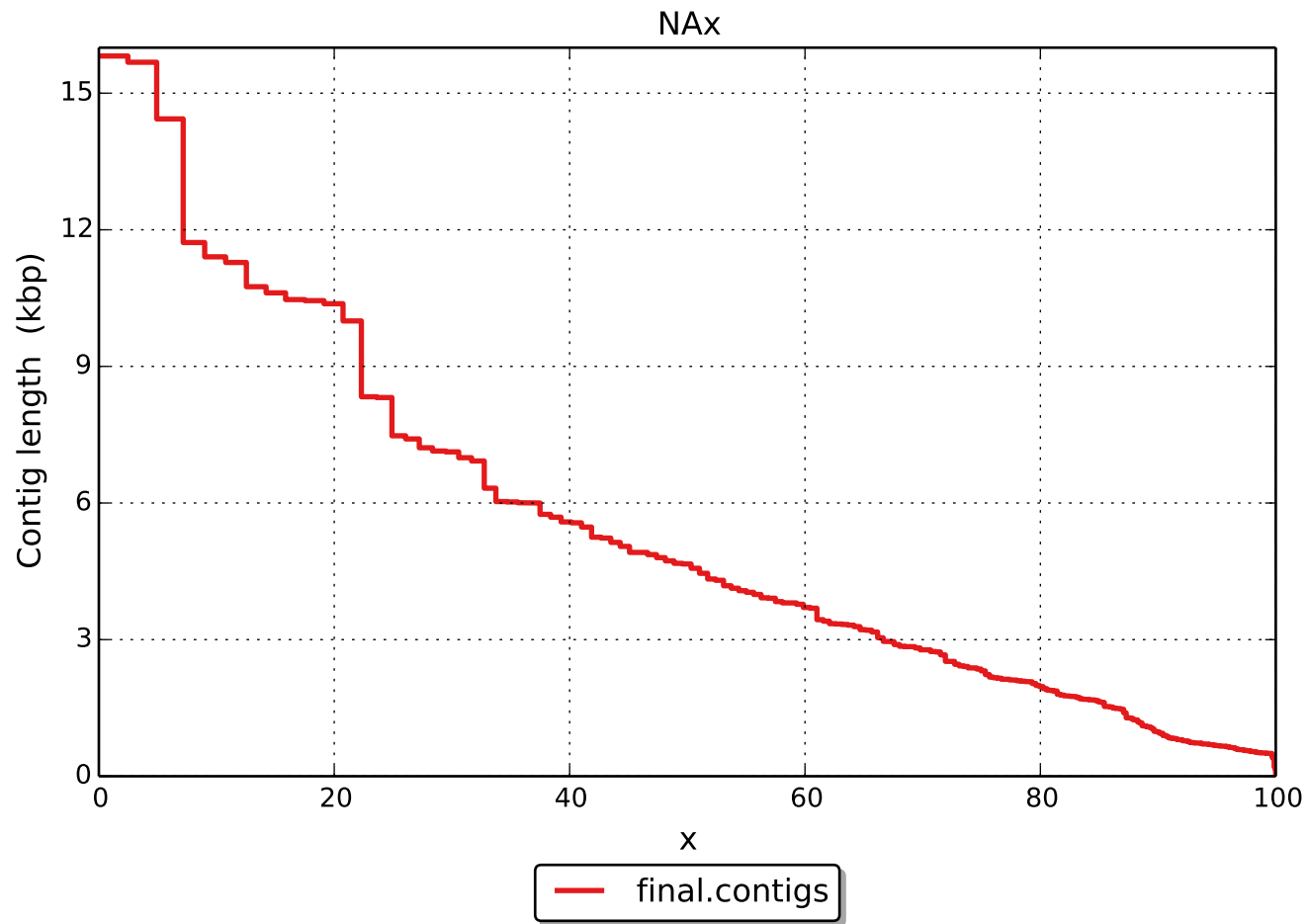












# NGAx

