

Report

	final.contigs
# contigs (>= 1000 bp)	296
# contigs (>= 5000 bp)	227
# contigs (>= 10000 bp)	166
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	9
Total length (>= 1000 bp)	4658666
Total length (>= 5000 bp)	4448638
Total length (>= 10000 bp)	4010989
Total length (>= 25000 bp)	2193685
Total length (>= 50000 bp)	587006
# contigs	304
Largest contig	95788
Total length	4664548
Reference length	4641652
GC (℥)	50.79
Reference GC (℥)	50.79
N50	23895
NG50	23895
N75	14777
NG75	15066
L50	63
LG50	63
L75	125
LG75	124
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	99.956
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	95788
NA50	23895
NGA50	23895
NA75	14777
NGA75	15066
LA50	63
LGA50	63
LA75	125
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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

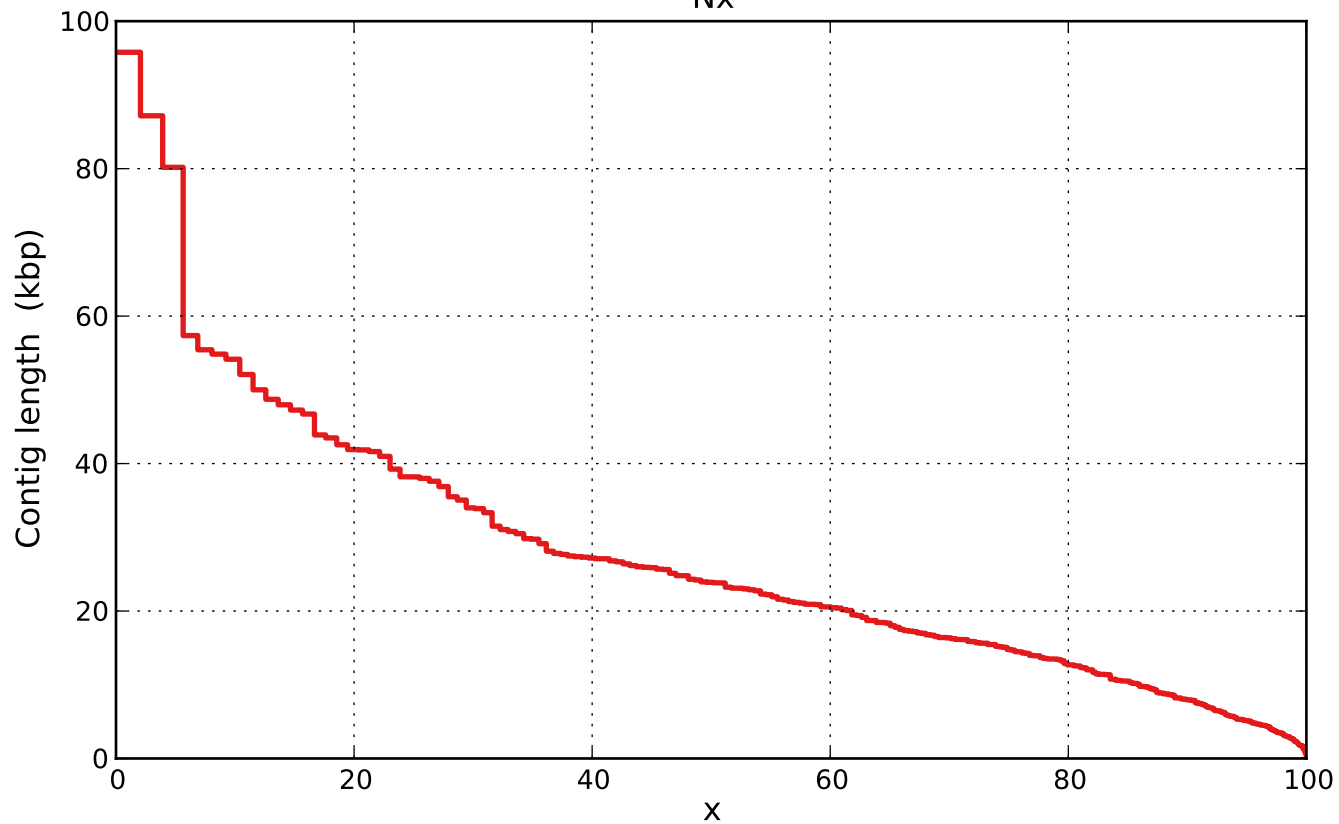
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

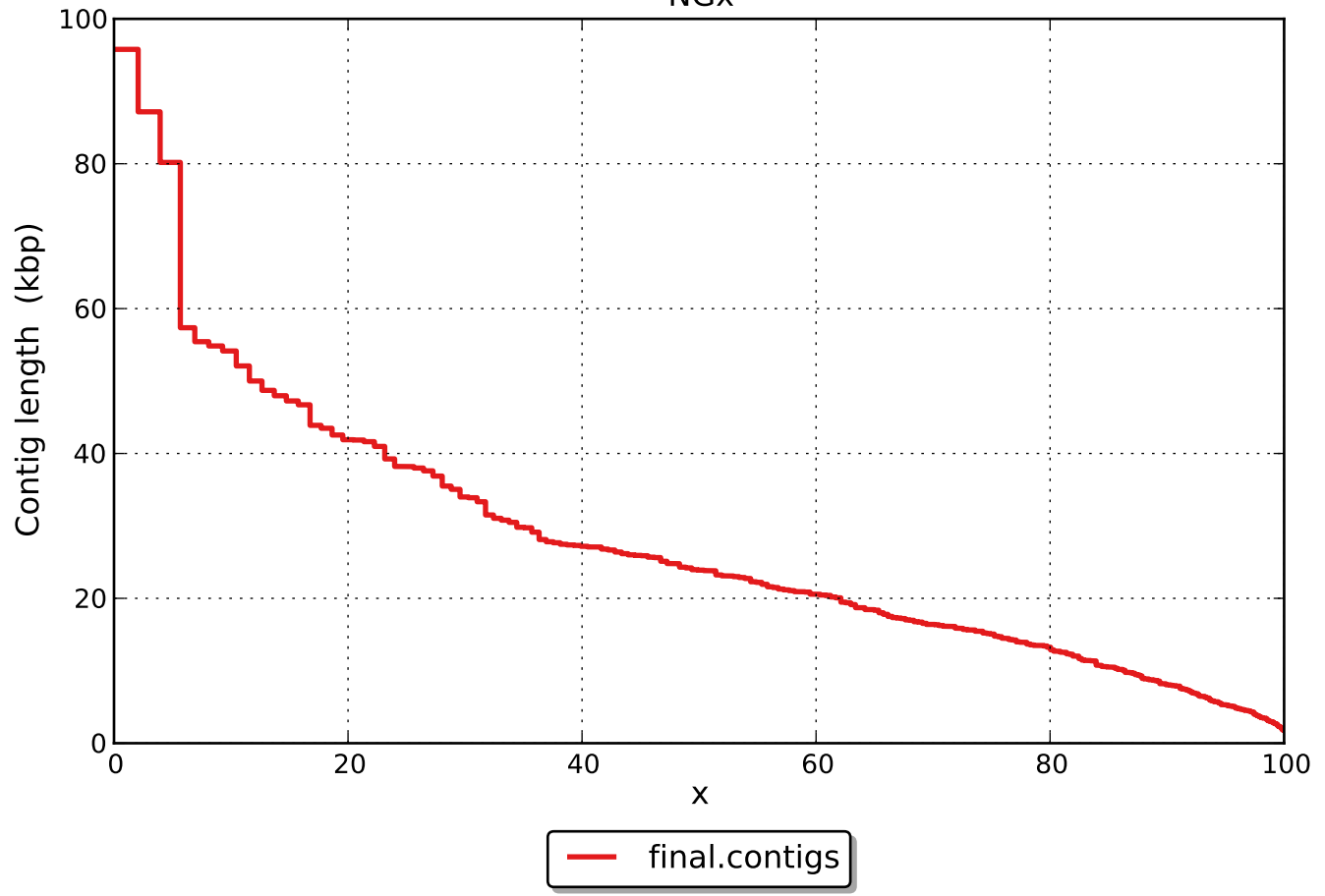
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

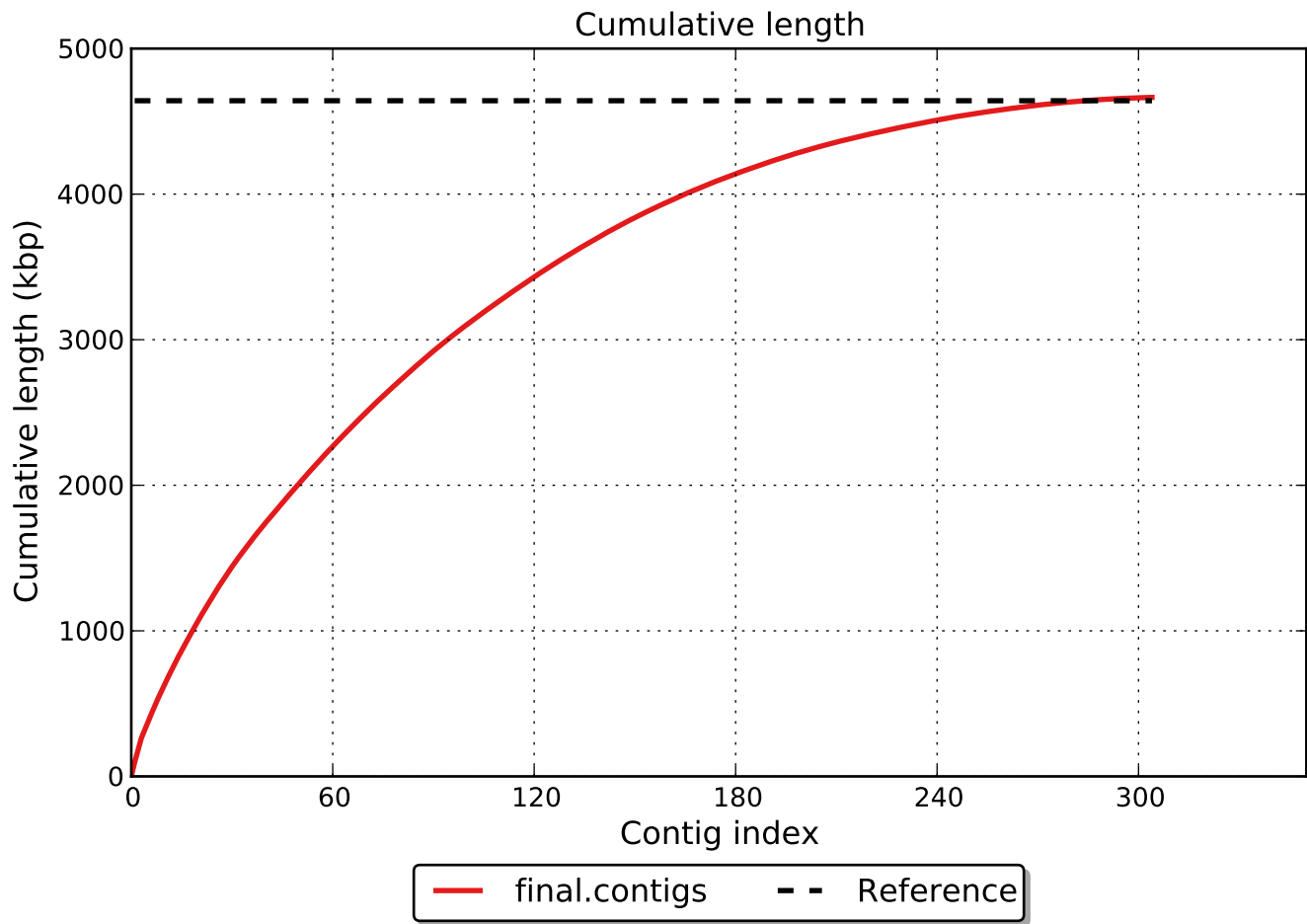
Nx



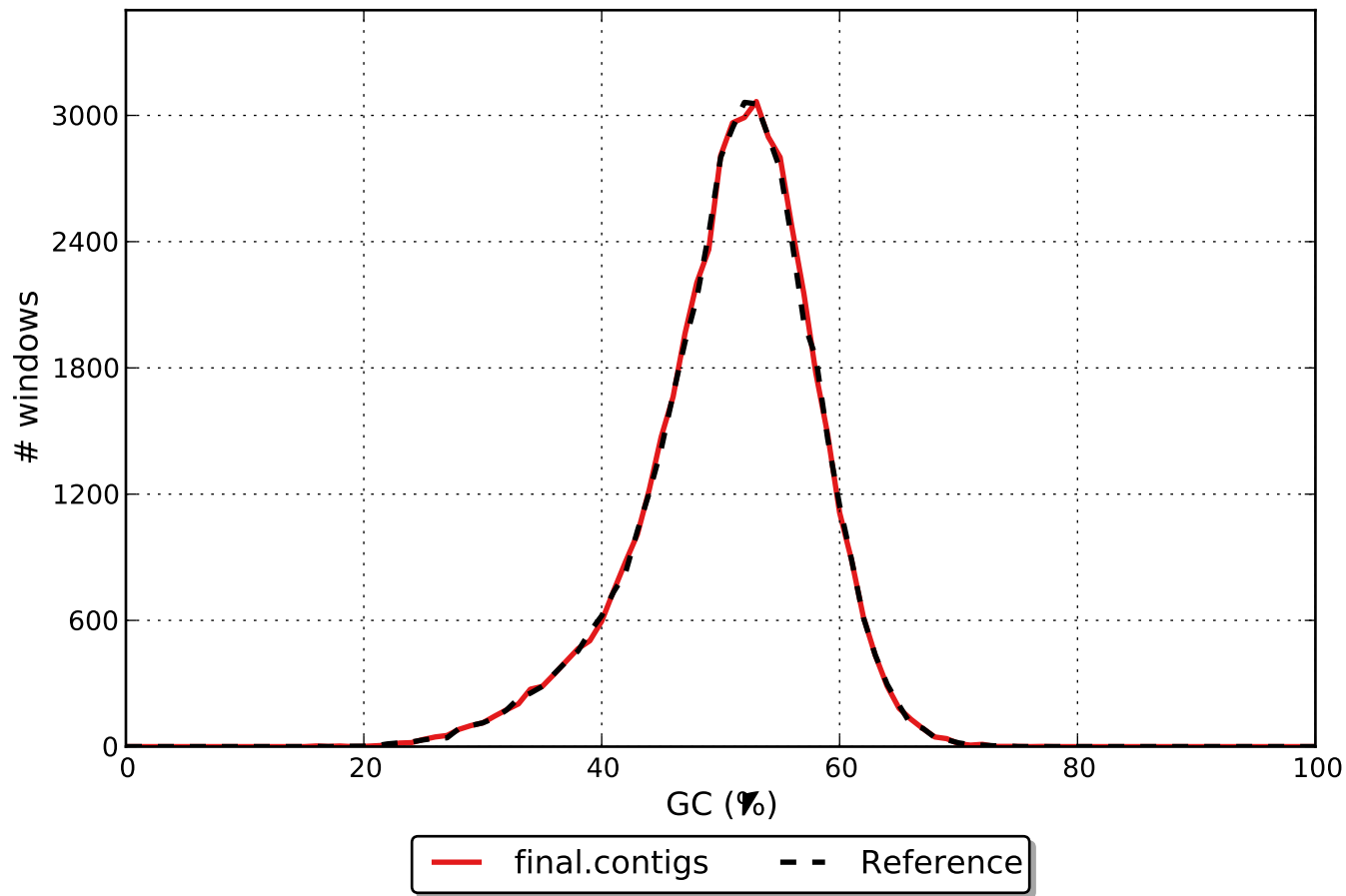
— final.contigs

NGx





GC content

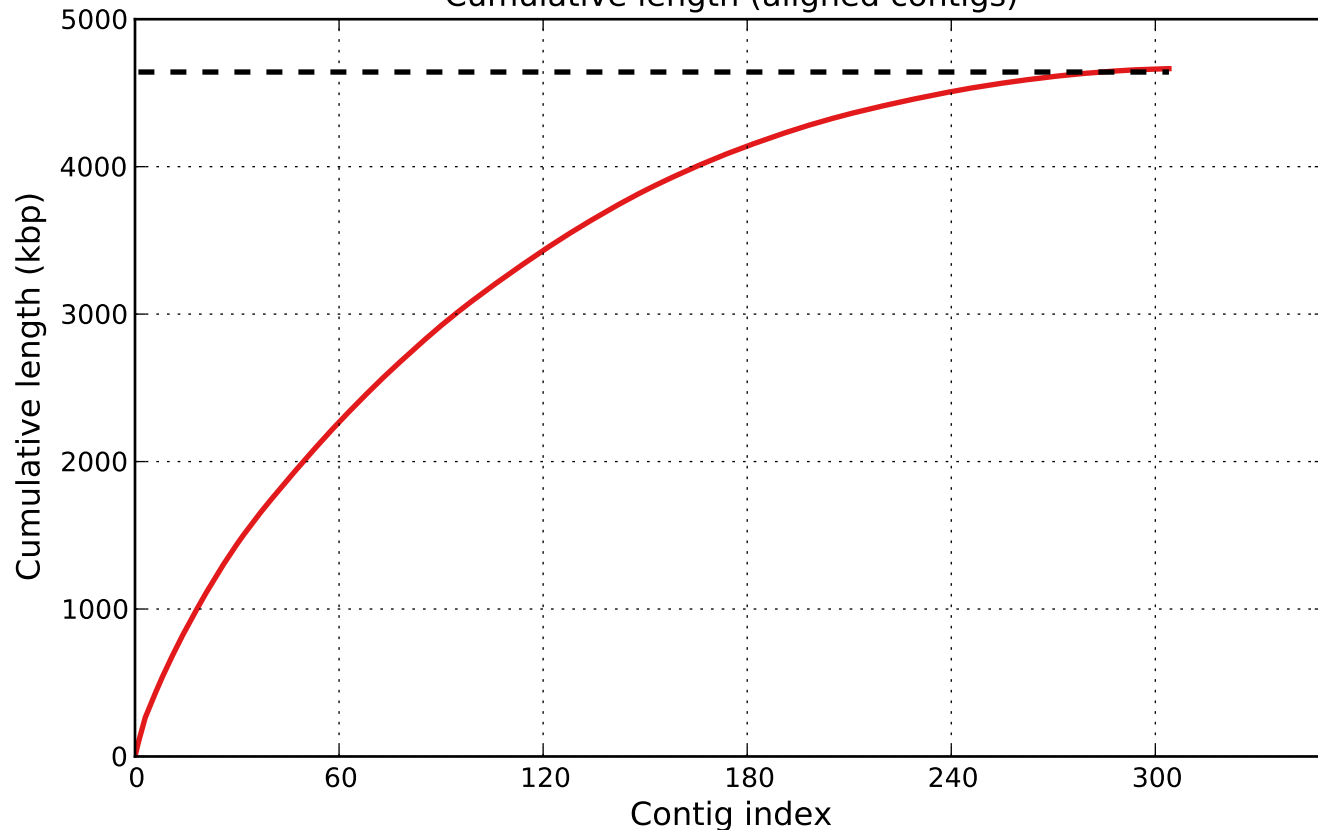


# Misassemblies



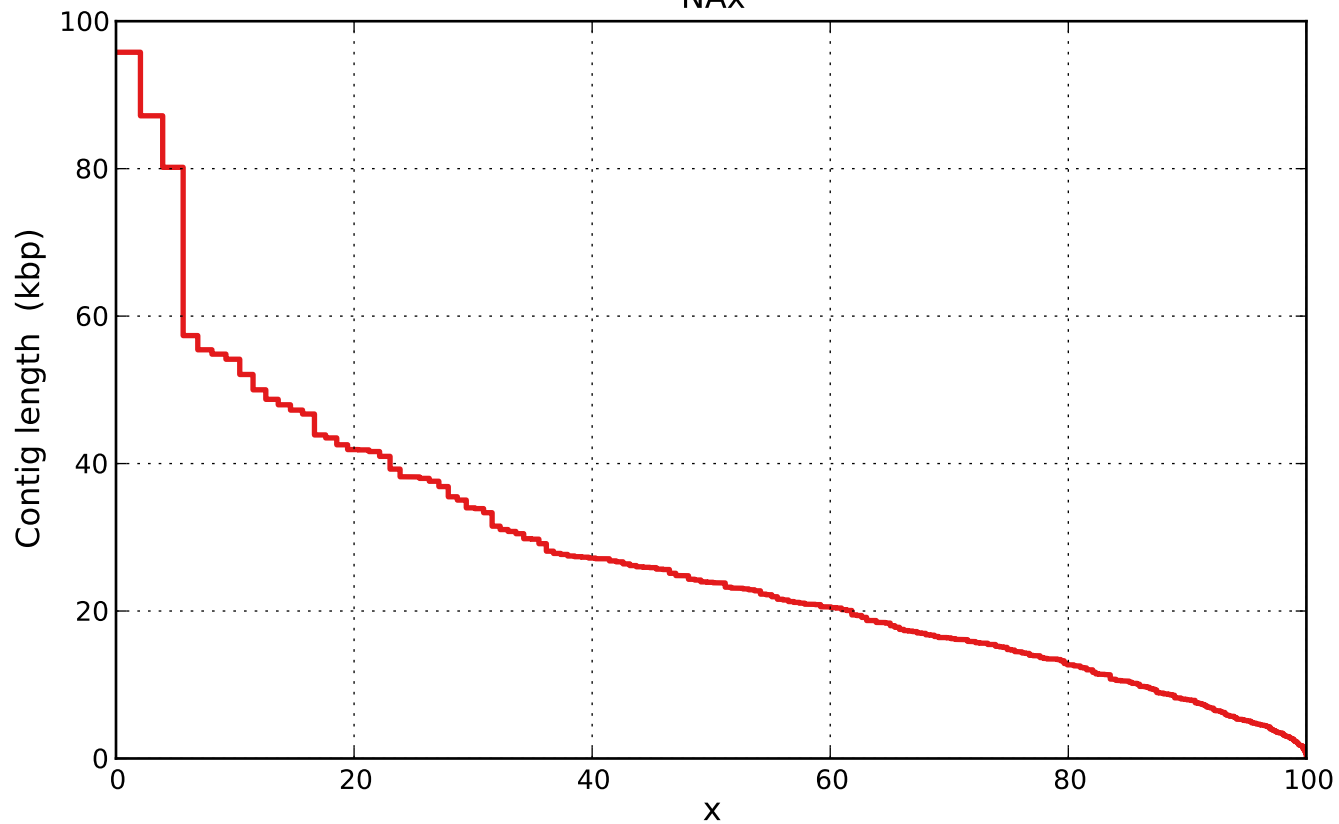


Cumulative length (aligned contigs)



— final.contigs    - - Reference

NAx



— final.contigs

# NGAx

