

Report

	final.contigs
# contigs (>= 1000 bp)	1357
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1938734
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4271
Largest contig	4826
Total length	4001715
Reference length	4641652
GC (℥)	50.74
Reference GC (℥)	50.79
N50	984
NG50	887
N75	722
NG75	615
L50	1420
LG50	1762
L75	2613
LG75	3335
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	80.766
Duplication ratio	1.067
# N's per 100 kbp	0.00
# mismatches per 100 kbp	184.37
# indels per 100 kbp	0.05
Largest alignment	4826
NA50	984
NGA50	887
NA75	722
NGA75	615
LA50	1420
LGA50	1762
LA75	2613
LGA75	3335

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	6912
# indels	2
# short indels	2
# long indels	0
Indels length	2

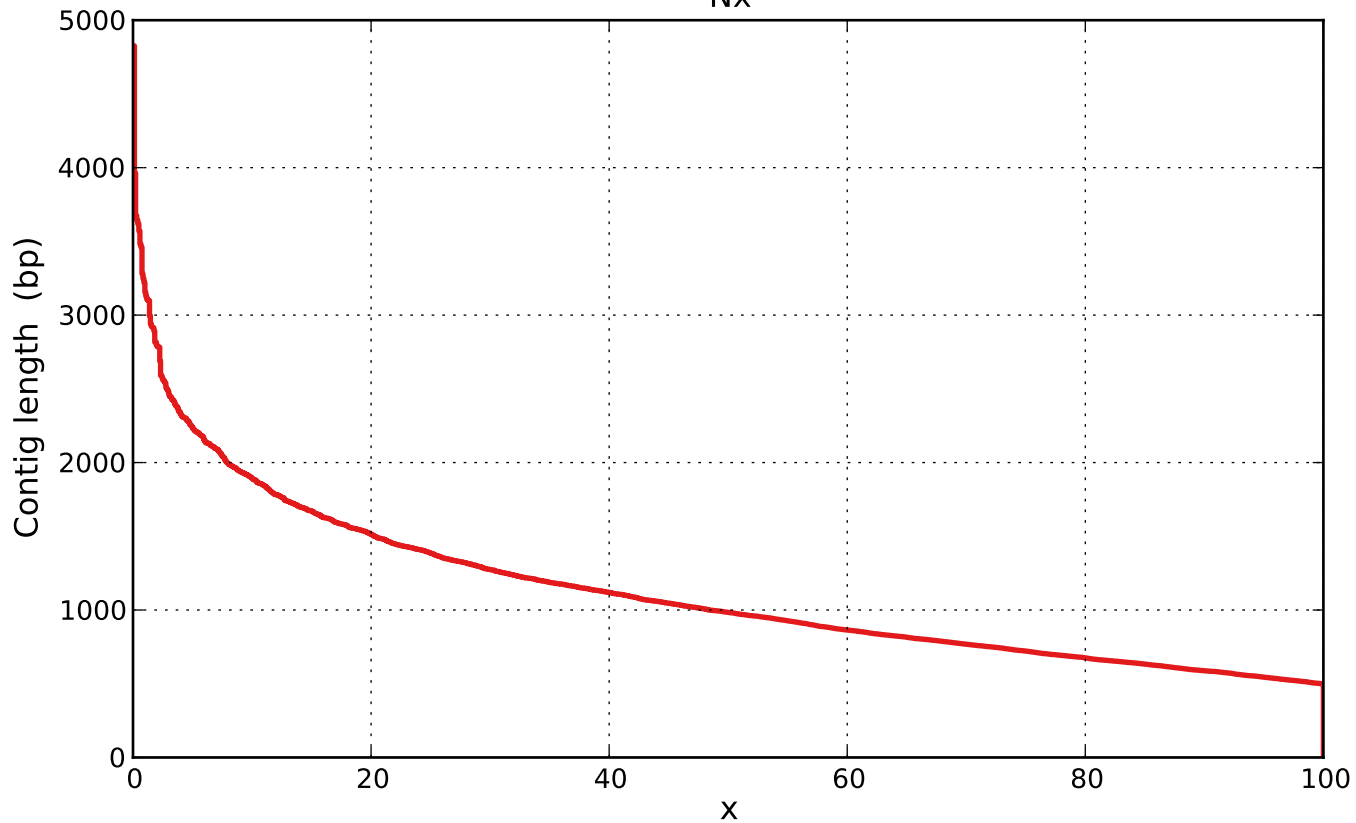
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

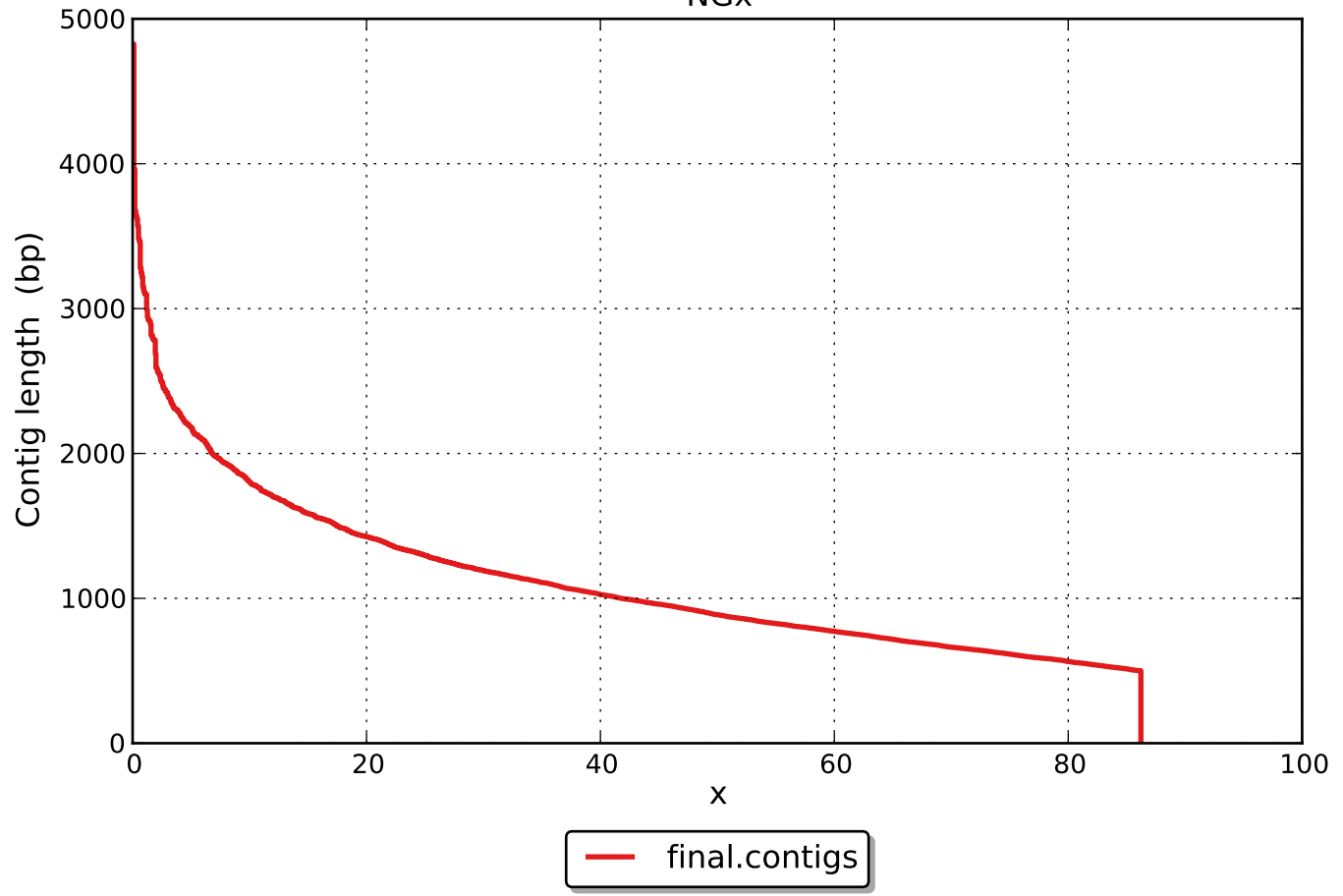
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

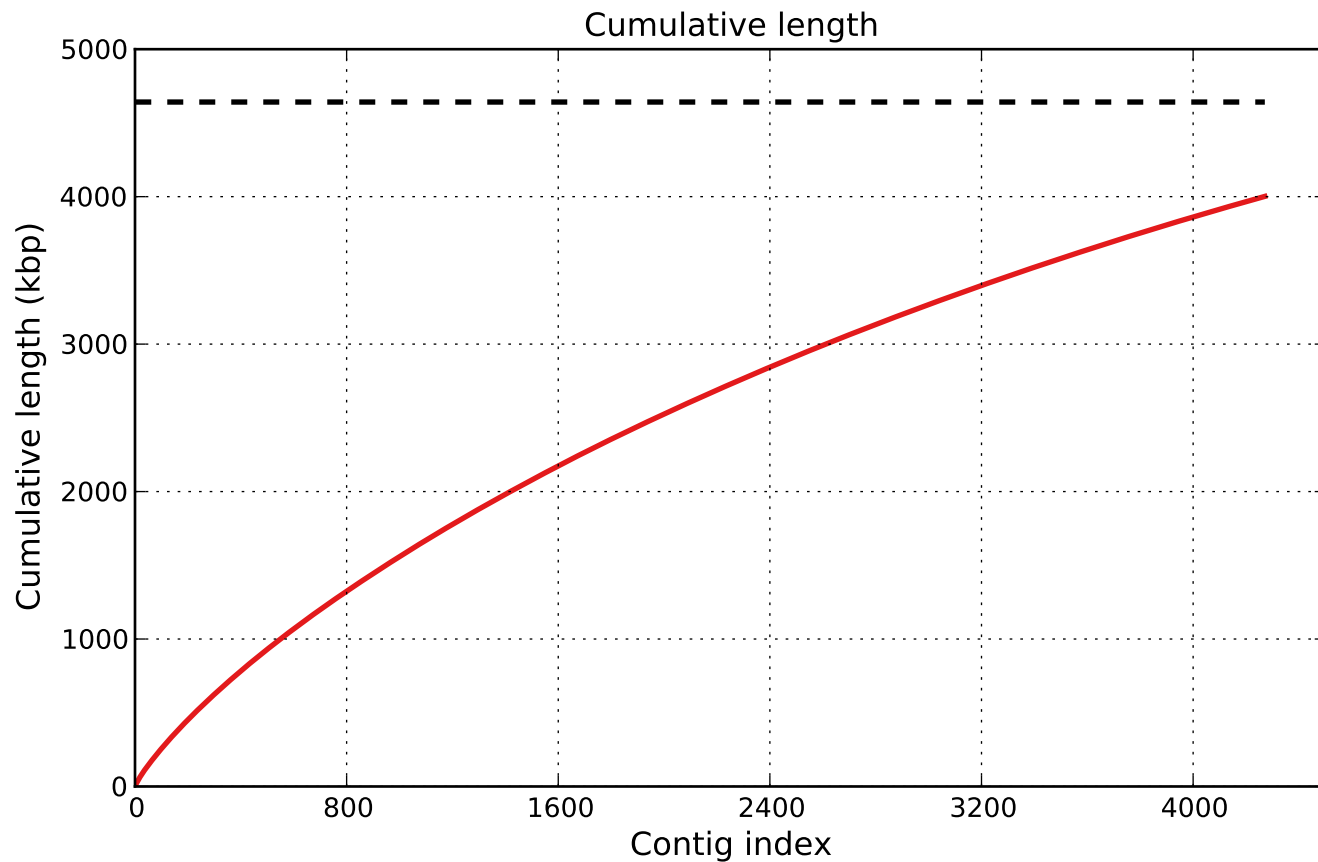
Nx



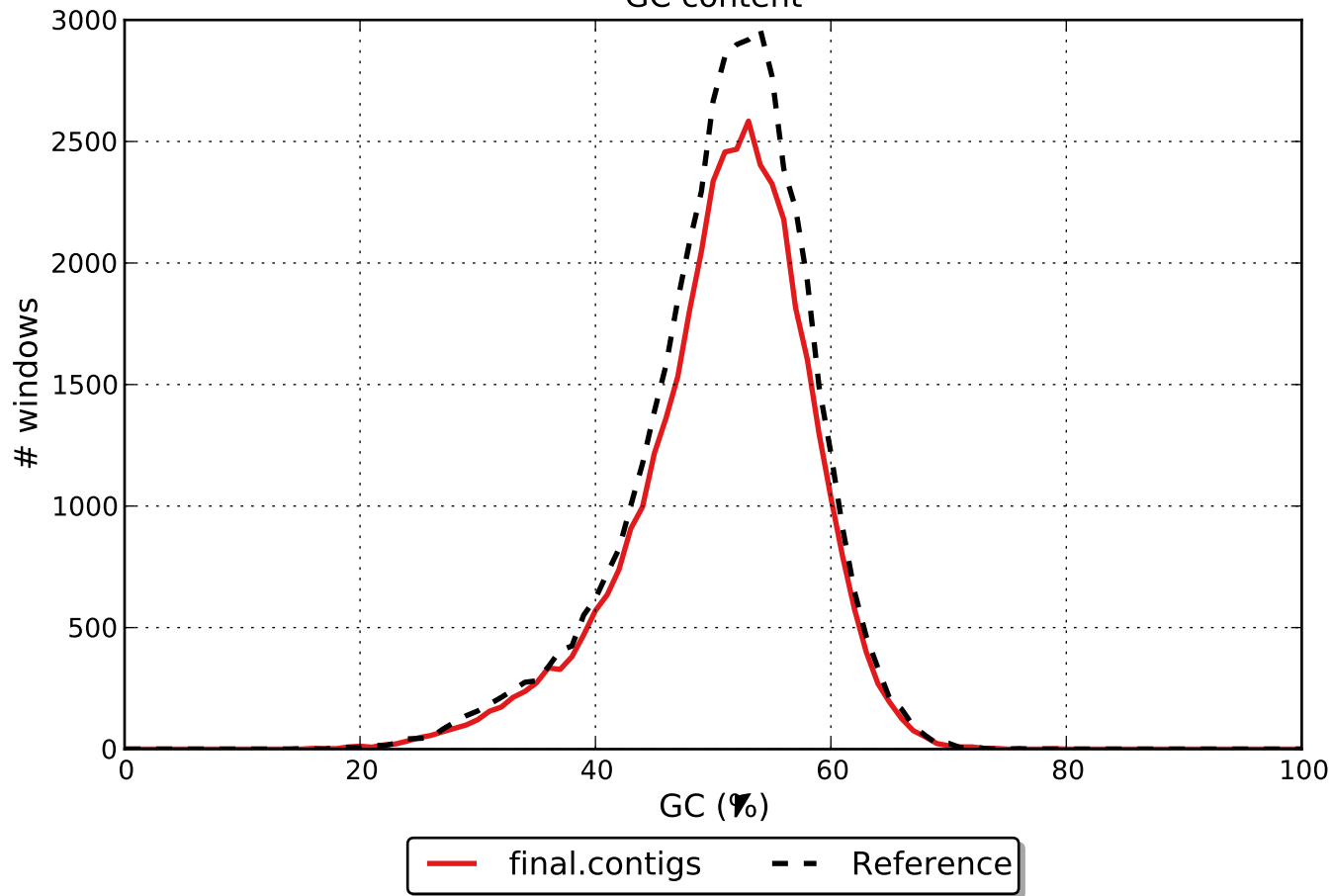
— final.contigs

NGx





GC content

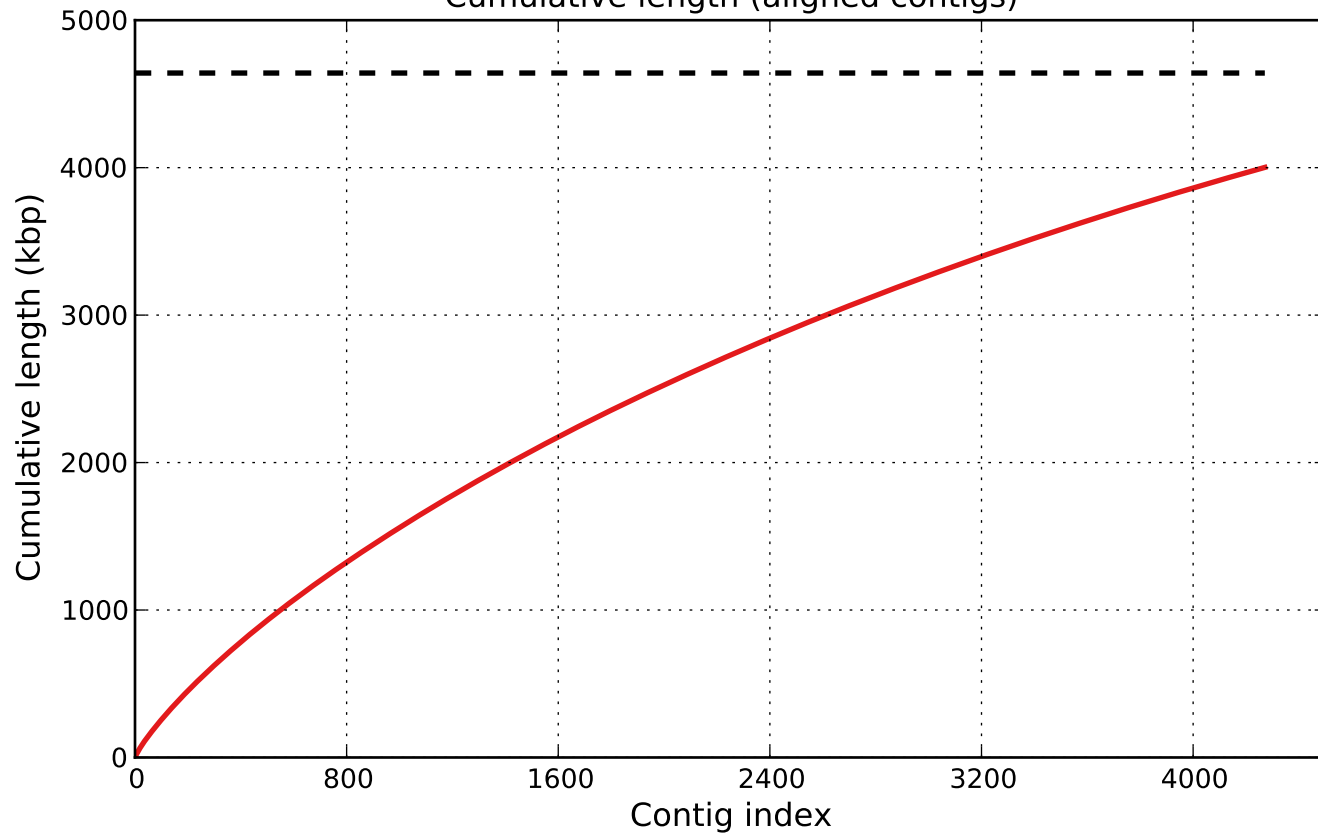


# Misassemblies

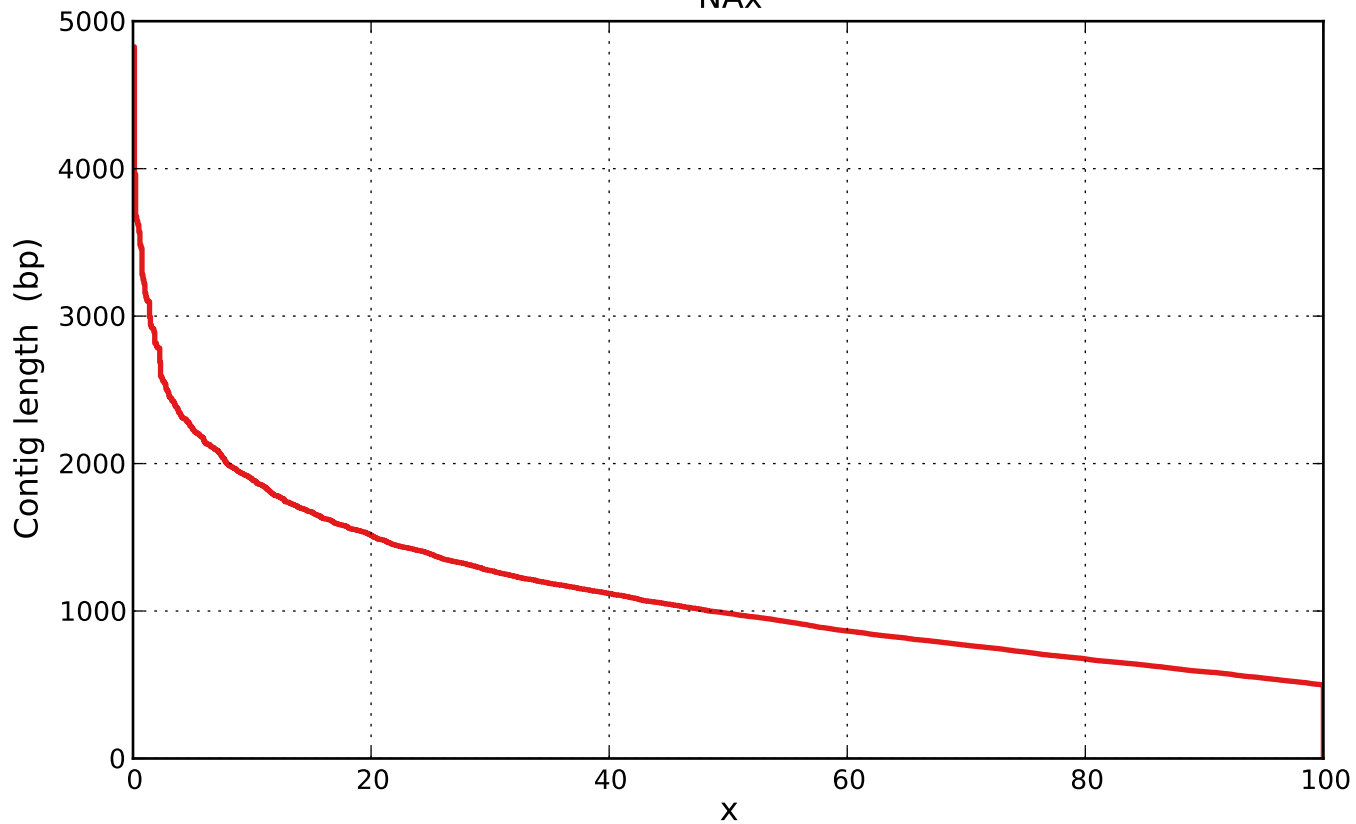




Cumulative length (aligned contigs)



NAx



— final.contigs

NGAx

