

Report

	final.contigs
# contigs (>= 1000 bp)	1368
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2118029
Total length (>= 5000 bp)	5220
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3310
Largest contig	5220
Total length	3502697
Reference length	4641652
GC (℥)	50.77
Reference GC (℥)	50.79
N50	1159
NG50	911
N75	803
NG75	508
L50	1027
LG50	1582
L75	1940
LG75	3268
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	7102
# local misassemblies	6
# unaligned contigs	0 + 11 part
Unaligned length	734
Genome fraction (℥)	73.853
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	584.60
# indels per 100 kbp	9.77
Largest alignment	5220
NA50	1158
NGA50	910
NA75	802
NGA75	506
LA50	1028
LGA50	1584
LA75	1943
LGA75	3273

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

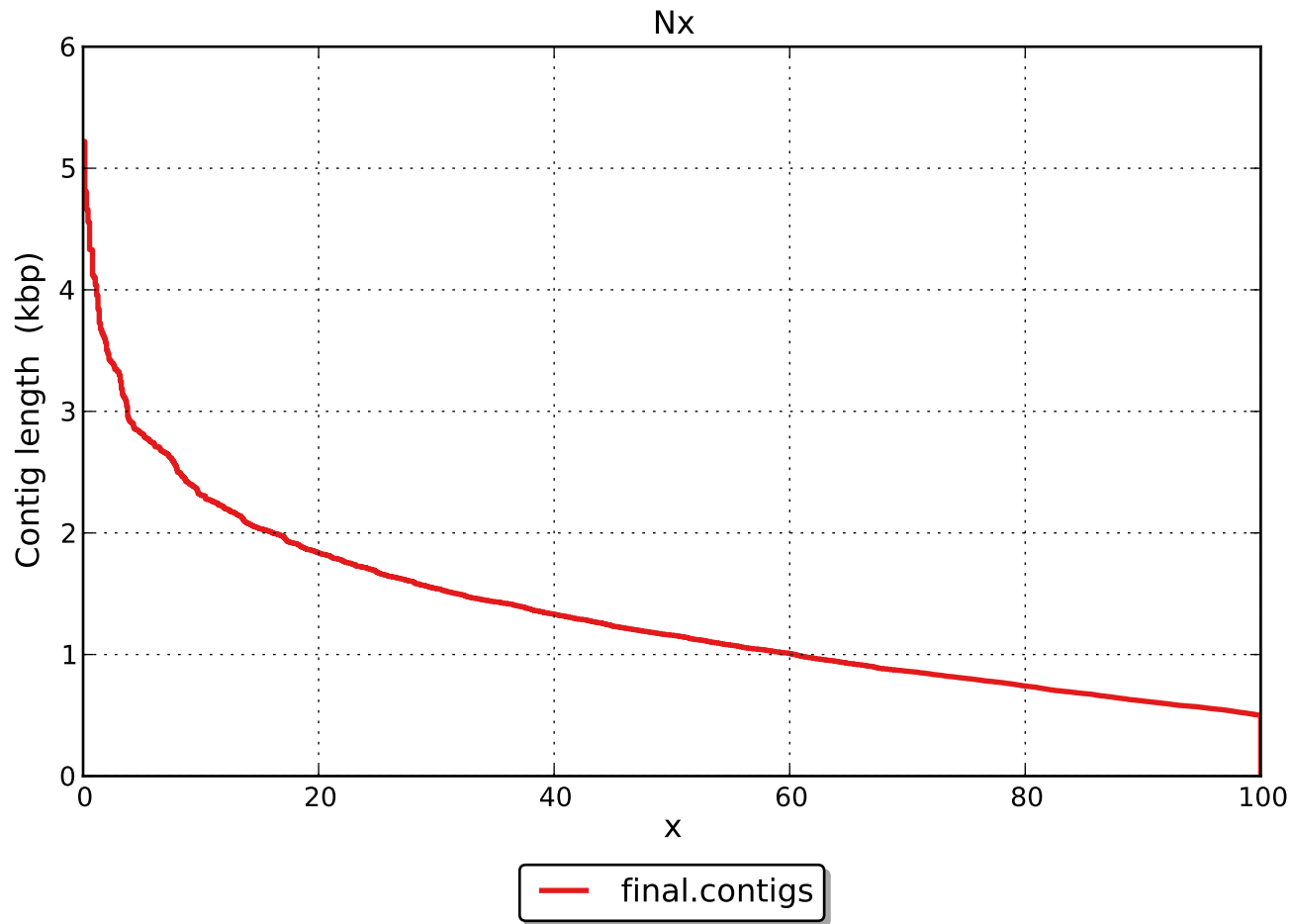
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	5
Misassembled contigs length	7102
# local misassemblies	6
# mismatches	20040
# indels	335
# short indels	332
# long indels	3
Indels length	518

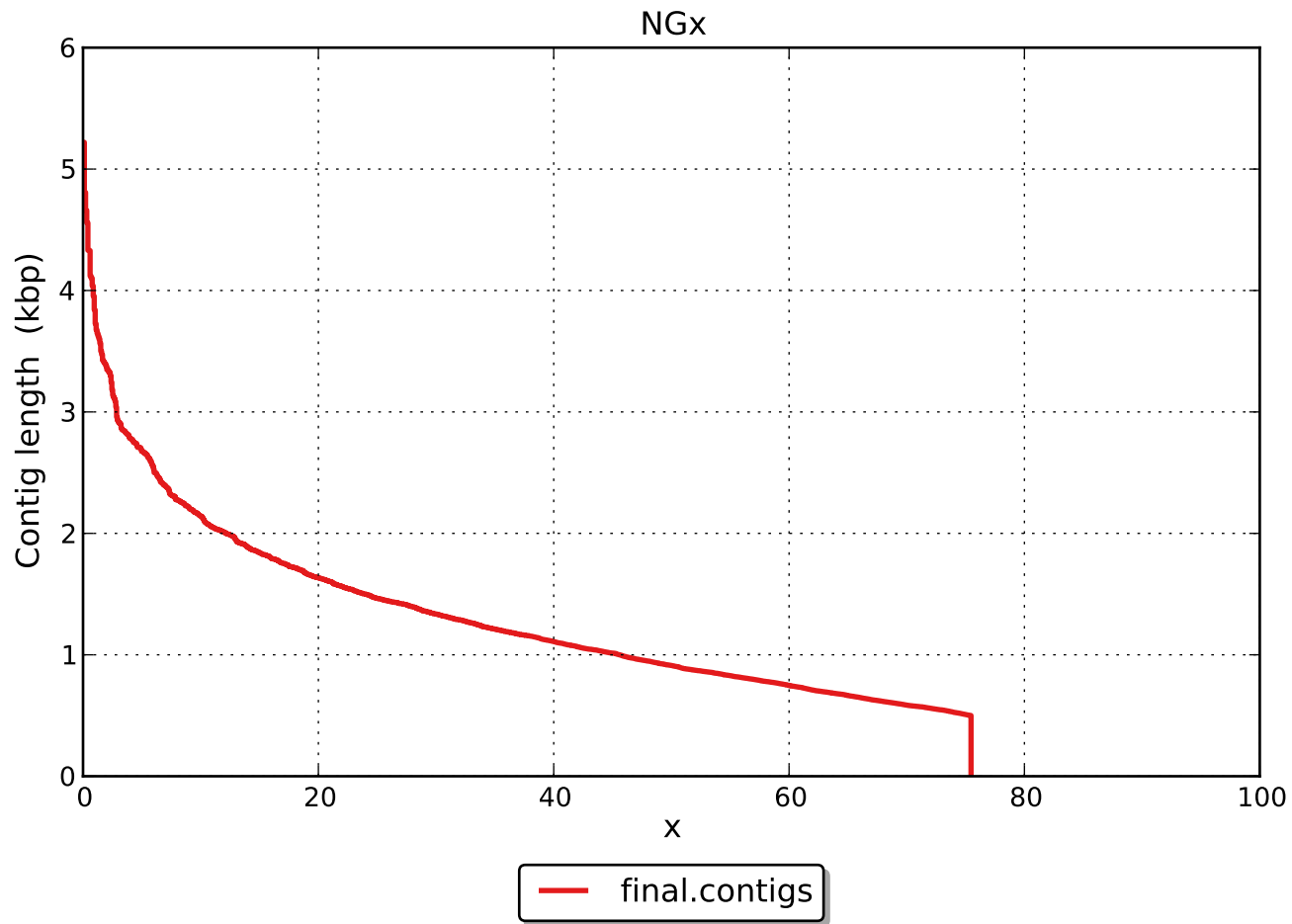
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

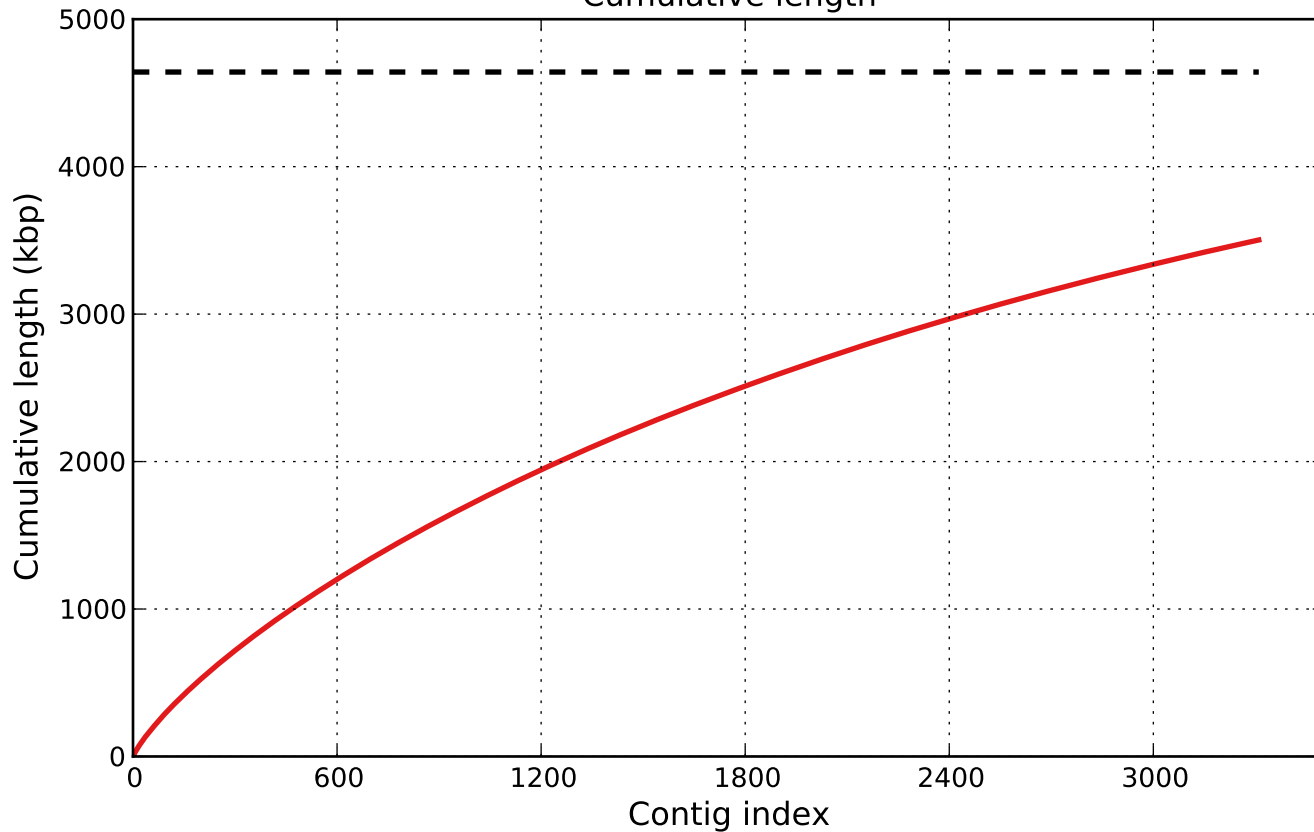
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	734
# N's	0

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).



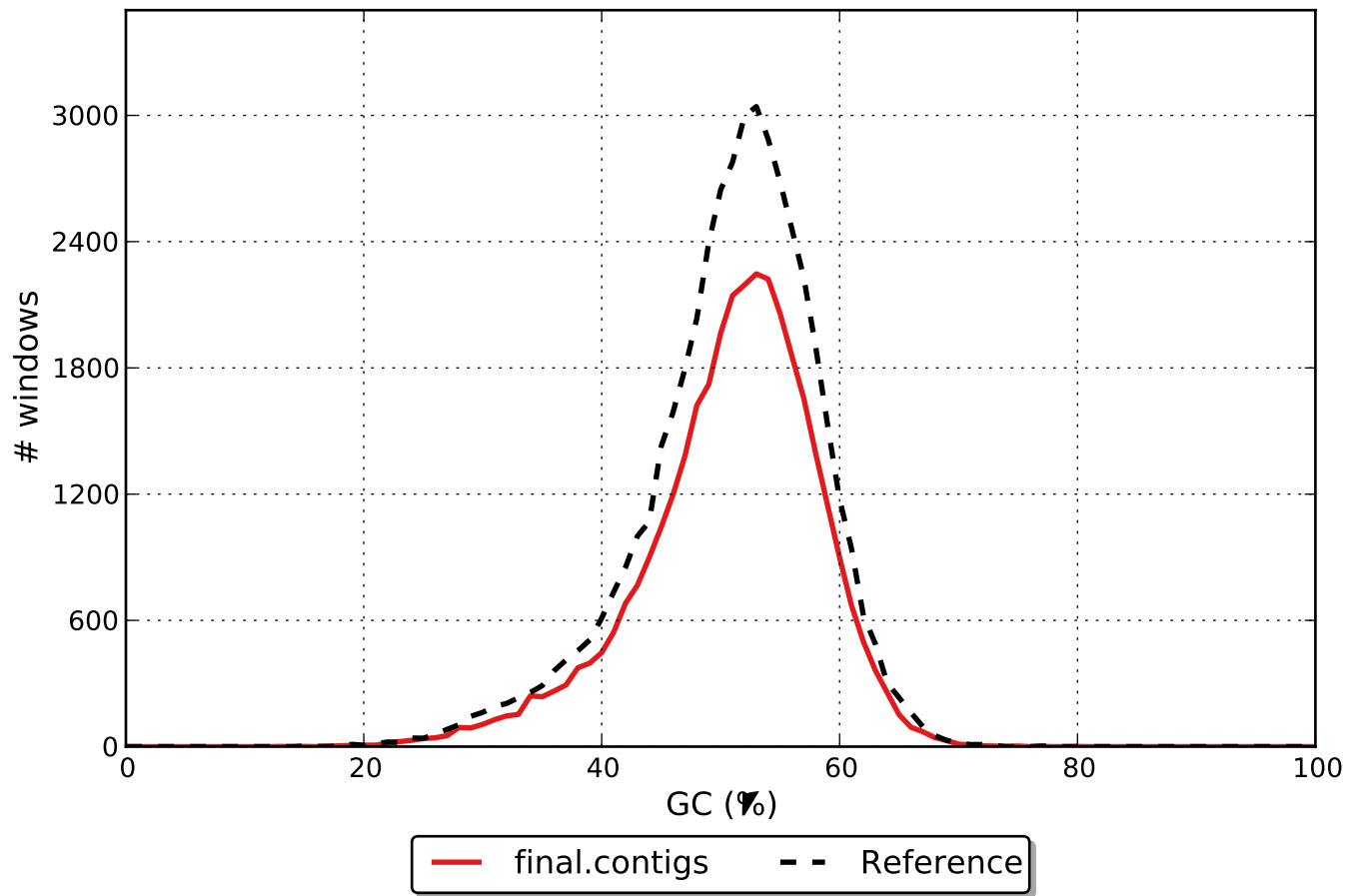


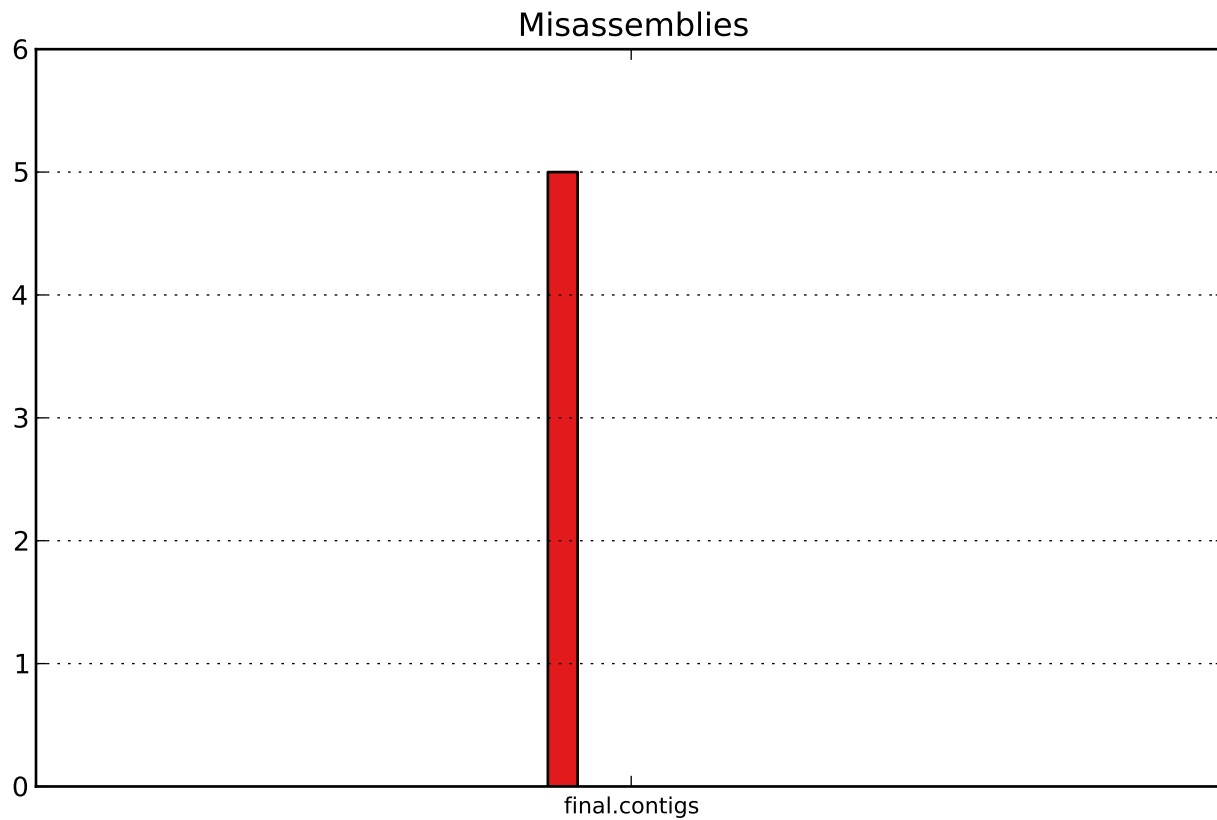
Cumulative length



— final.contigs    - - Reference

# GC content

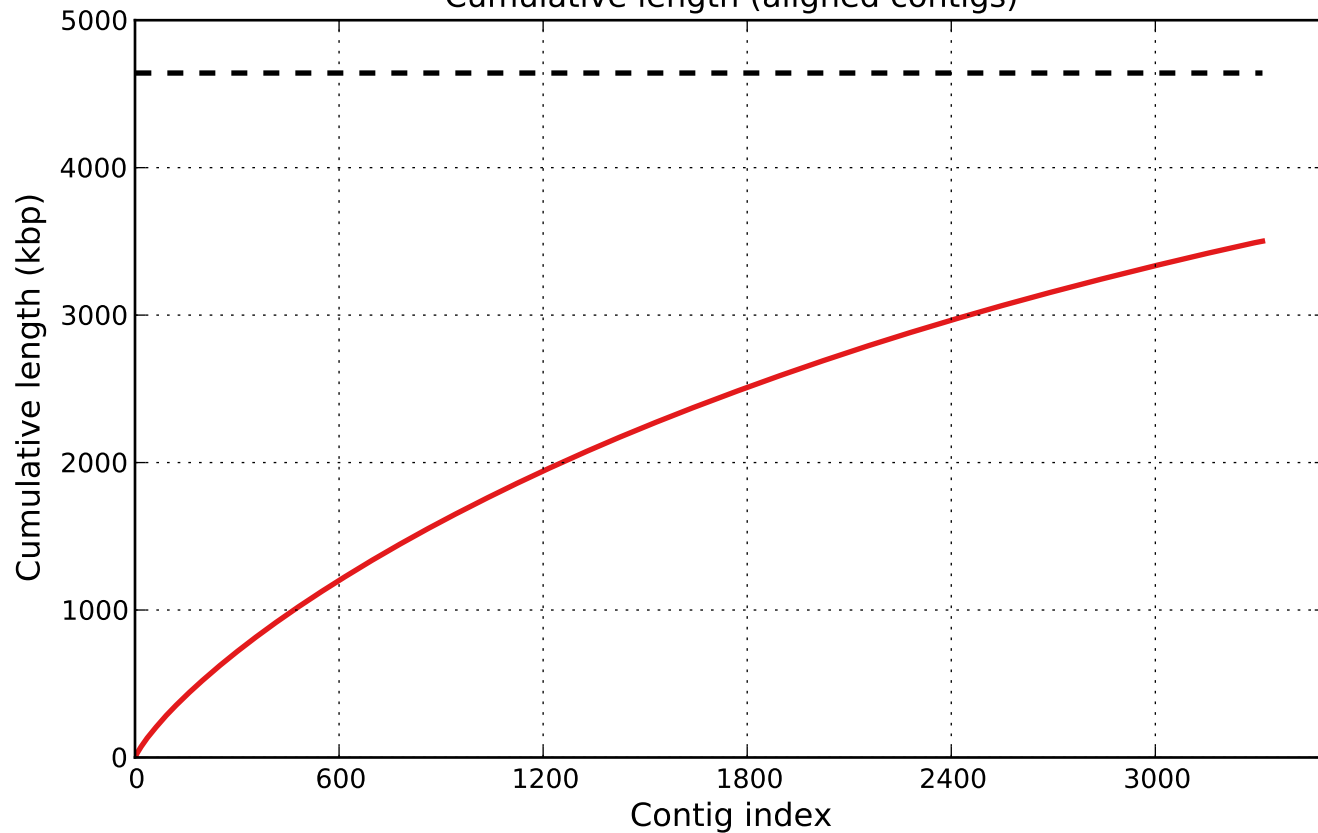




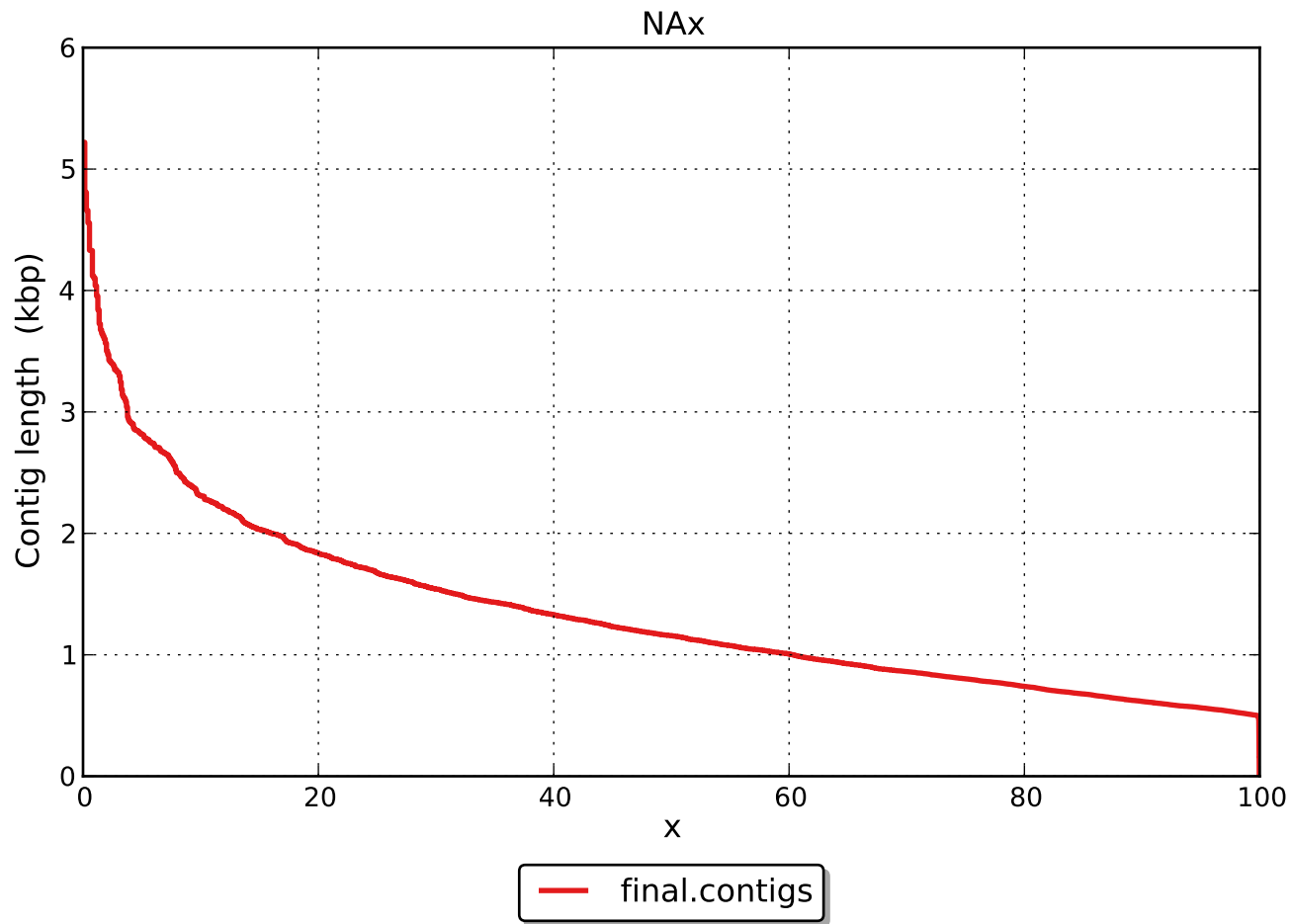
 # relocations



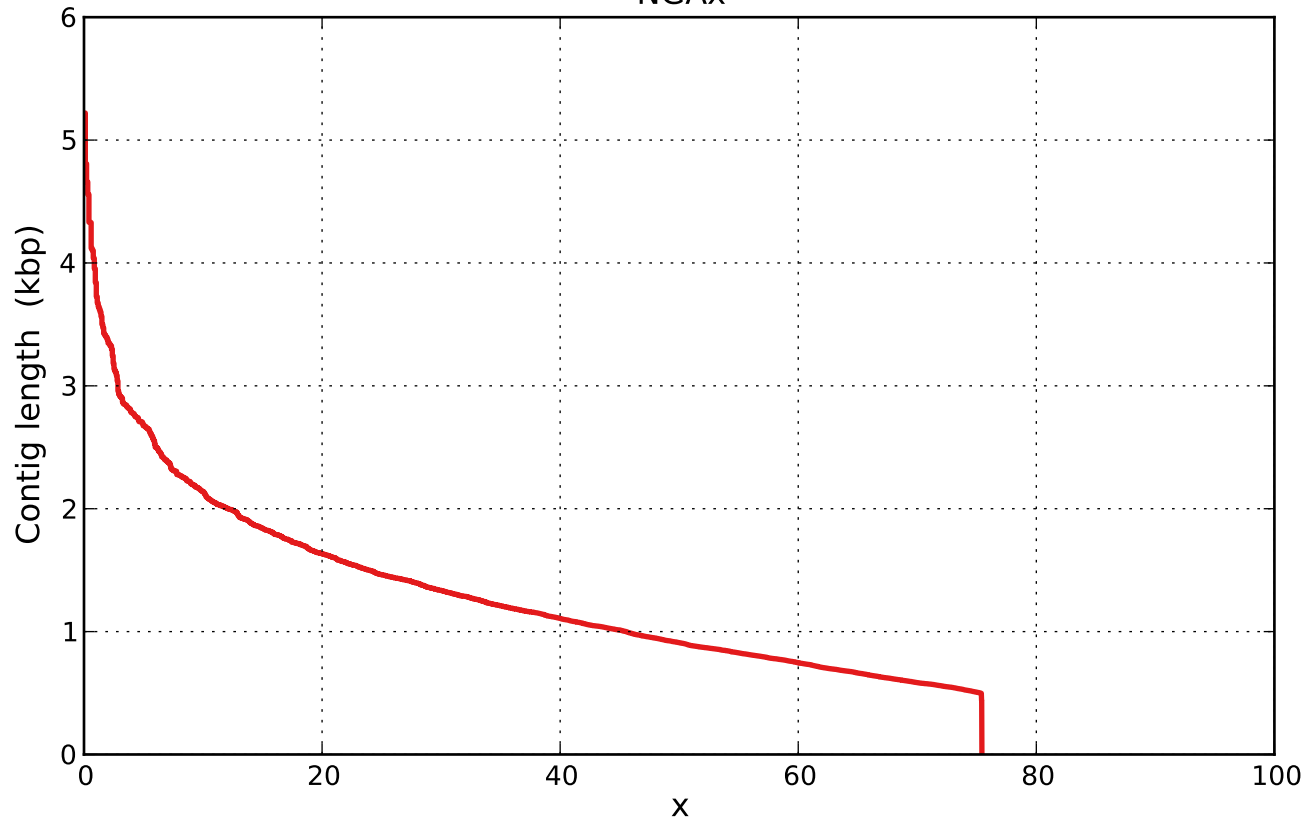
Cumulative length (aligned contigs)



— final.contigs    - - Reference



NGAx



— final.contigs