

Report

	final.contigs
# contigs (>= 1000 bp)	1729
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2967536
Total length (>= 5000 bp)	16001
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3552
Largest contig	5370
Total length	4275519
Reference length	4641652
GC (℥)	50.77
Reference GC (℥)	50.79
N50	1396
NG50	1291
N75	909
NG75	797
L50	1024
LG50	1161
L75	1981
LG75	2303
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	88.347
Duplication ratio	1.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.12
# indels per 100 kbp	0.00
Largest alignment	5370
NA50	1396
NGA50	1291
NA75	909
NGA75	797
LA50	1024
LGA50	1161
LA75	1981
LGA75	2303

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

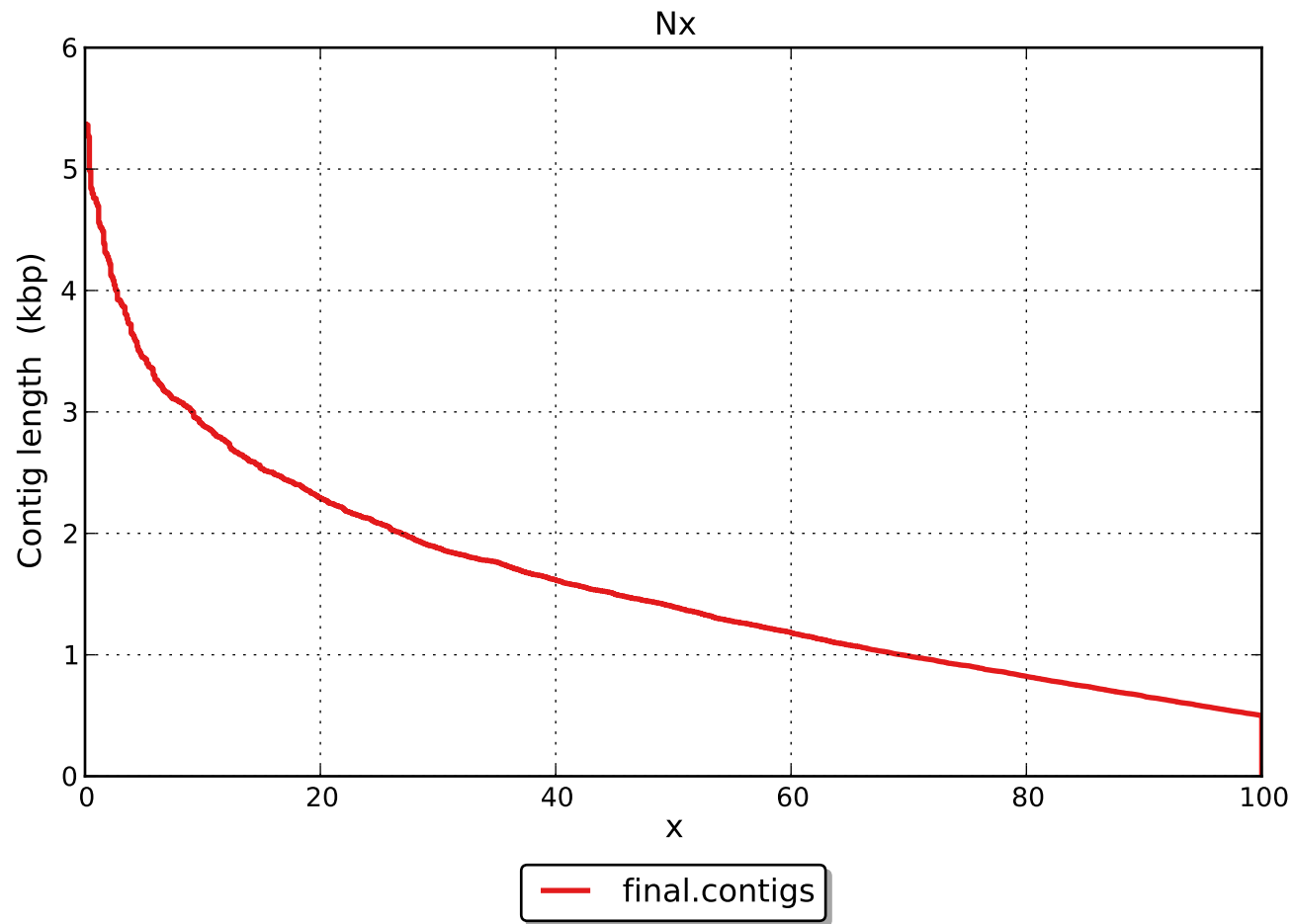
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	907
# indels	0
# short indels	0
# long indels	0
Indels length	0

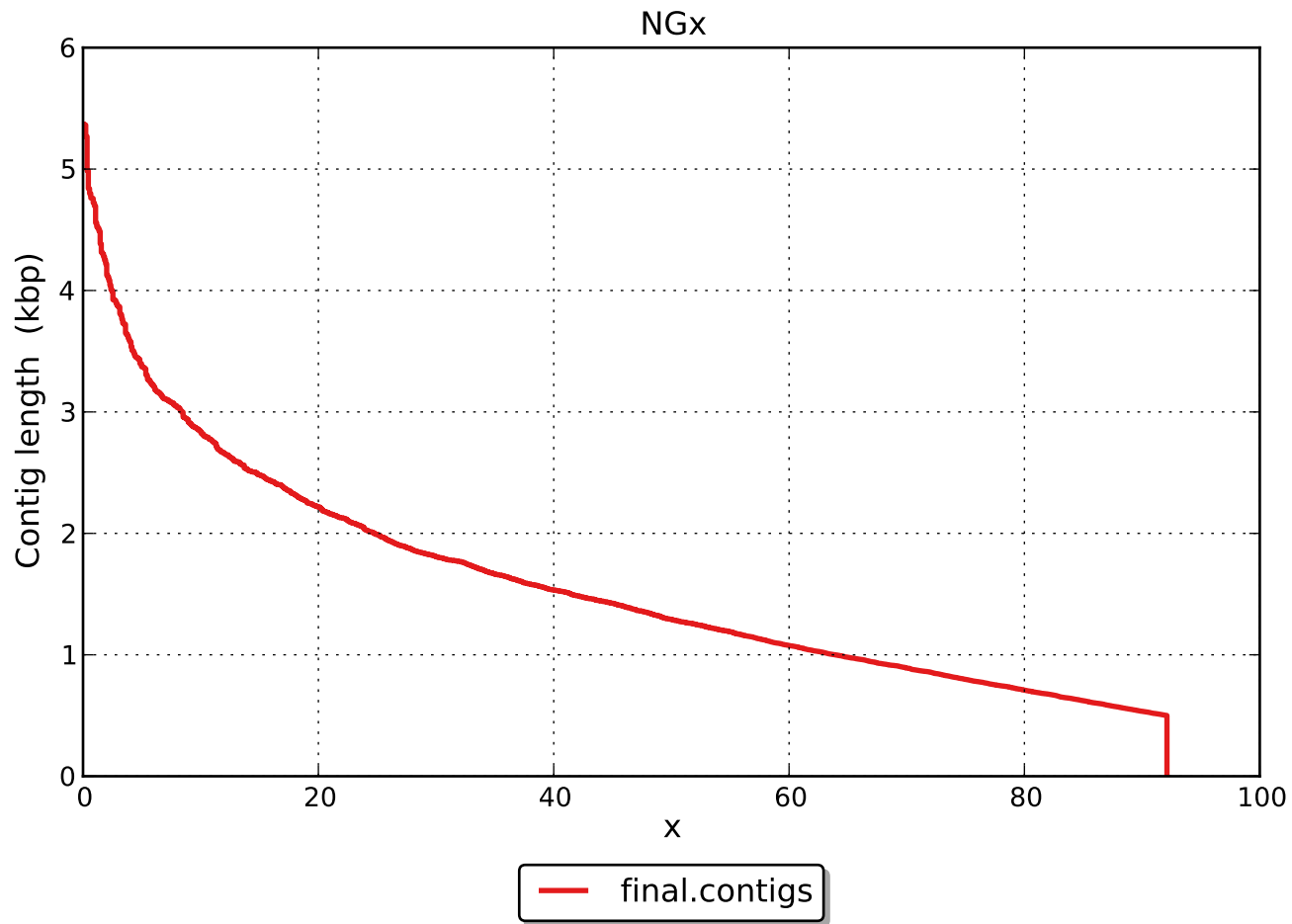
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

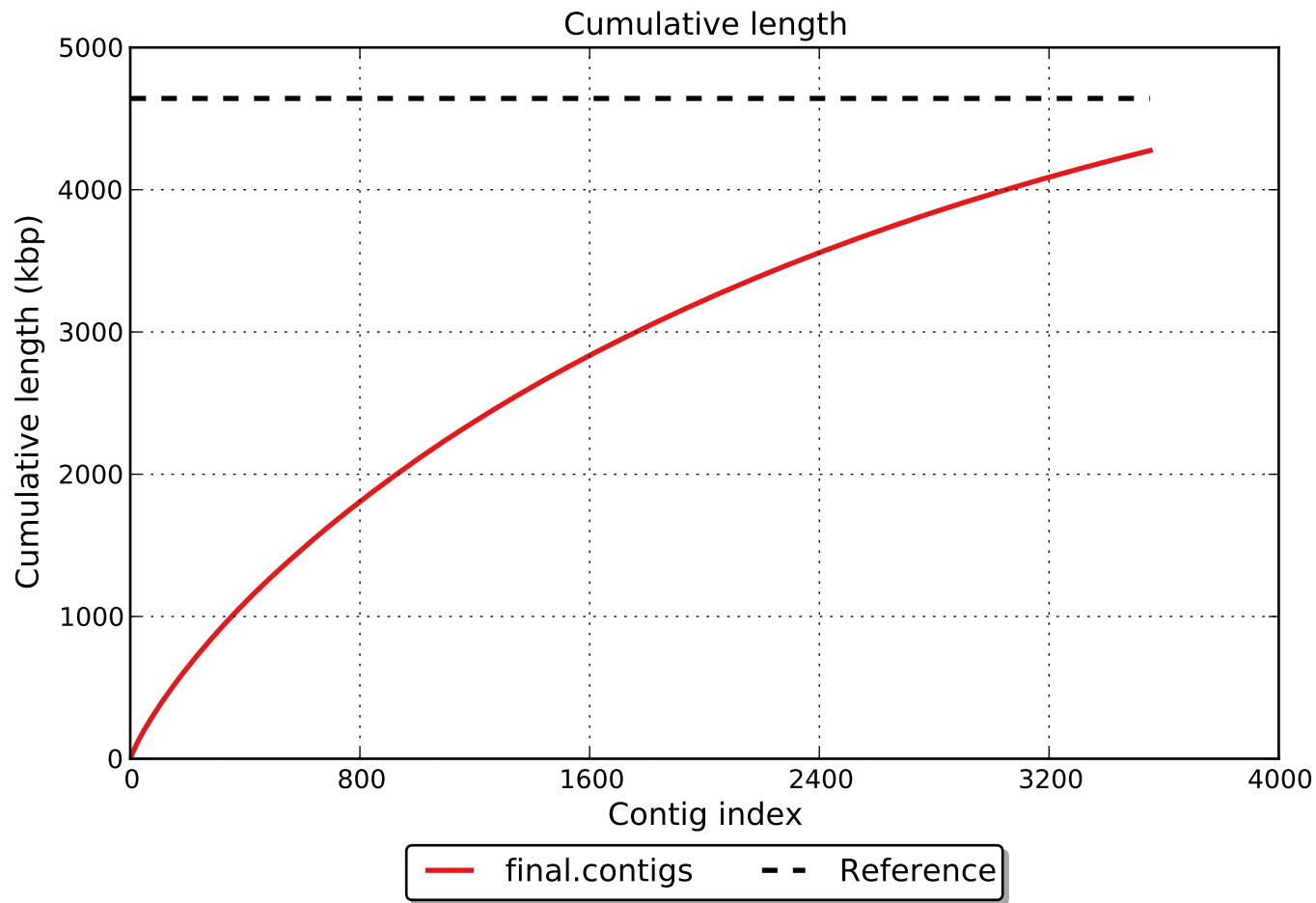
## Unaligned report

	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

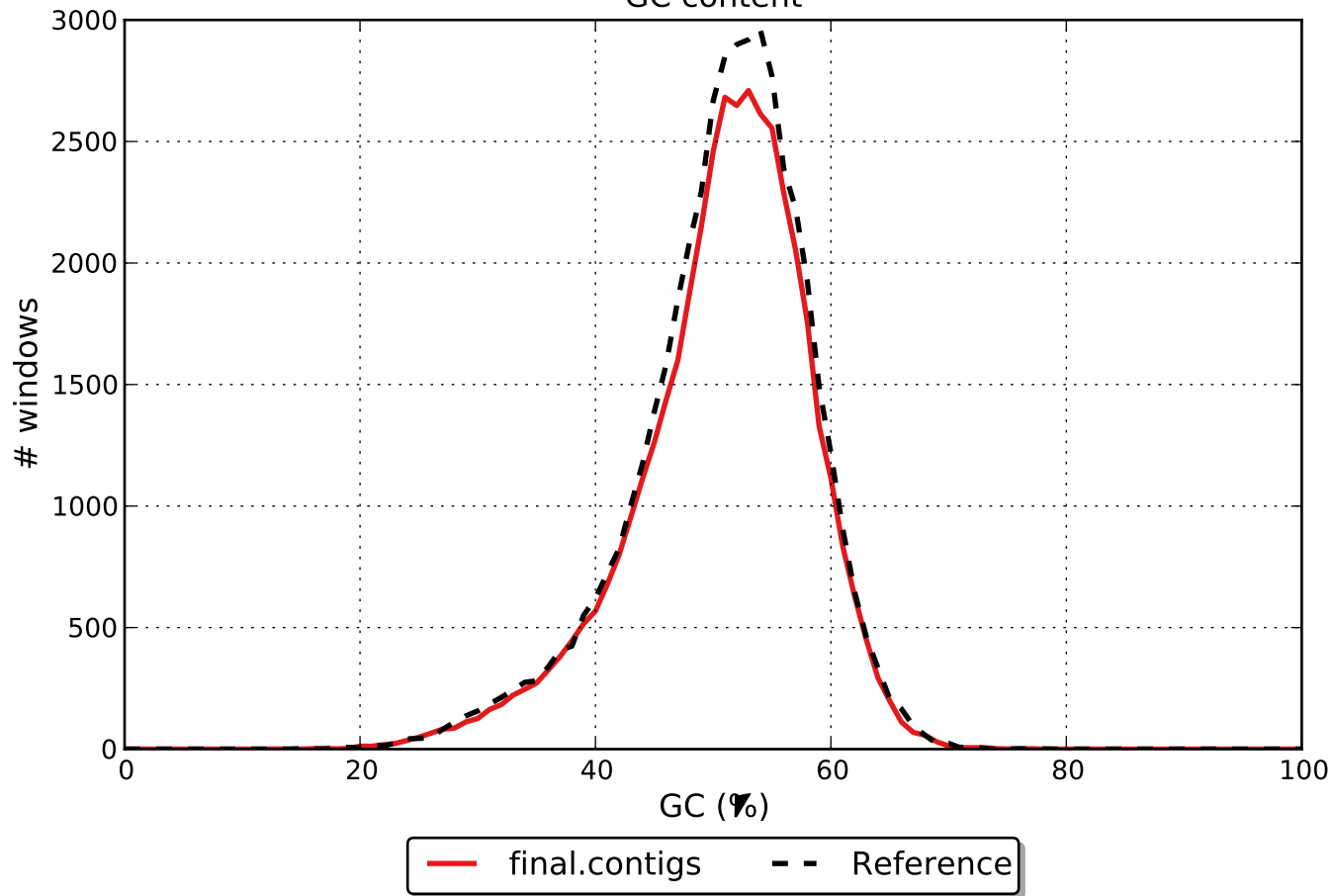
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



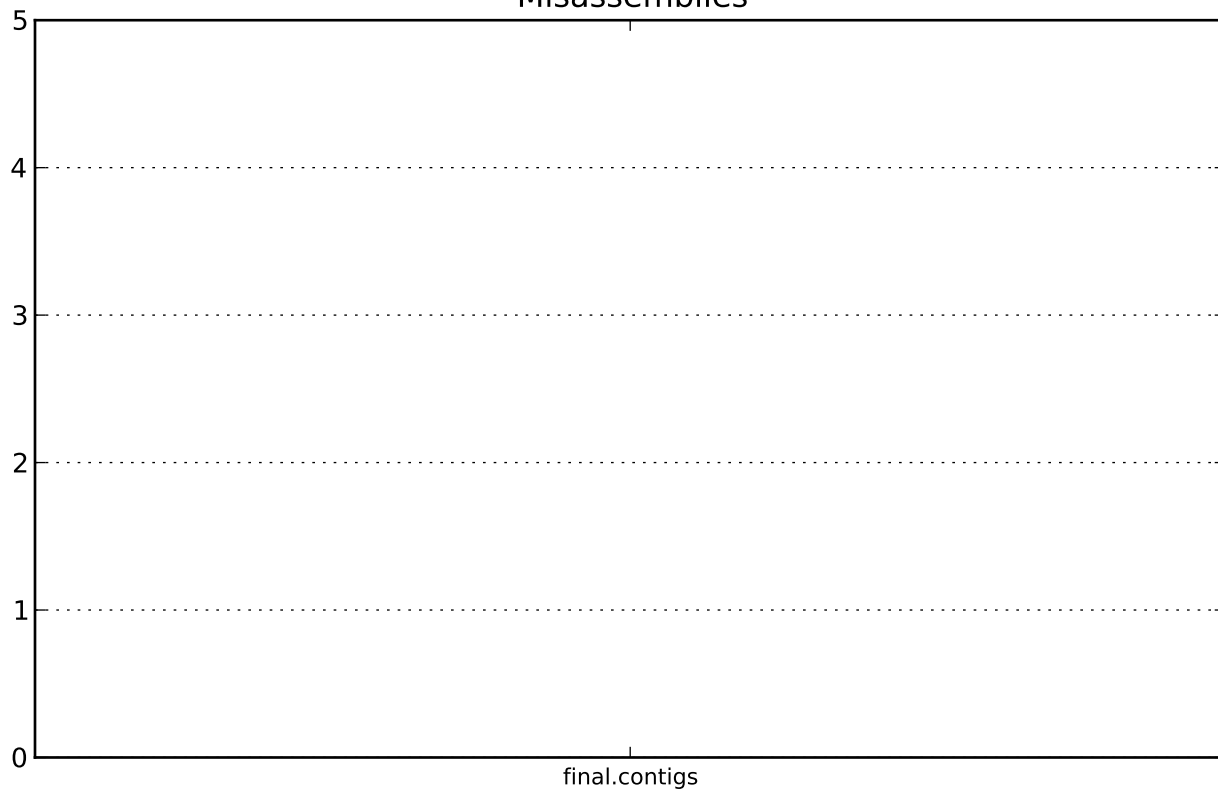




GC content

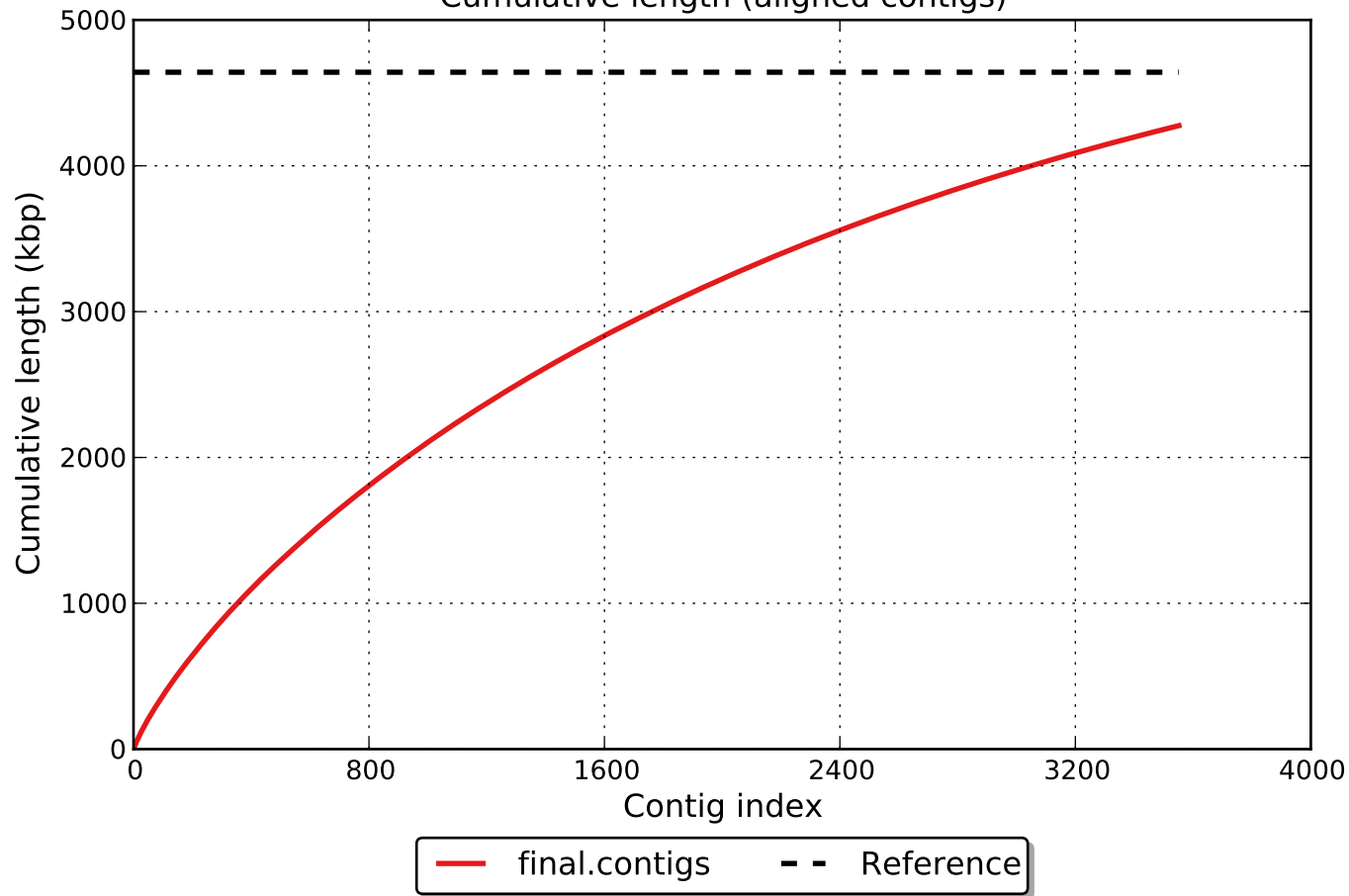


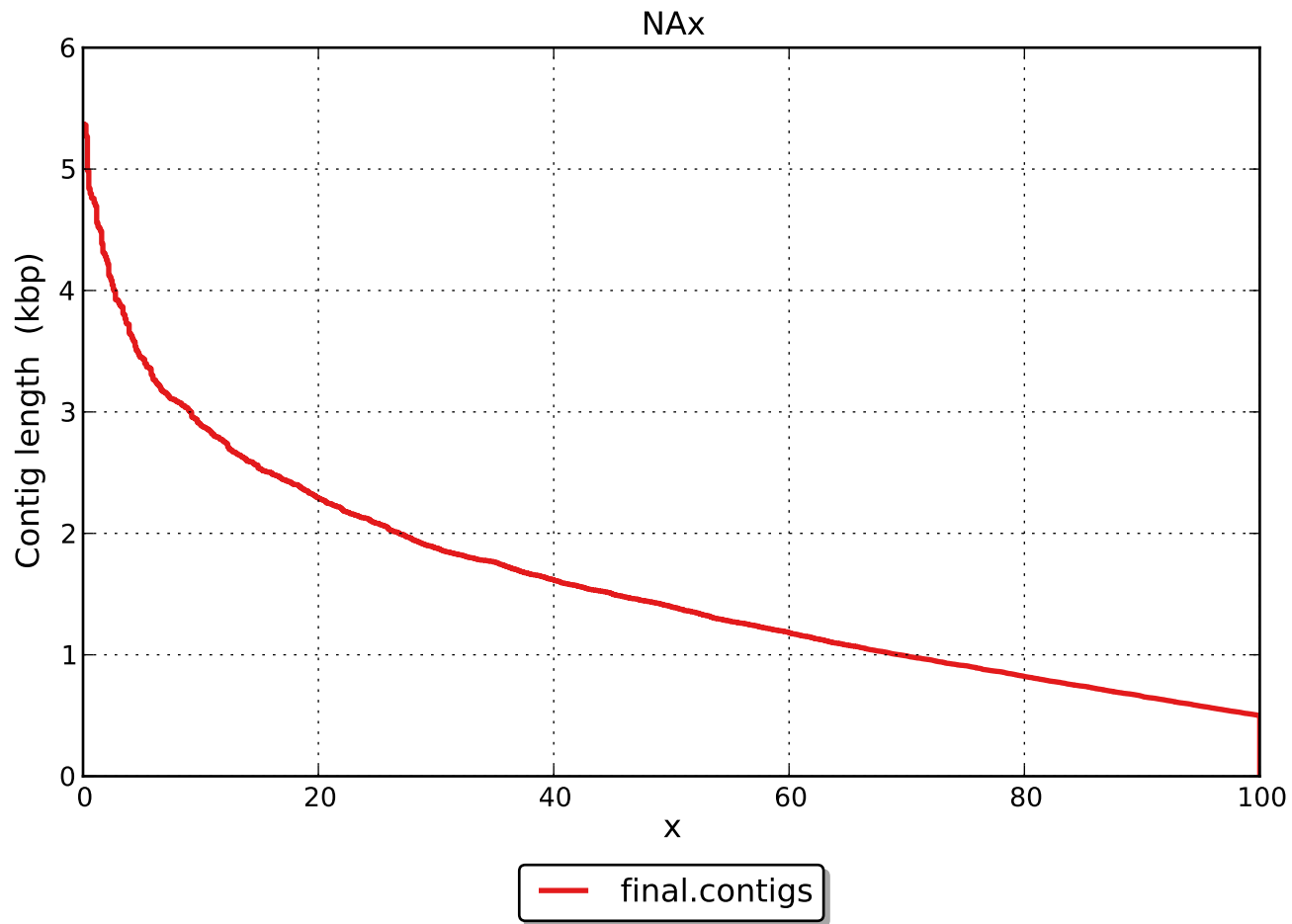
# Misassemblies



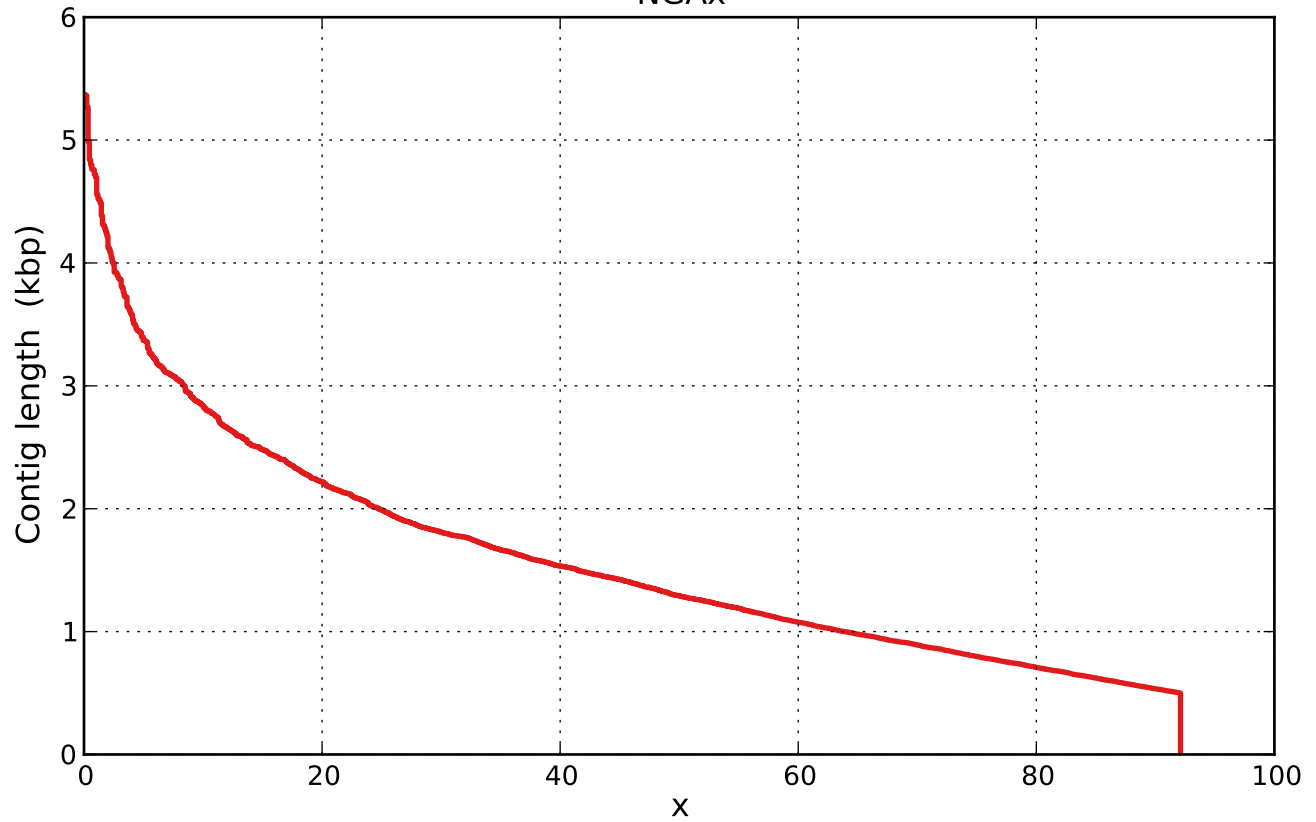


Cumulative length (aligned contigs)





NGAx



— final.contigs