

# Report

	final.contigs
# contigs (>= 0 bp)	5222
# contigs (>= 1000 bp)	1126
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	3995685
Total length (>= 1000 bp)	1659247
Total length (>= 5000 bp)	5490
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3425
Largest contig	5490
Total length	3278442
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	1006
NG50	770
N75	731
L50	1107
LG50	1884
L75	2068
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	9227
# local misassemblies	0
# unaligned contigs	1145 + 15 part
Unaligned length	941536
Genome fraction (%)	49.841
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	577.32
# indels per 100 kbp	0.13
Largest alignment	5093
NA50	838
NGA50	506
LA50	1220
LGA50	2248

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

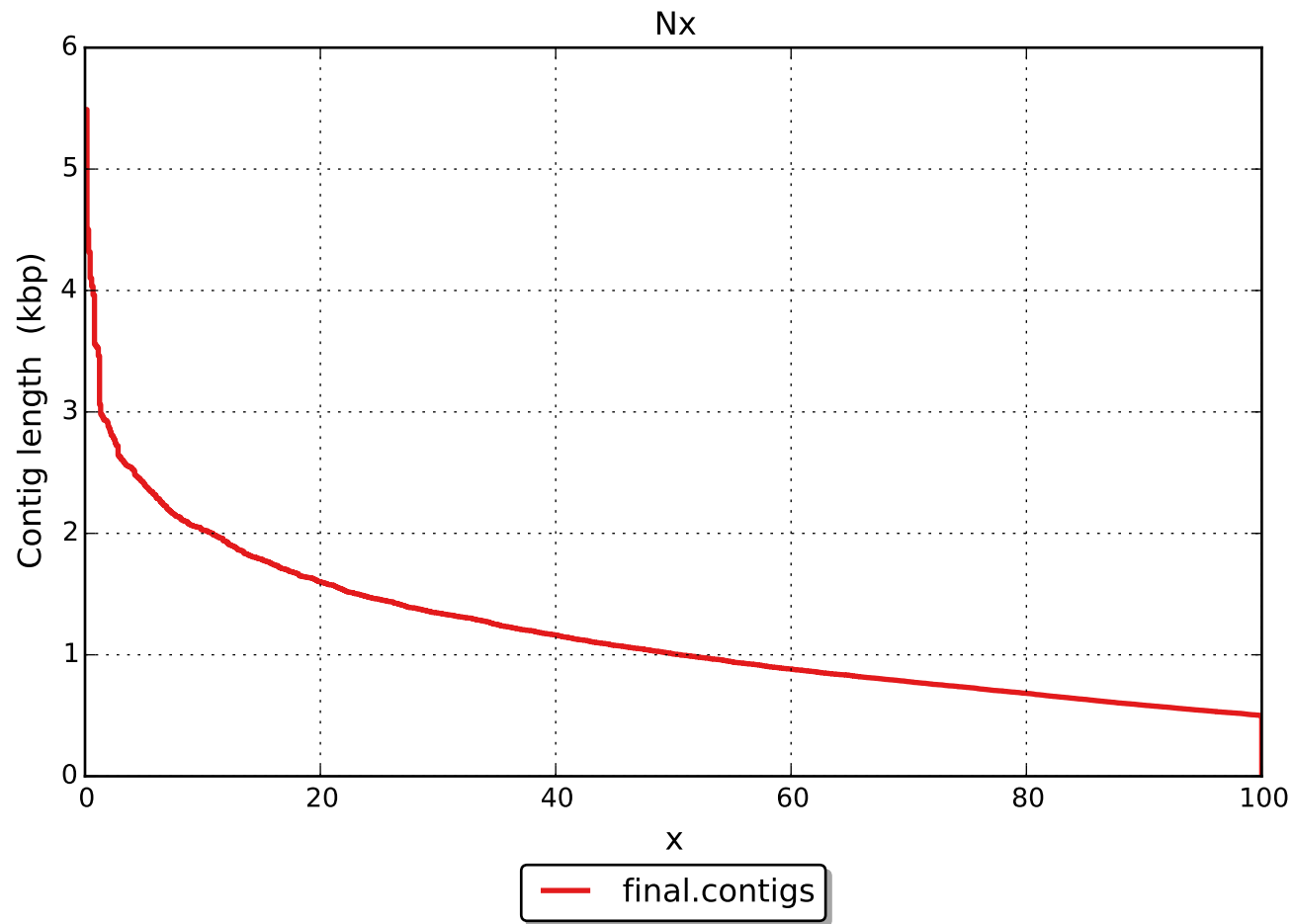
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	9227
# local misassemblies	0
# mismatches	13356
# indels	3
# short indels	3
# long indels	0
Indels length	3

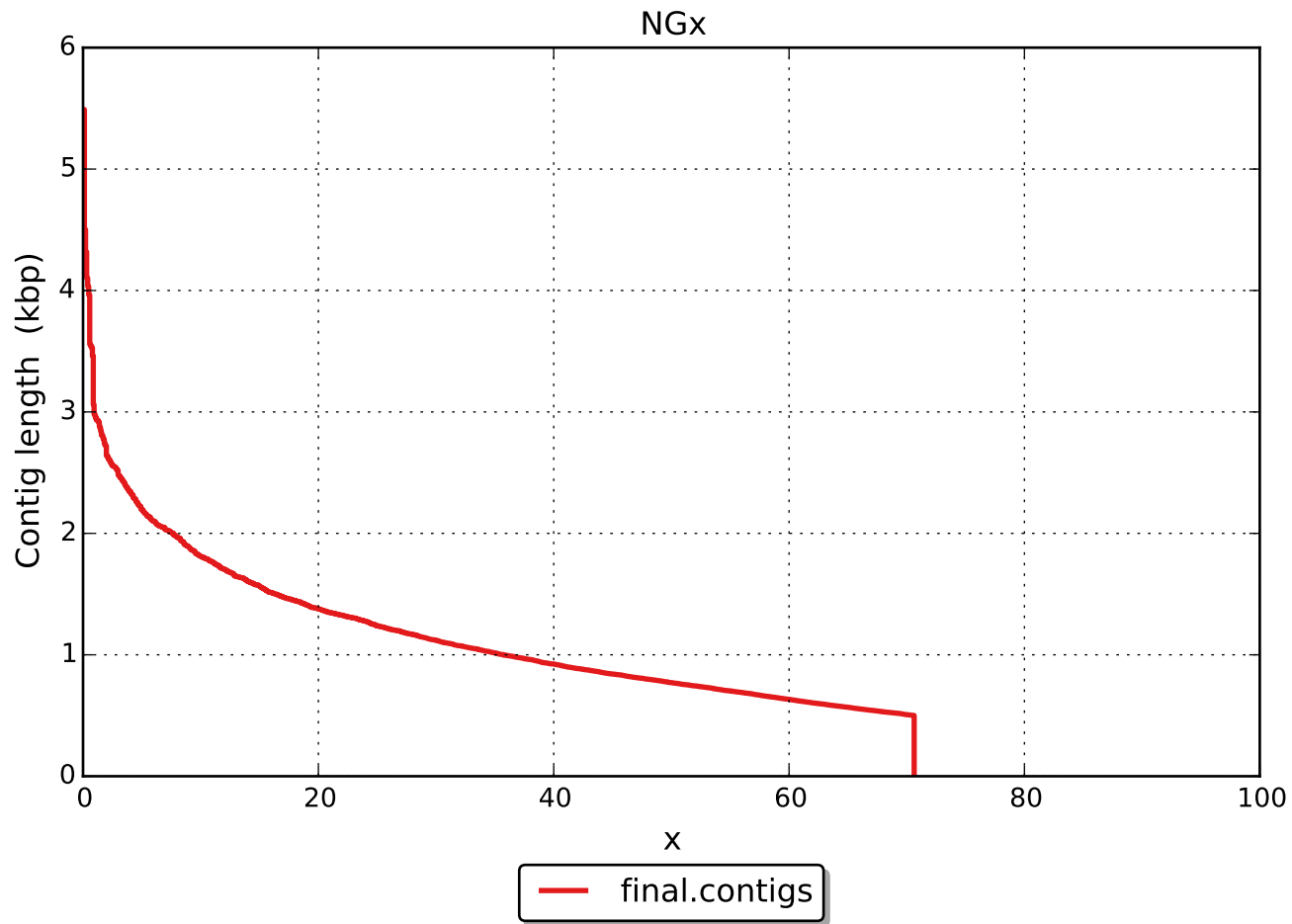
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

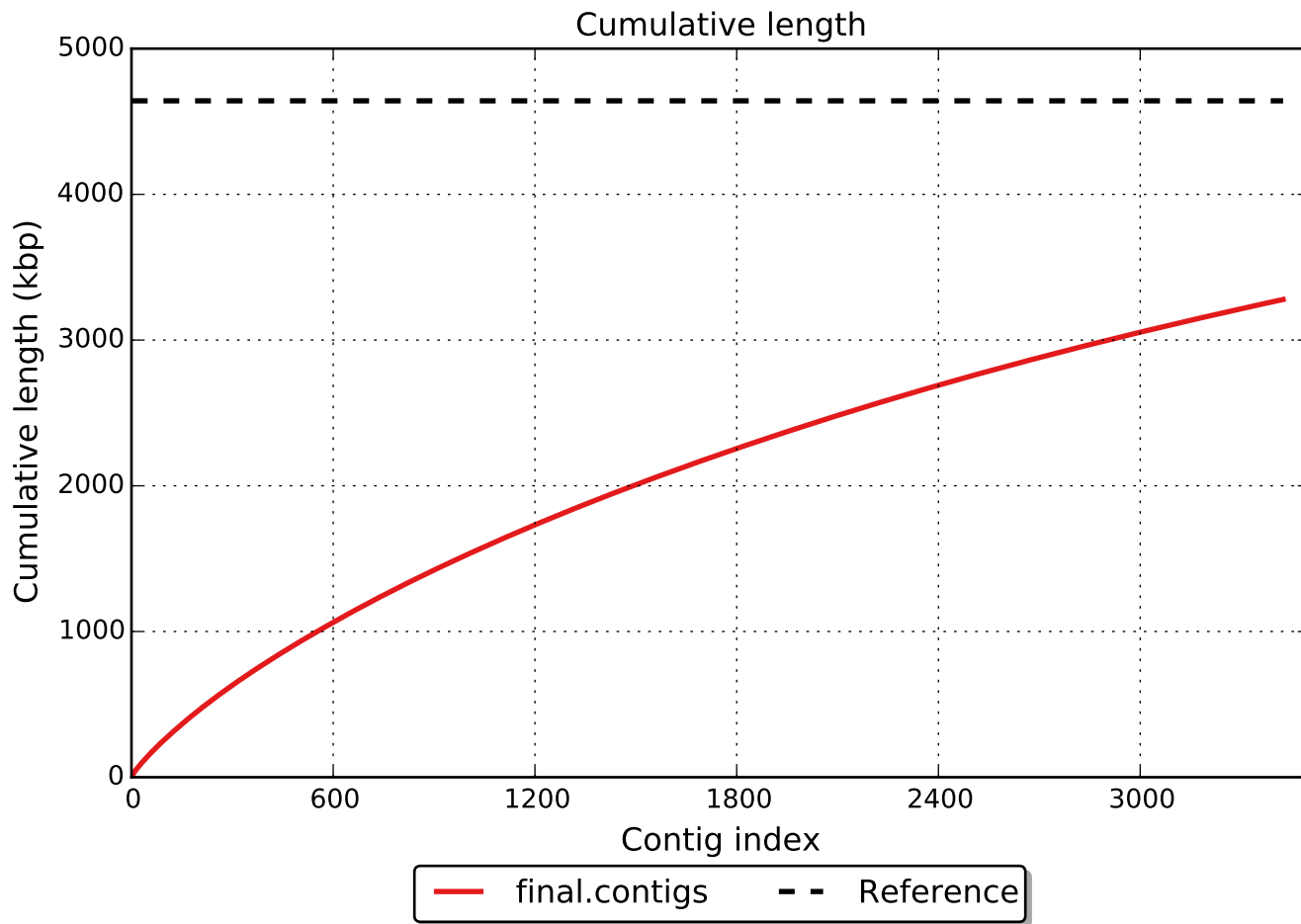
## Unaligned report

	final.contigs
# fully unaligned contigs	1145
Fully unaligned length	935481
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	3
Partially unaligned length	6055
# N's	0

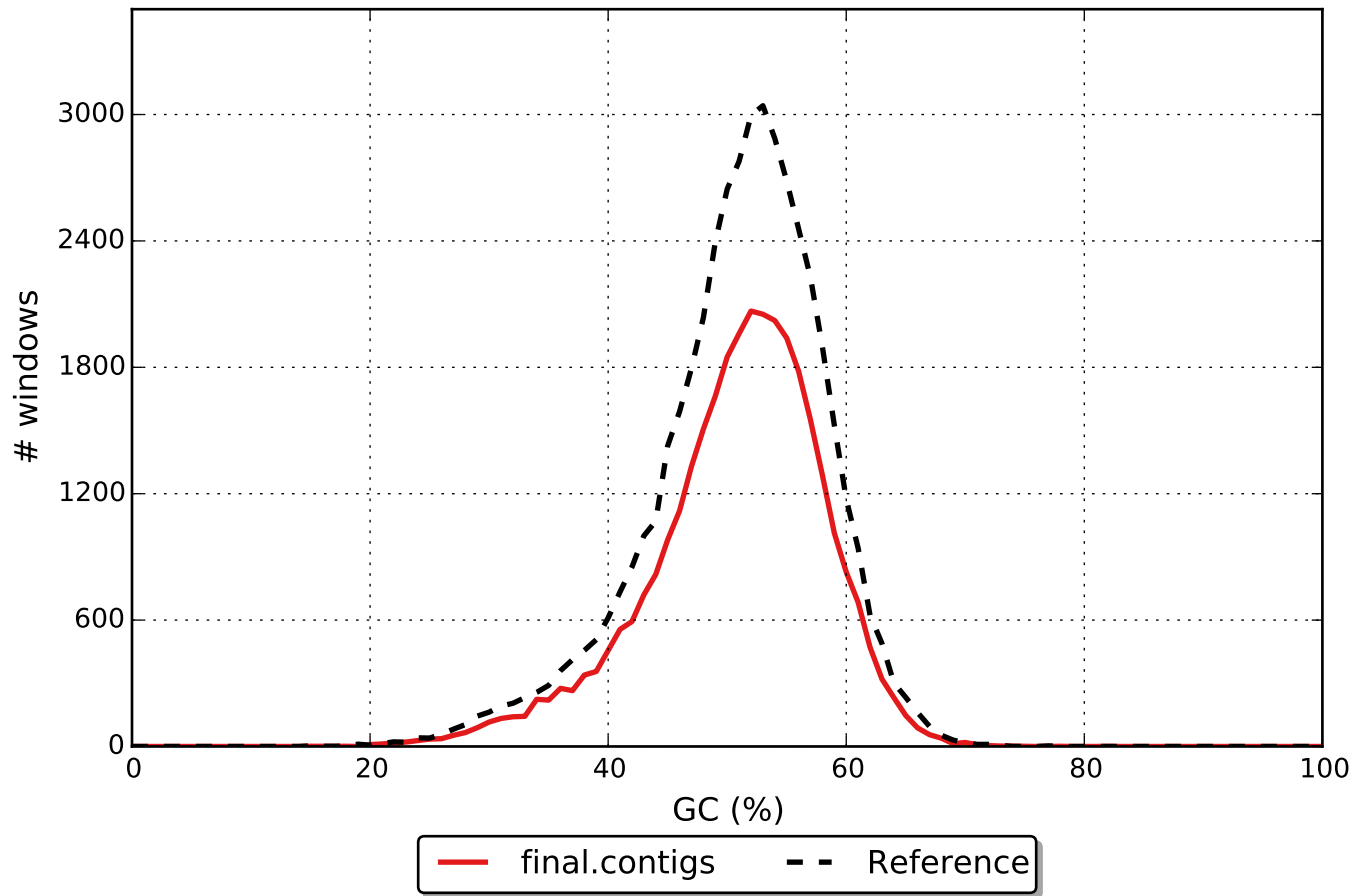
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

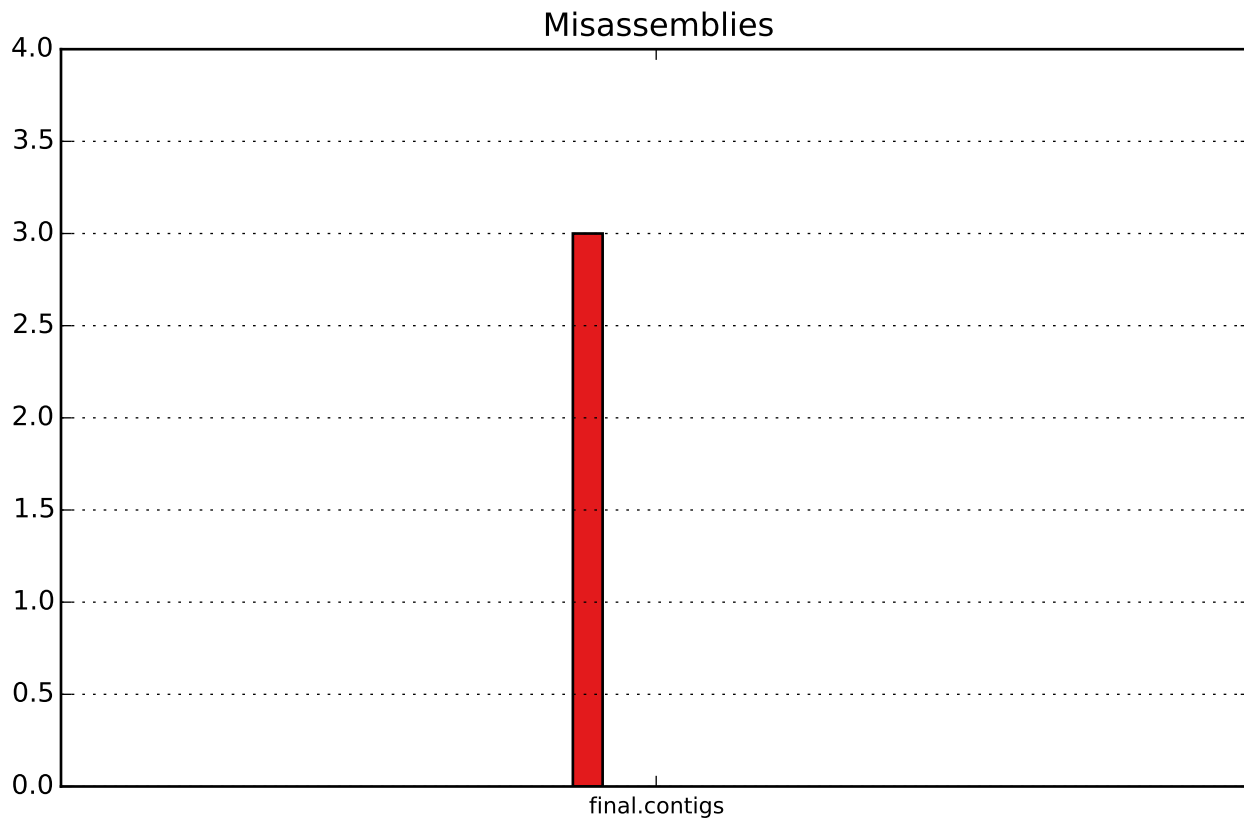






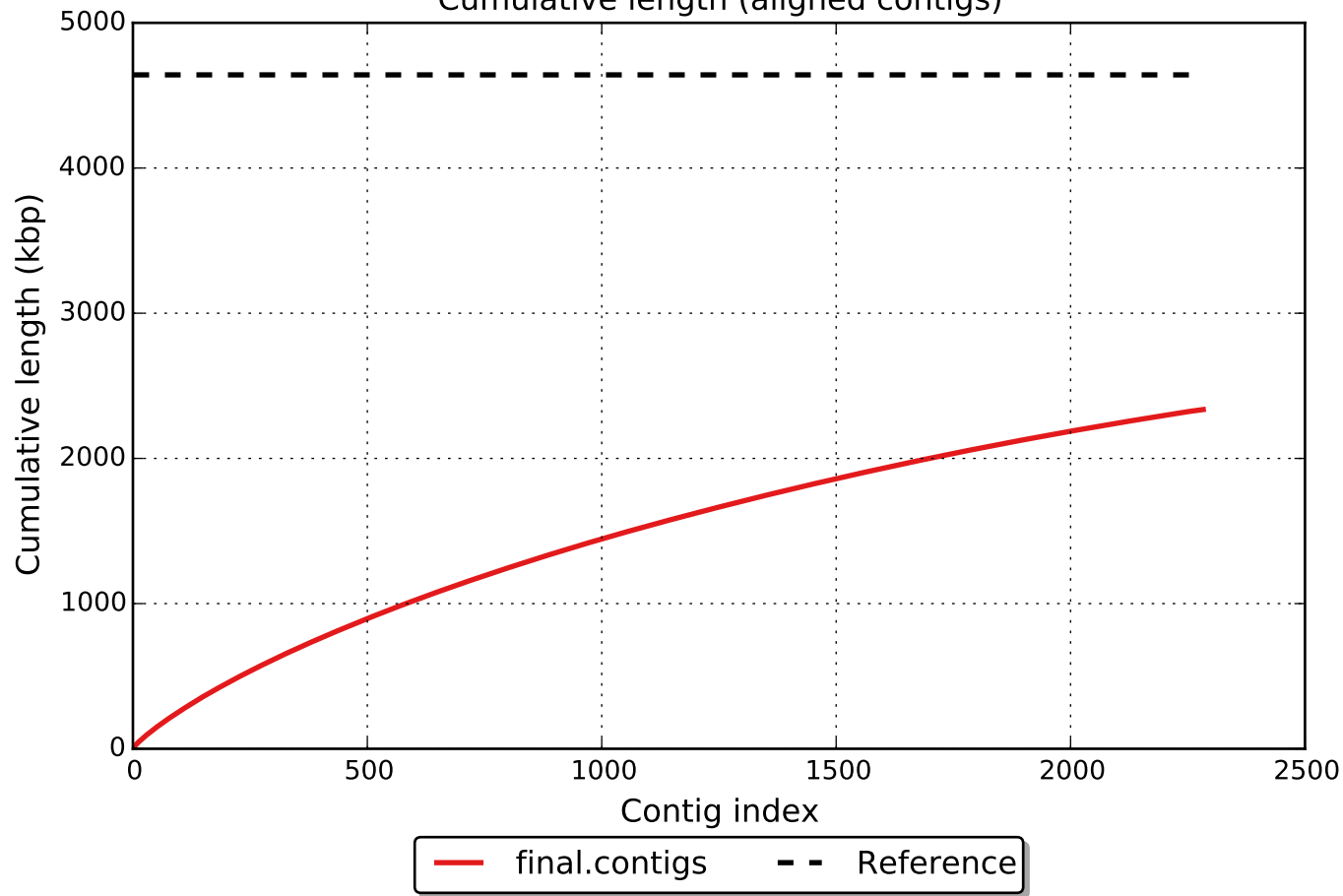
GC content

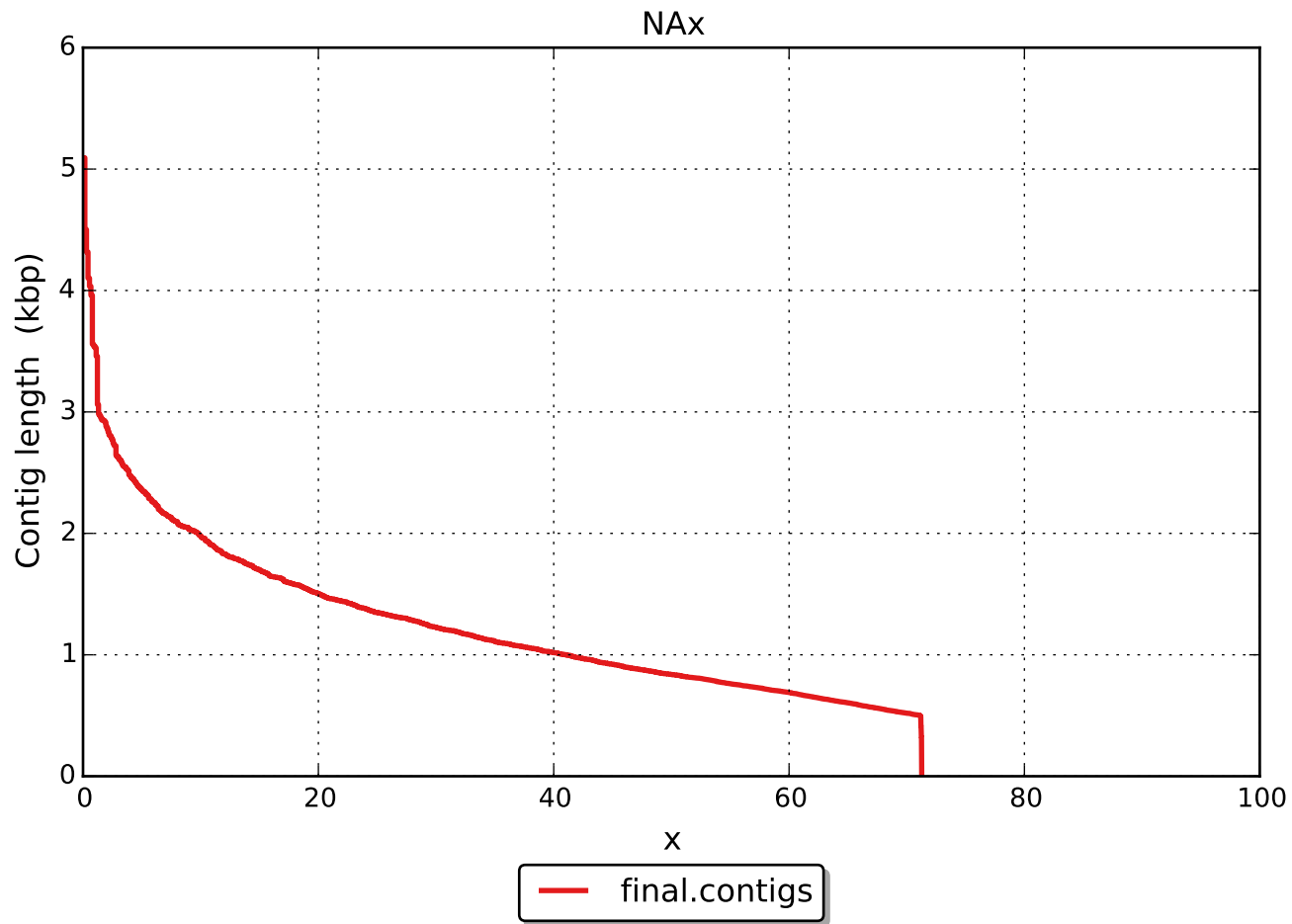






Cumulative length (aligned contigs)





NGAx

