

## Report

	final.contigs
# contigs (>= 1000 bp)	1296
# contigs (>= 5000 bp)	206
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4074219
Total length (>= 5000 bp)	1418015
Total length (>= 10000 bp)	158362
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1743
Largest contig	18957
Total length	4393300
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.78
N50	3567
NG50	3440
N75	2127
NG75	1891
L50	392
LG50	428
L75	789
LG75	882
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	507
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.436
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	514.14
# indels per 100 kbp	0.05
Largest alignment	18957
NA50	3567
NGA50	3440
NA75	2127
NGA75	1891
LA50	392
LGA50	428
LA75	789
LGA75	882

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

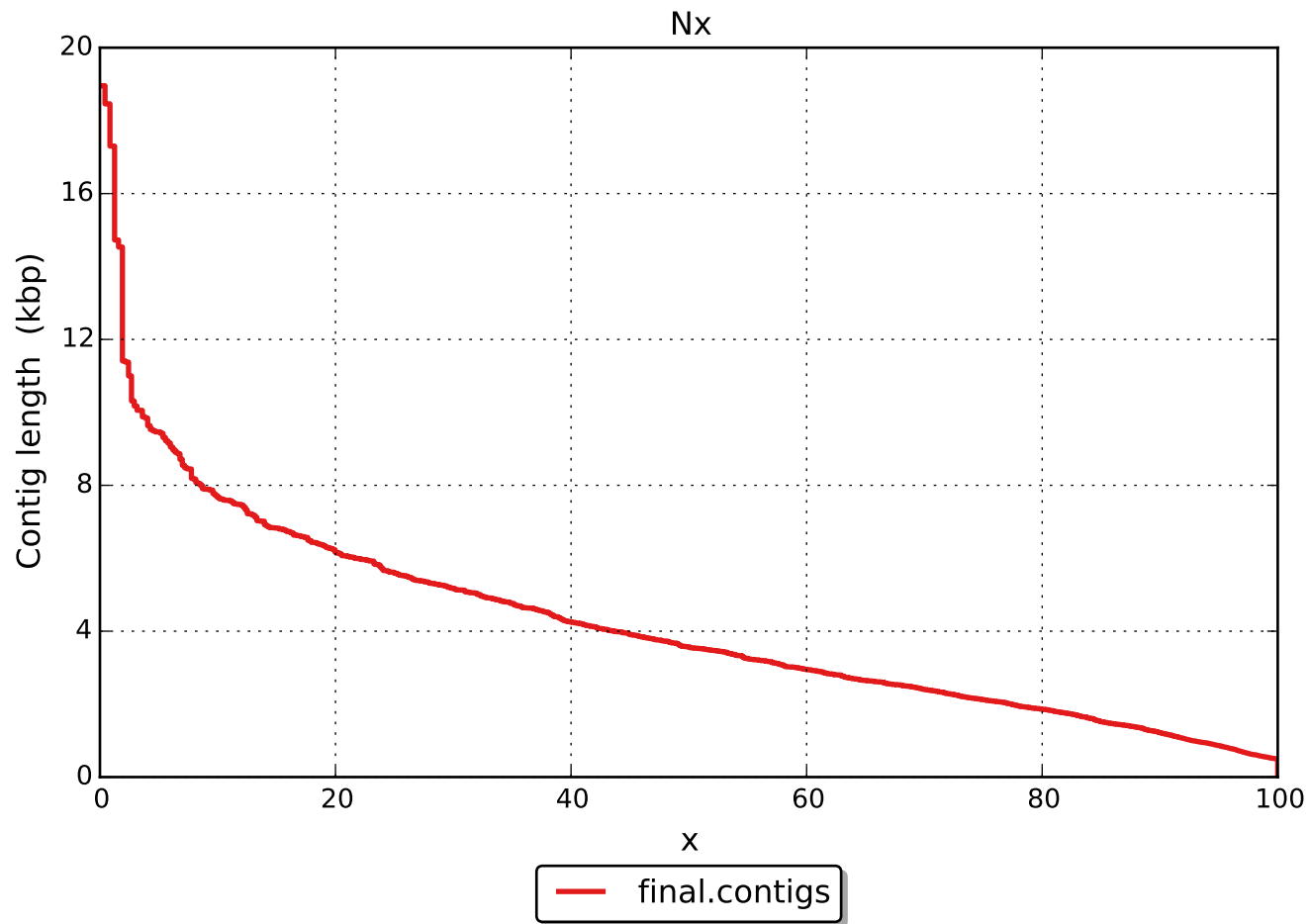
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	507
# local misassemblies	1
# mismatches	21821
# indels	2
# short indels	2
# long indels	0
Indels length	2

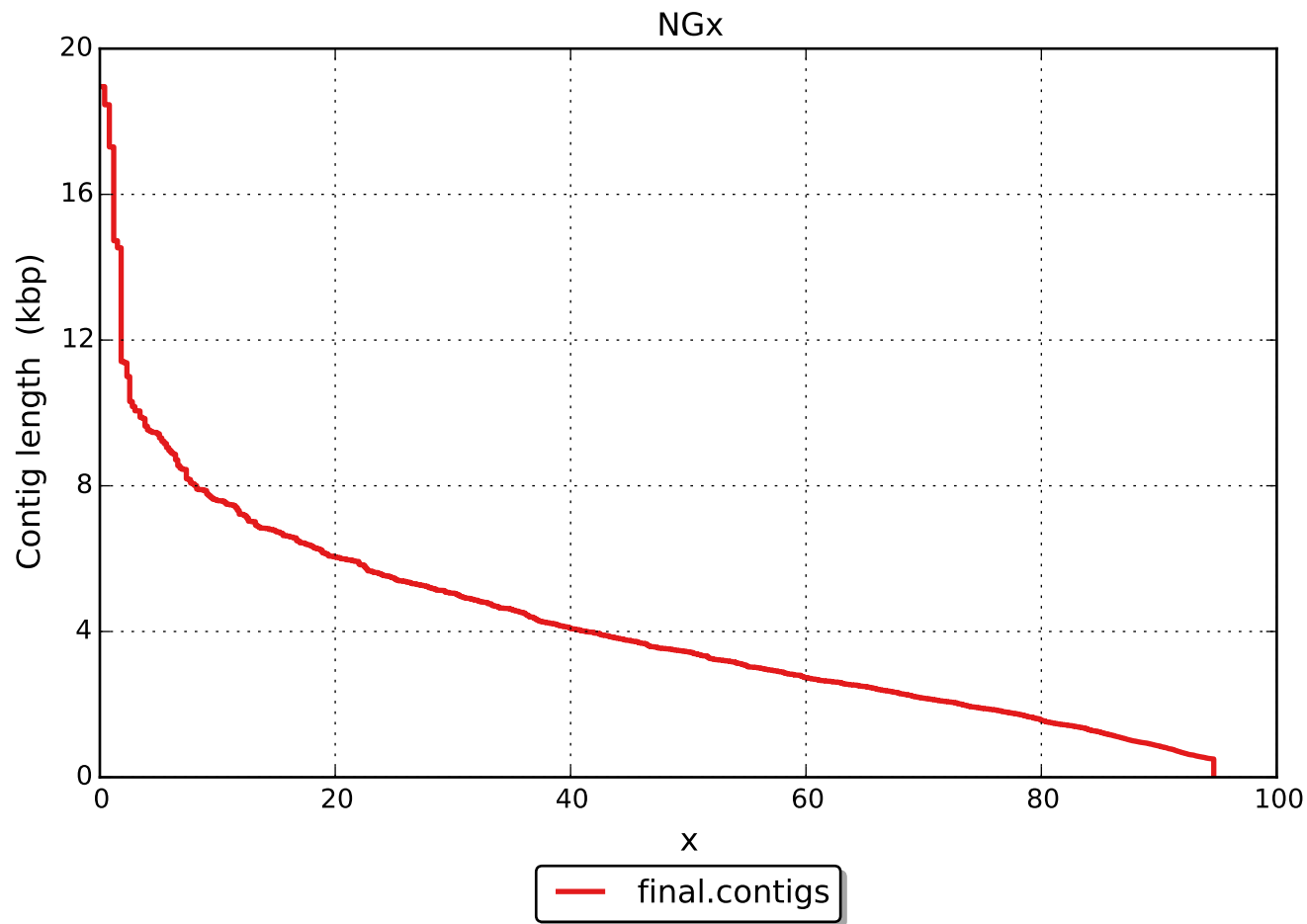
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

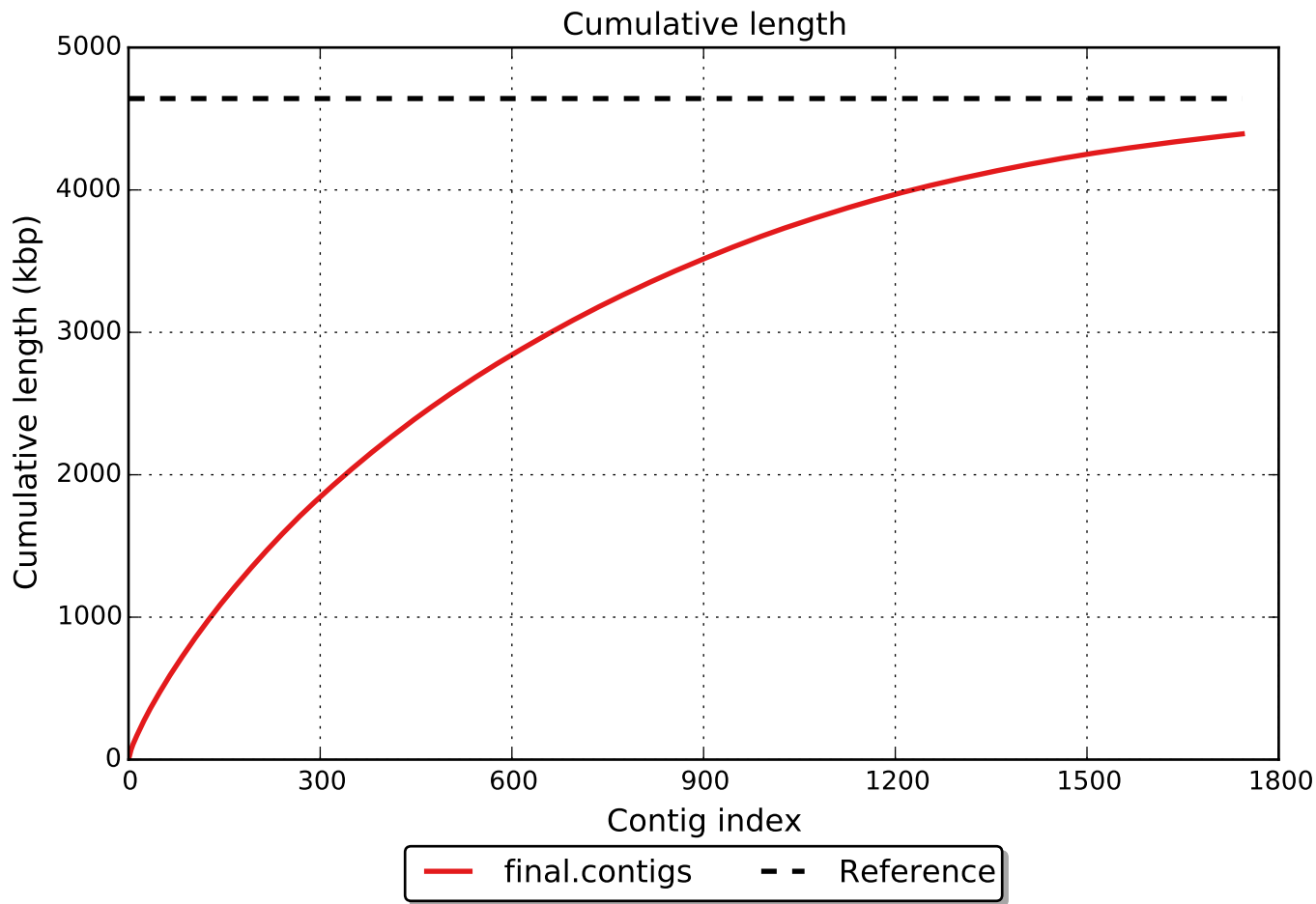
## Unaligned report

	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

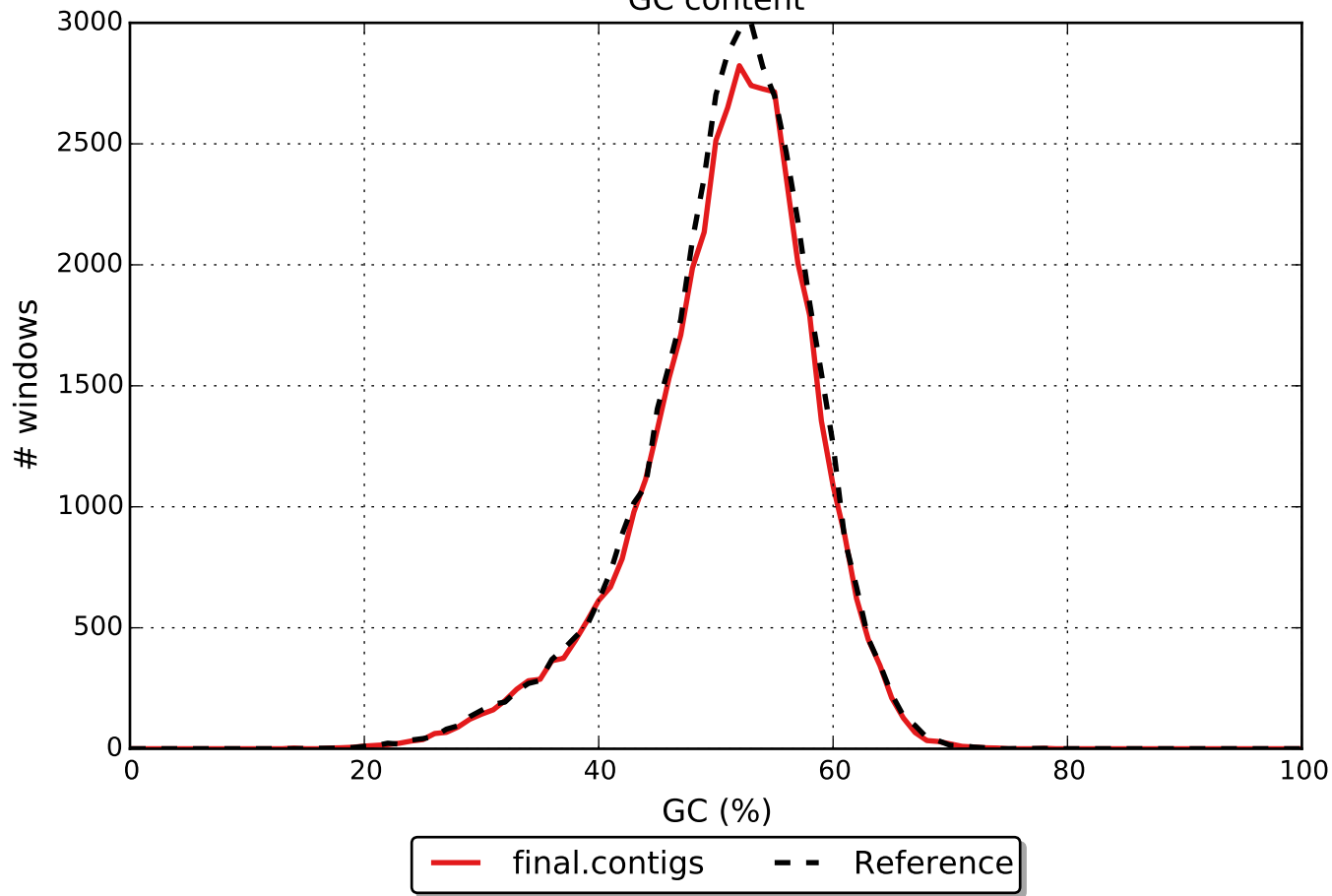
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

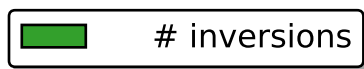
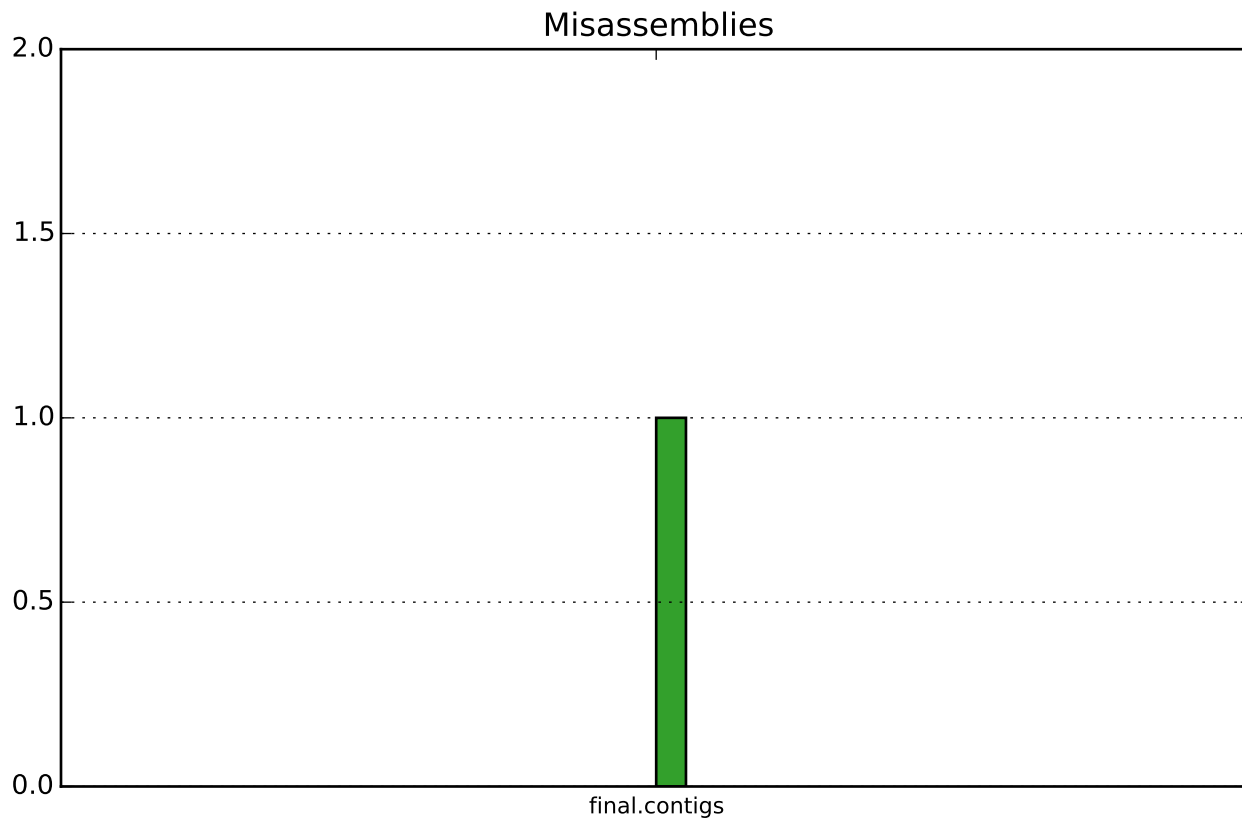






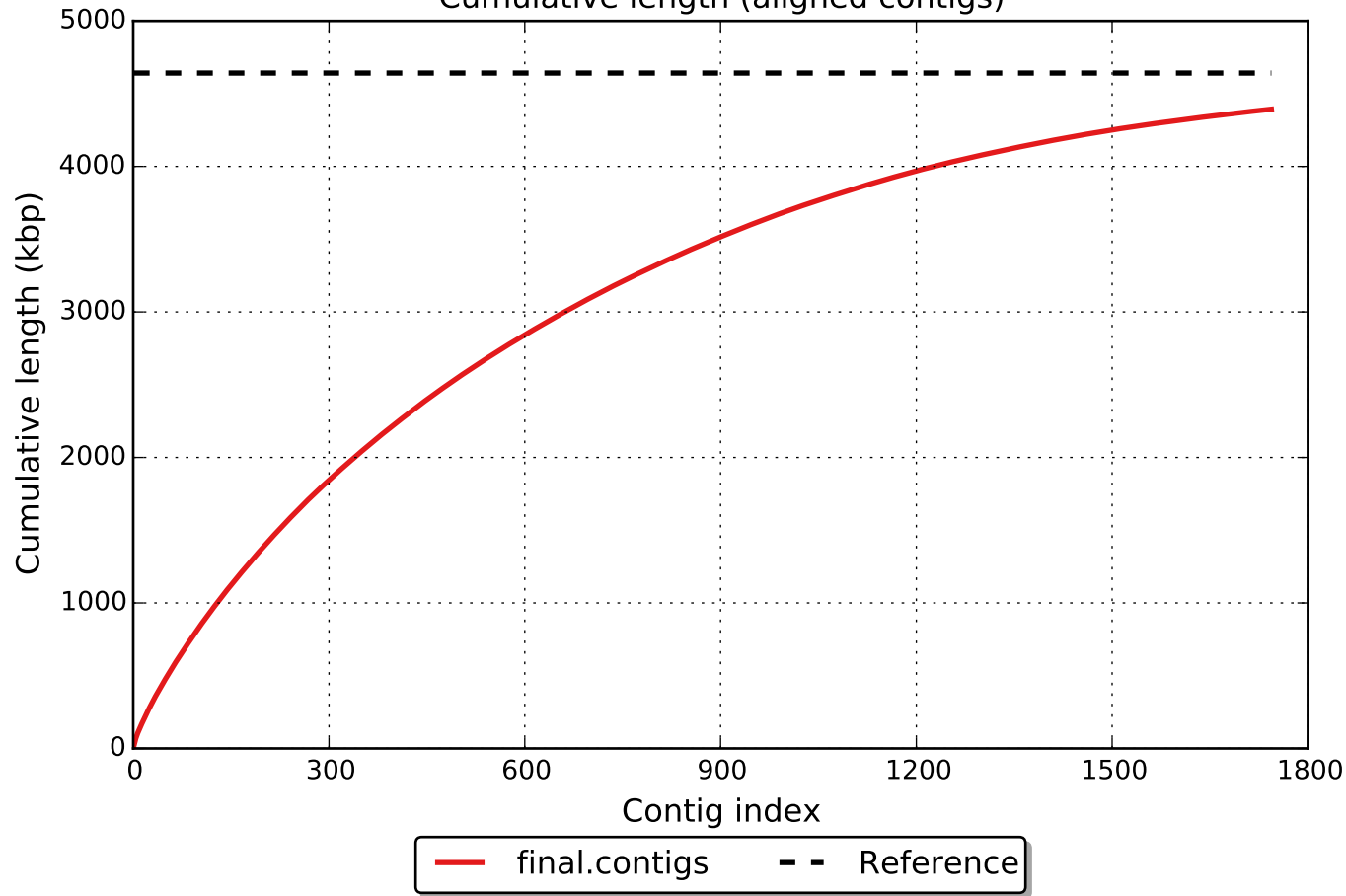
GC content

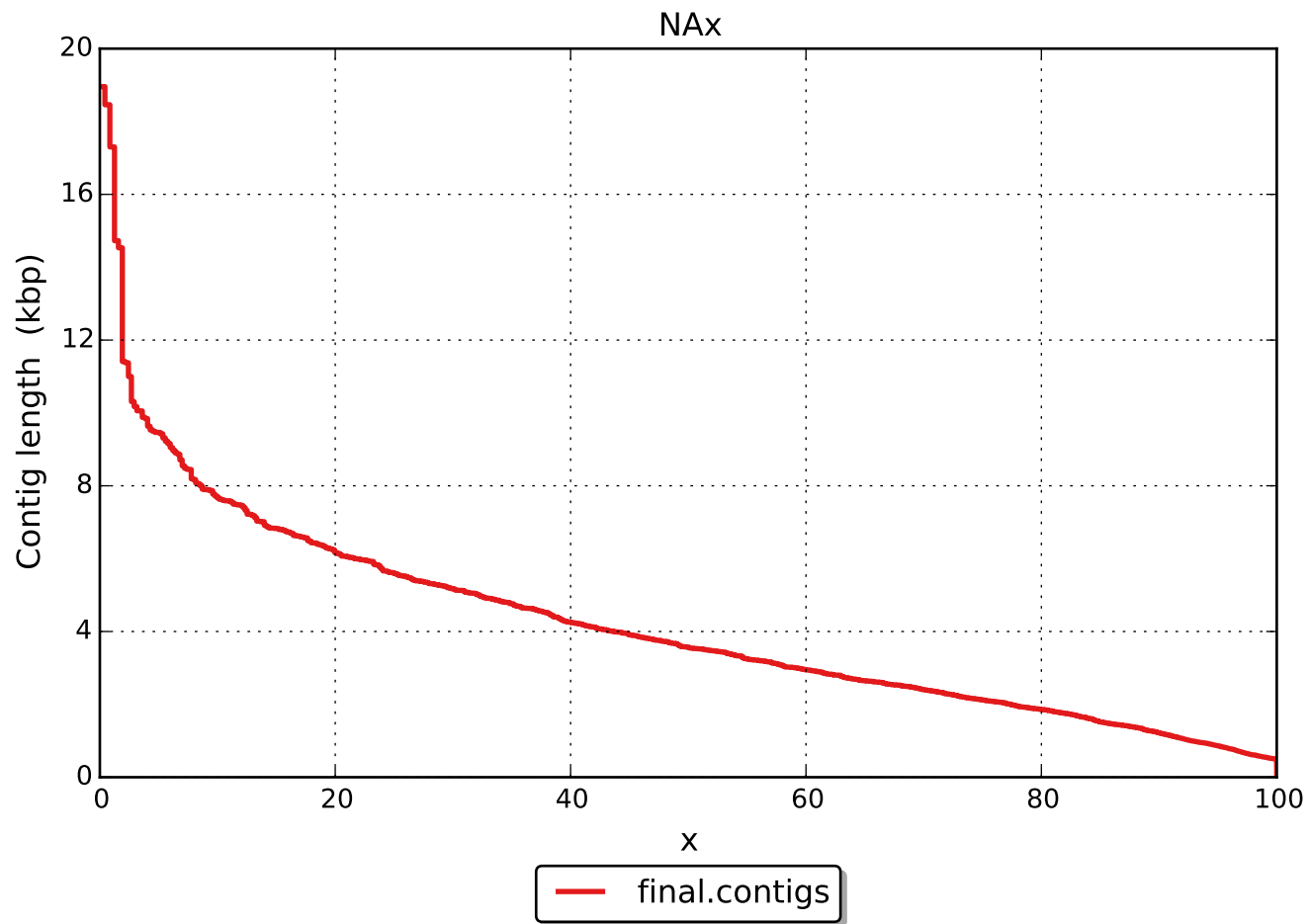






Cumulative length (aligned contigs)





NGAx

