

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	1697
# contigs ( $\geq 1000$ bp)	671
Total length ( $\geq 0$ bp)	2074893
Total length ( $\geq 1000$ bp)	1379814
# contigs	1697
Largest contig	8768
Total length	2074893
Reference length	1892775
GC (%)	32.31
Reference GC (%)	32.26
N50	1503
NG50	1725
N75	810
NG75	941
L50	384
LG50	328
L75	869
LG75	712
# misassemblies	16
# misassembled contigs	16
Misassembled contigs length	13747
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	316
Genome fraction (%)	89.317
Duplication ratio	1.227
# N's per 100 kbp	0.00
# mismatches per 100 kbp	837.70
# indels per 100 kbp	0.12
Largest alignment	8768
NA50	1498
NGA50	1725
NA75	807
NGA75	938
LA50	385
LGA50	328
LA75	869
LGA75	713

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).

## Misassemblies report

	final.contigs
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	16
Misassembled contigs length	13747
# local misassemblies	0
# mismatches	14162
# indels	2
# short indels	2
# long indels	0
Indels length	2

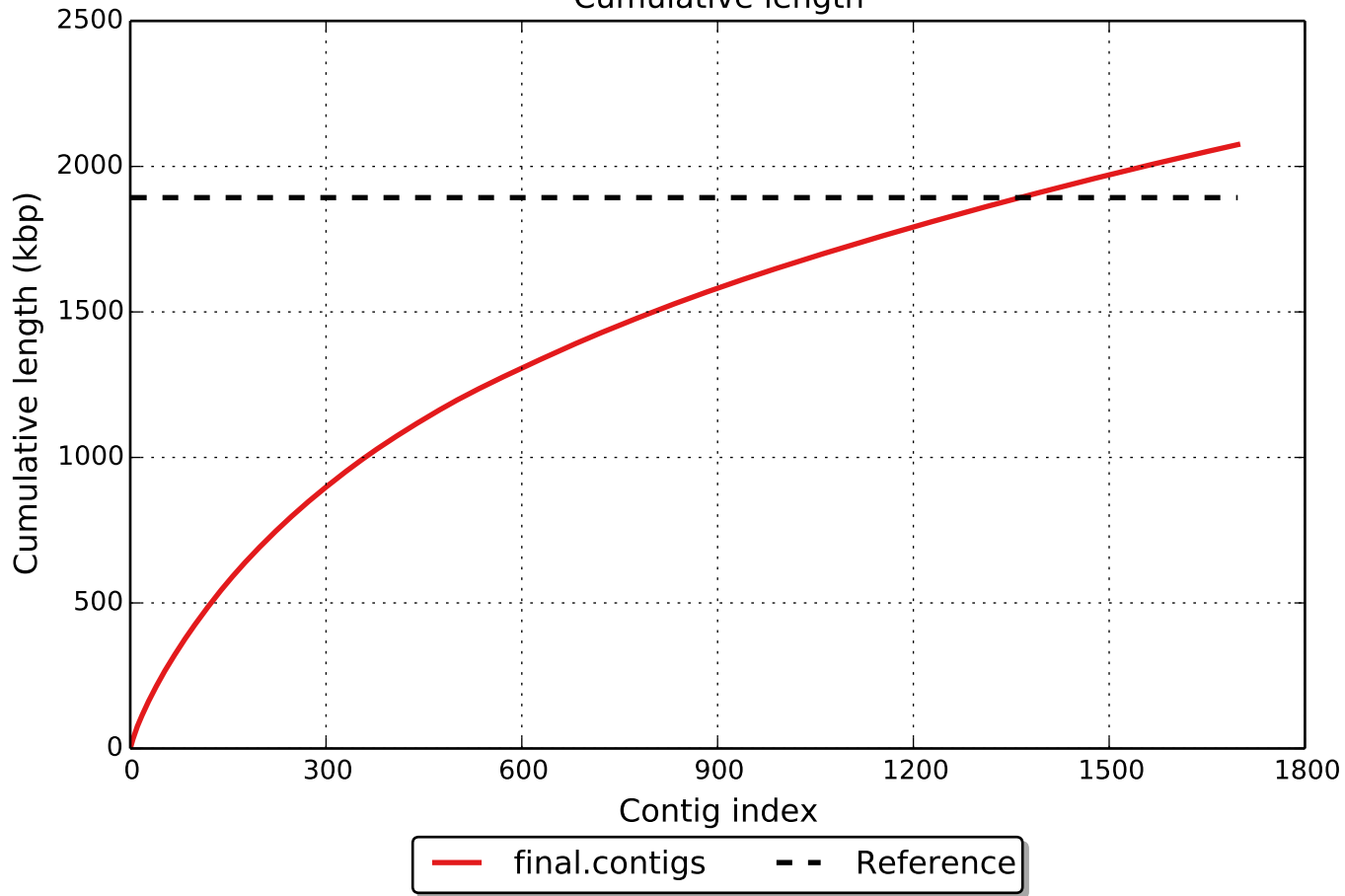
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

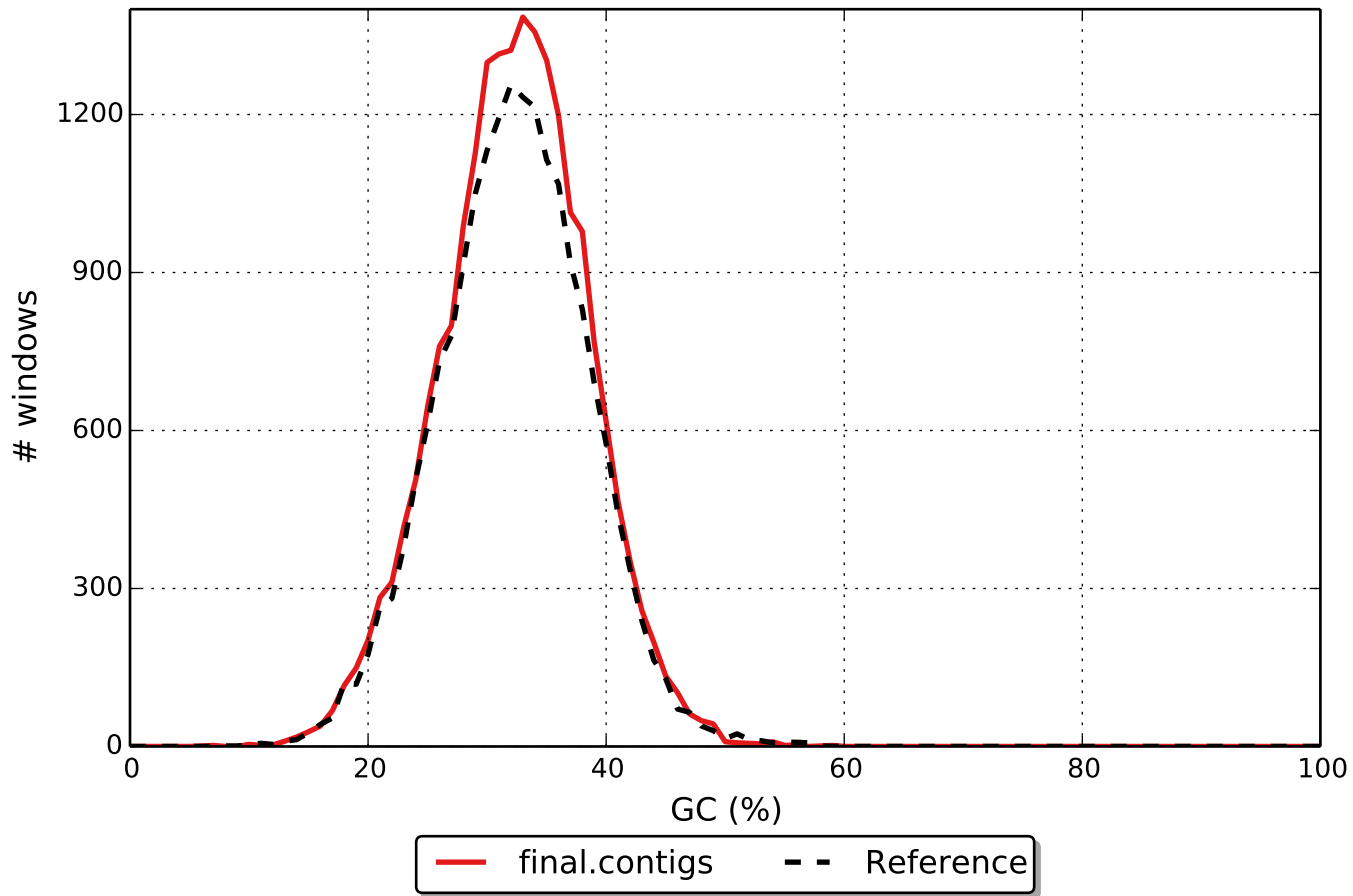
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	316
# N's	0

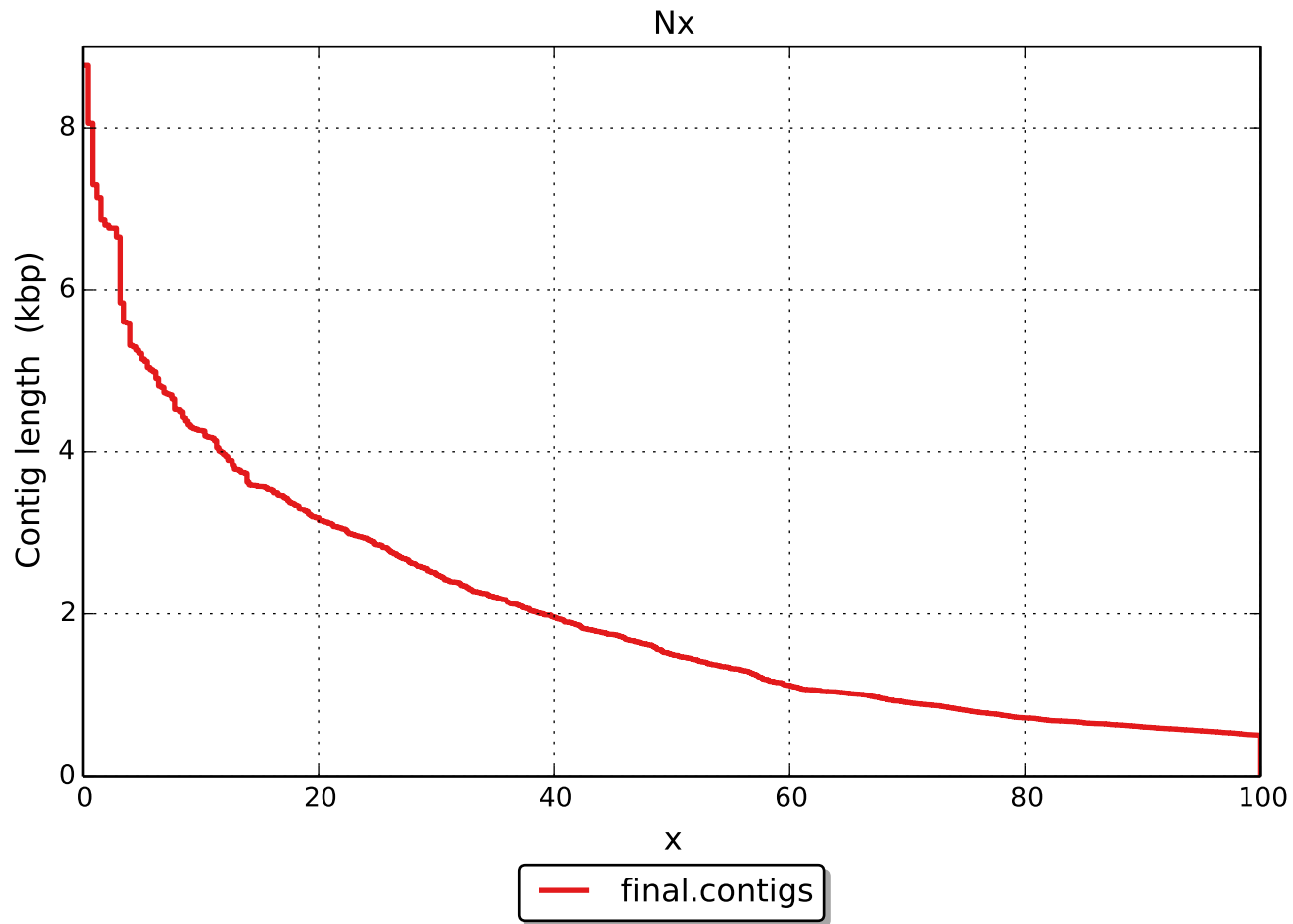
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Cumulative length

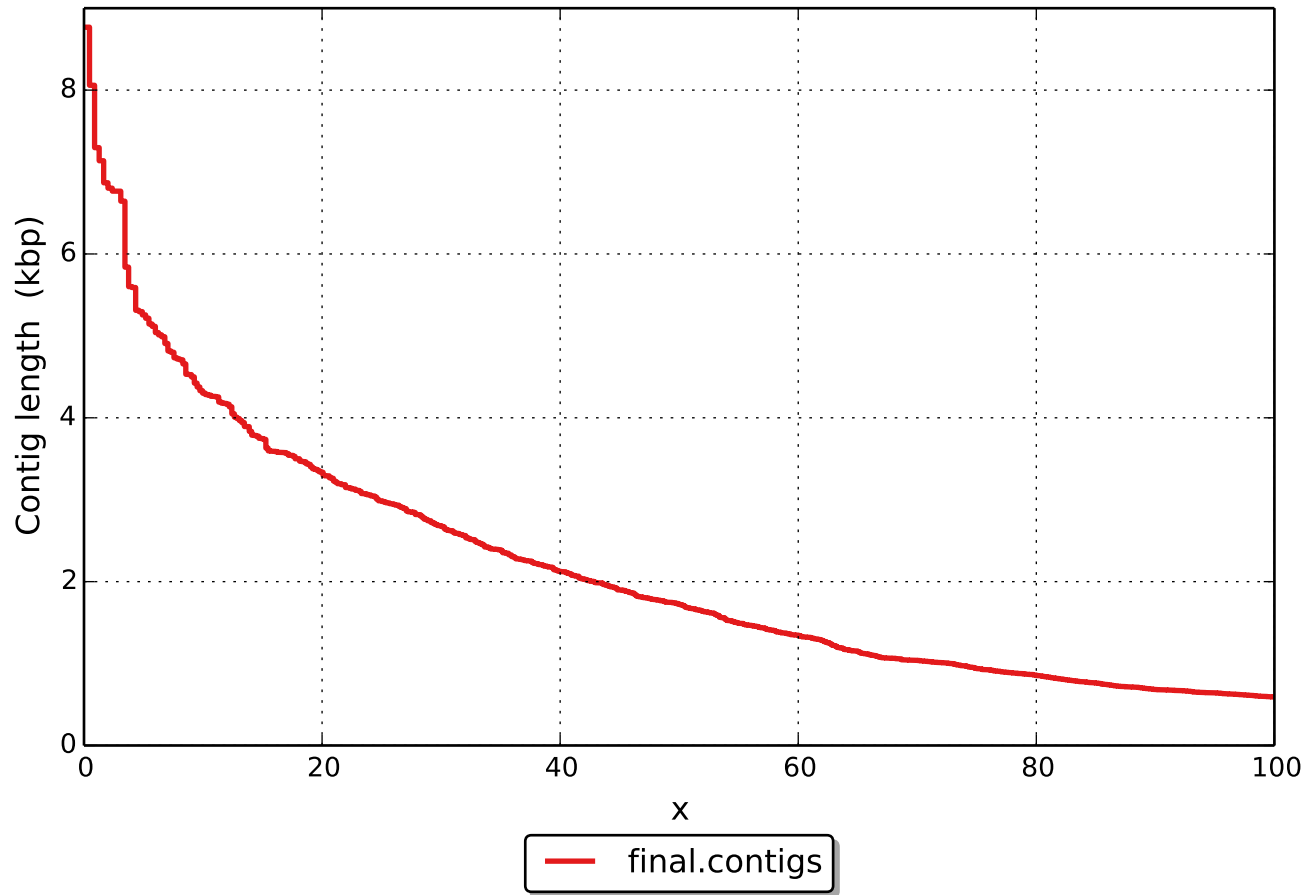


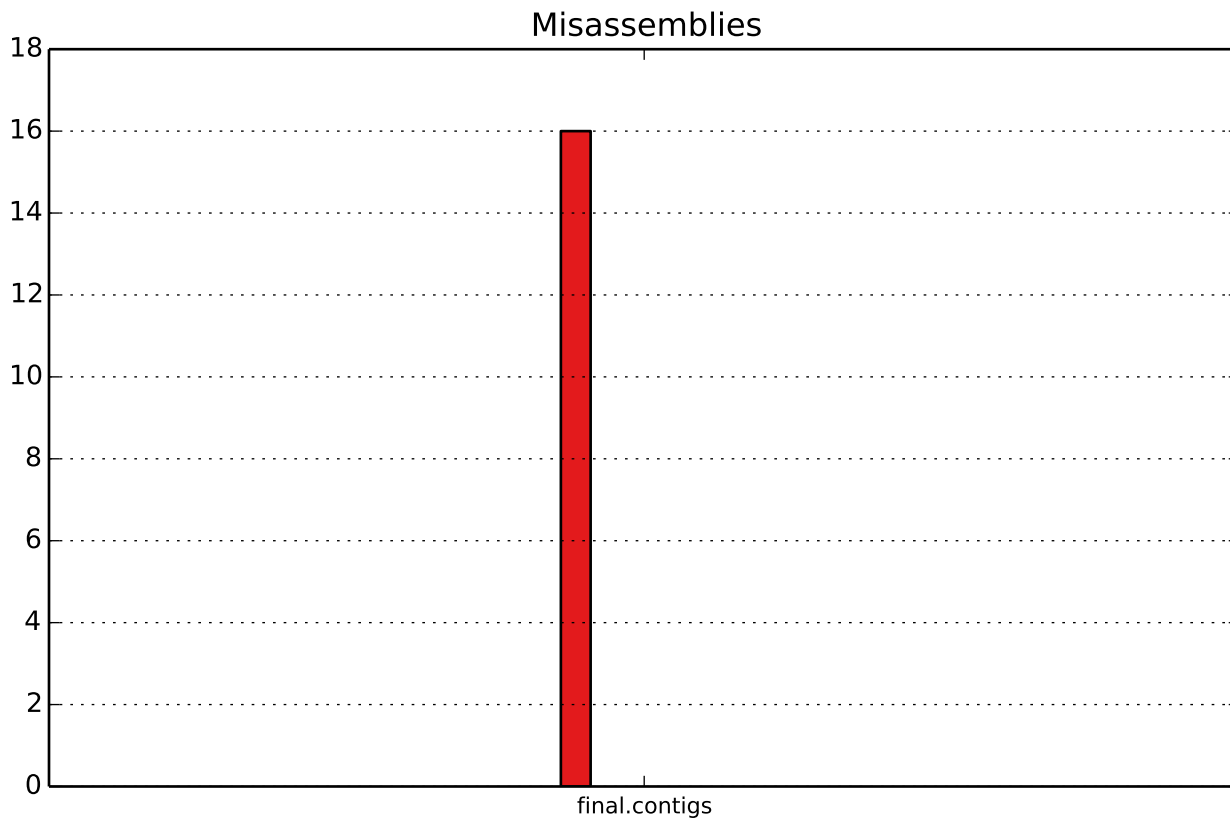
GC content





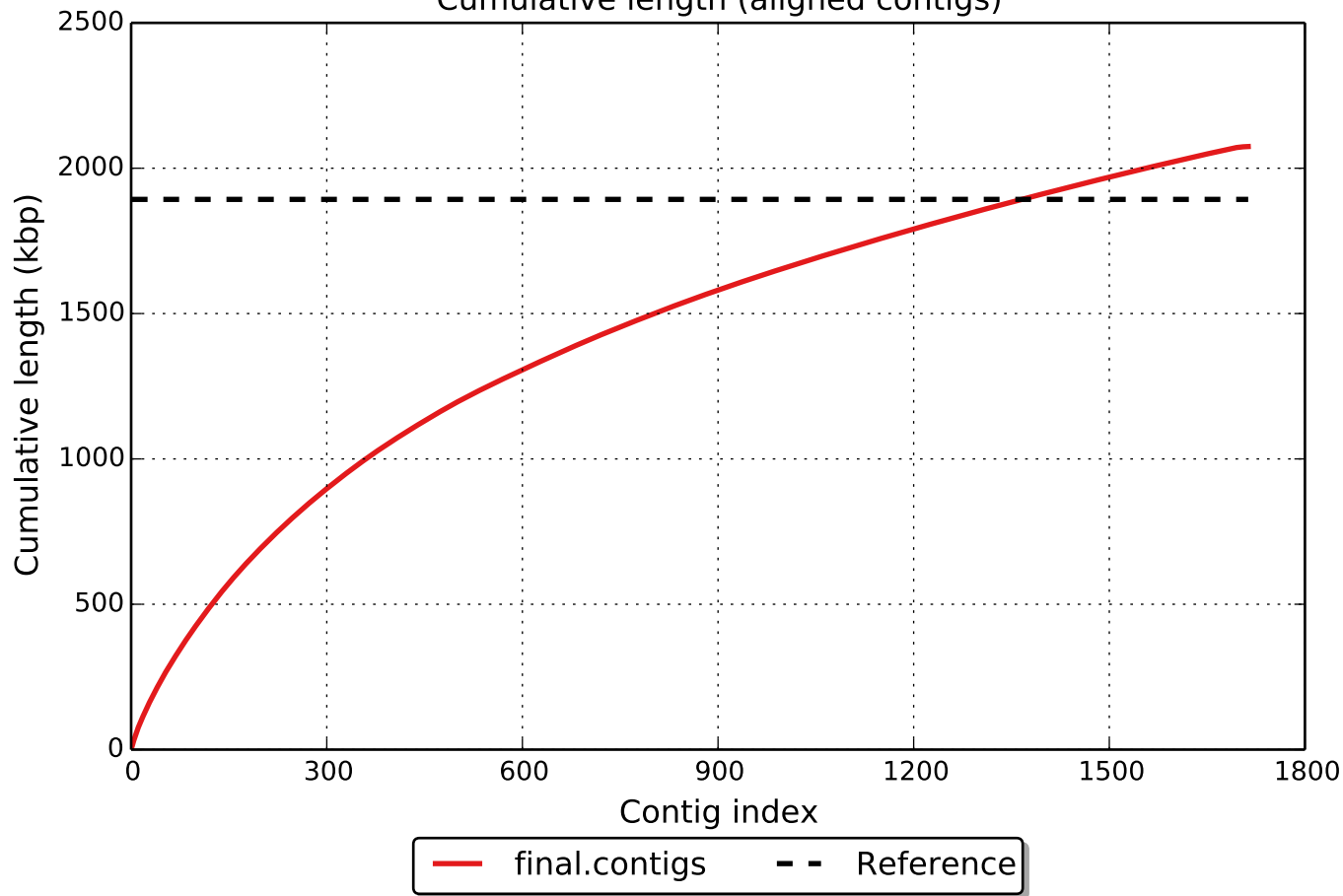
NGx

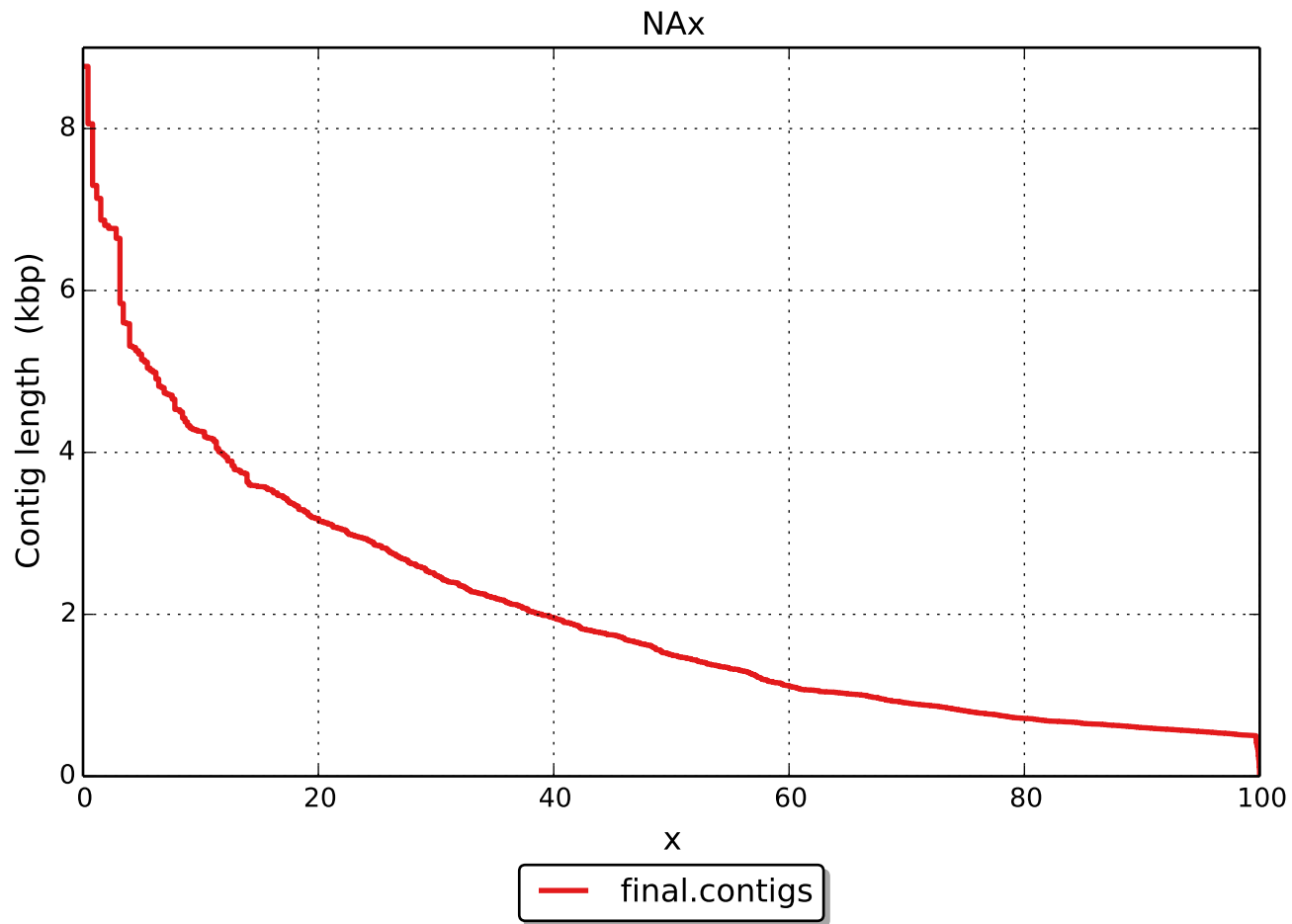






Cumulative length (aligned contigs)





# NGAx

