

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	826
# contigs ( $\geq 1000$ bp)	266
Total length ( $\geq 0$ bp)	826744
Total length ( $\geq 1000$ bp)	436254
# contigs	826
Largest contig	5316
Total length	826744
Reference length	641799
GC (%)	26.39
Reference GC (%)	26.30
N50	1045
NG50	1266
N75	733
NG75	926
L50	244
LG50	163
L75	484
LG75	313
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	7612
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	452
Genome fraction (%)	91.561
Duplication ratio	1.406
# N's per 100 kbp	0.00
# mismatches per 100 kbp	940.20
# indels per 100 kbp	0.68
Largest alignment	5316
NA50	1039
NGA50	1266
NA75	728
NGA75	920
LA50	244
LGA50	163
LA75	485
LGA75	314

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	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	7612
# local misassemblies	0
# mismatches	5525
# indels	4
# short indels	4
# long indels	0
Indels length	4

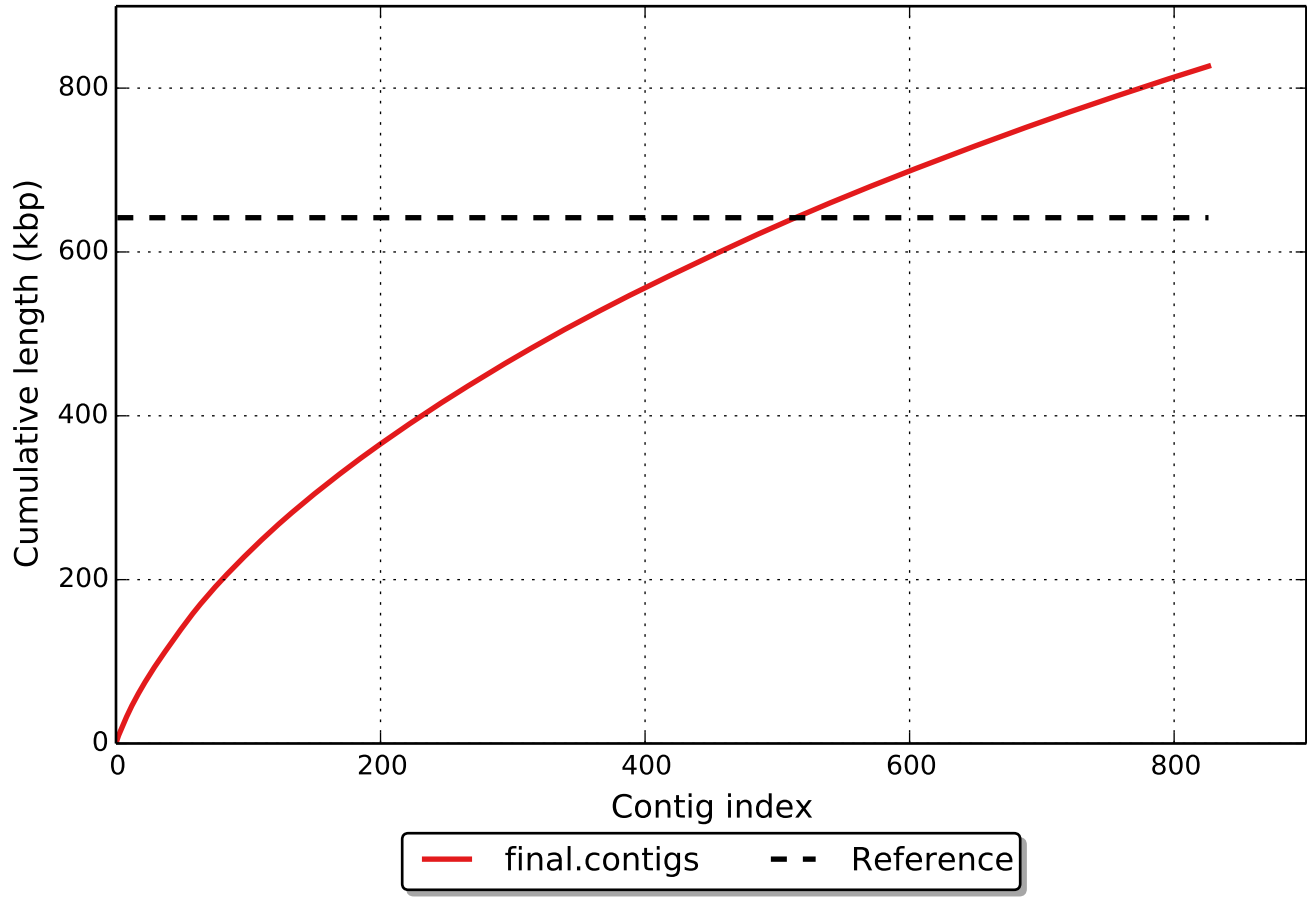
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

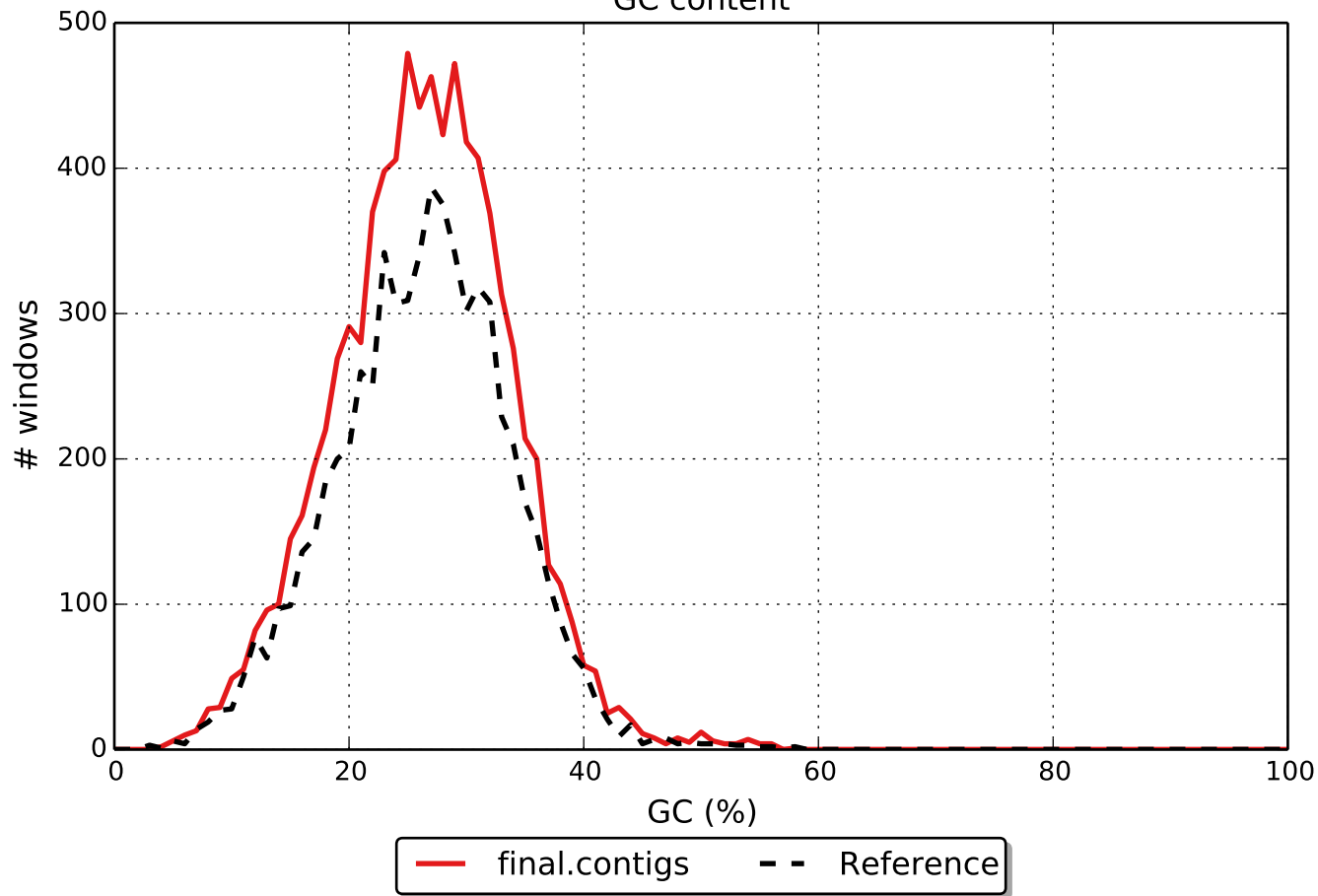
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	452
# N's	0

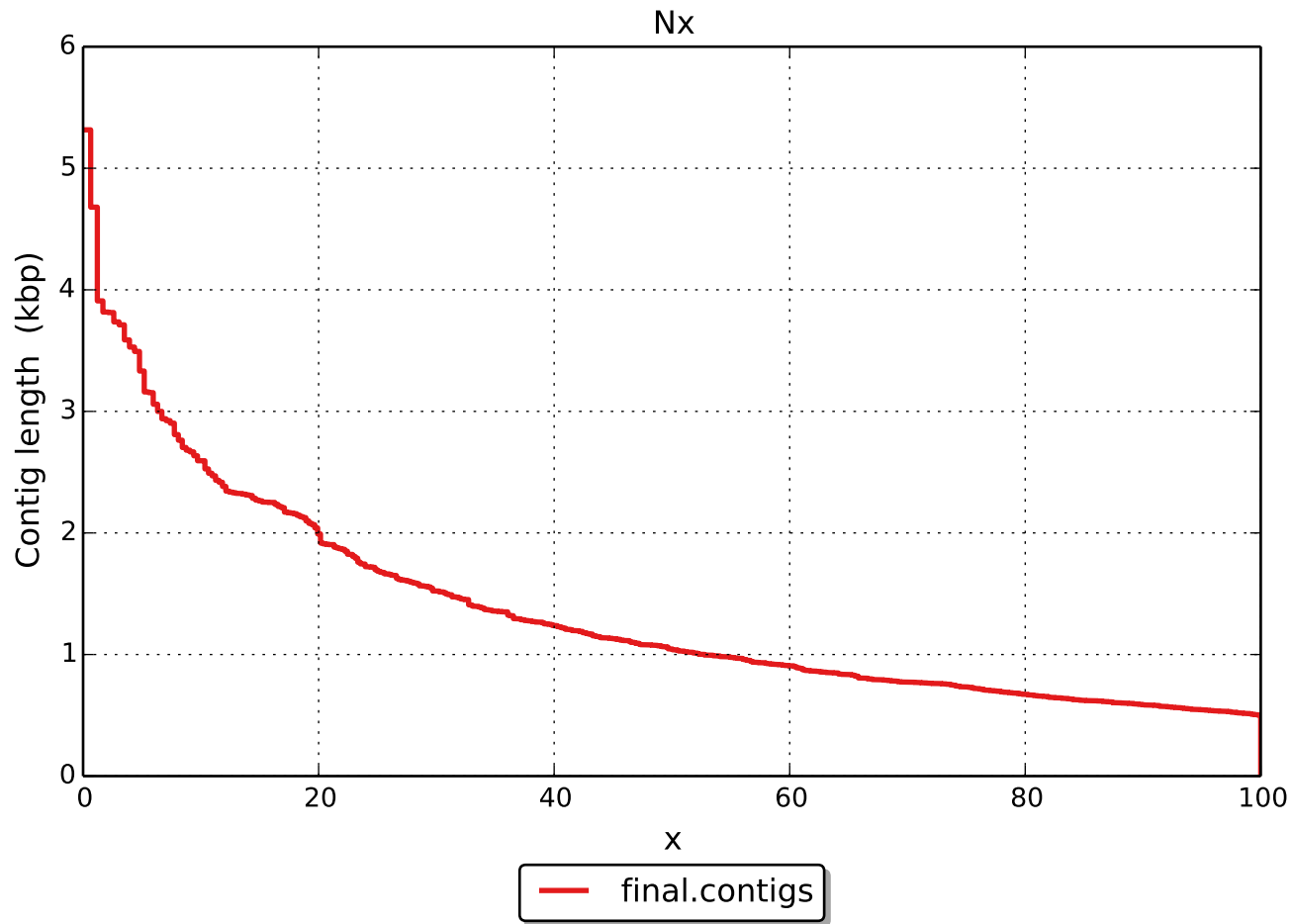
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

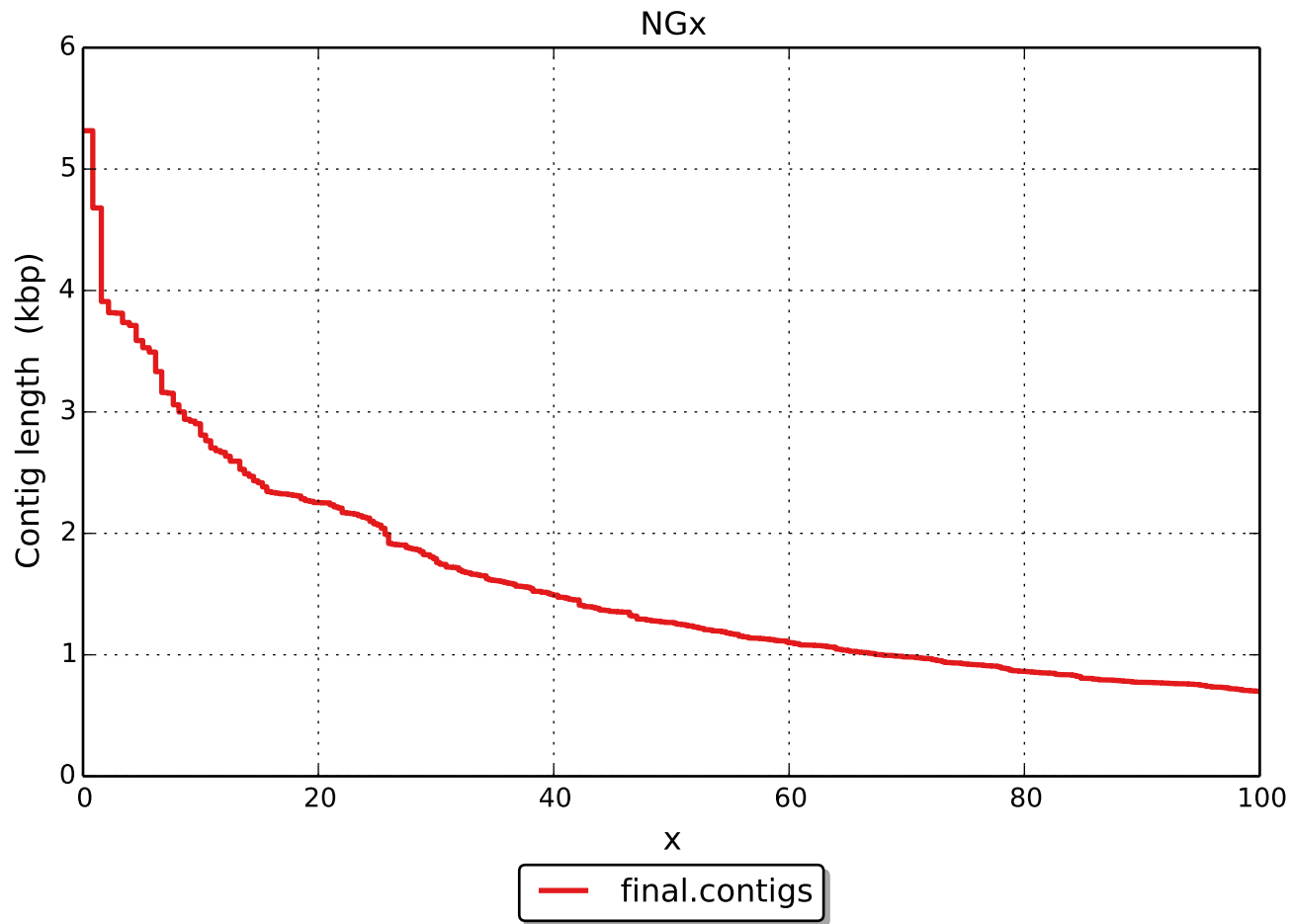
Cumulative length

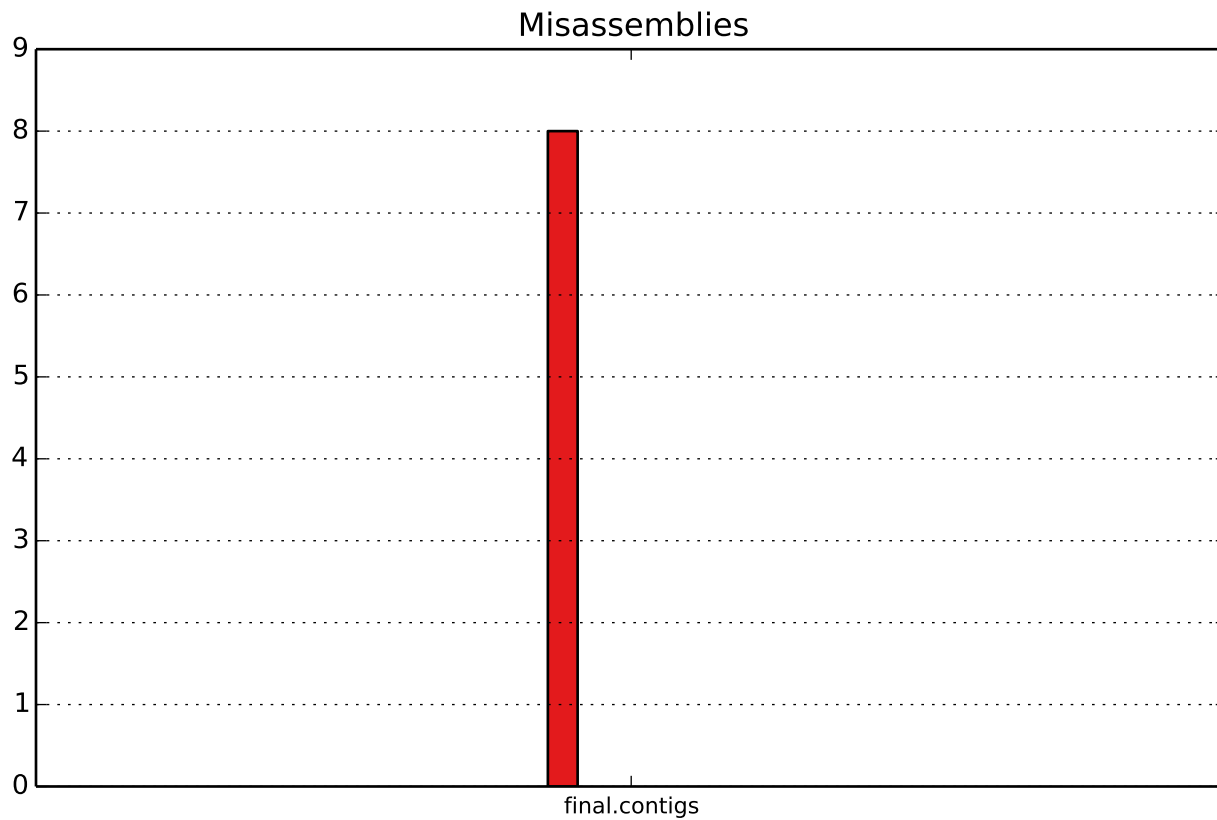


GC content

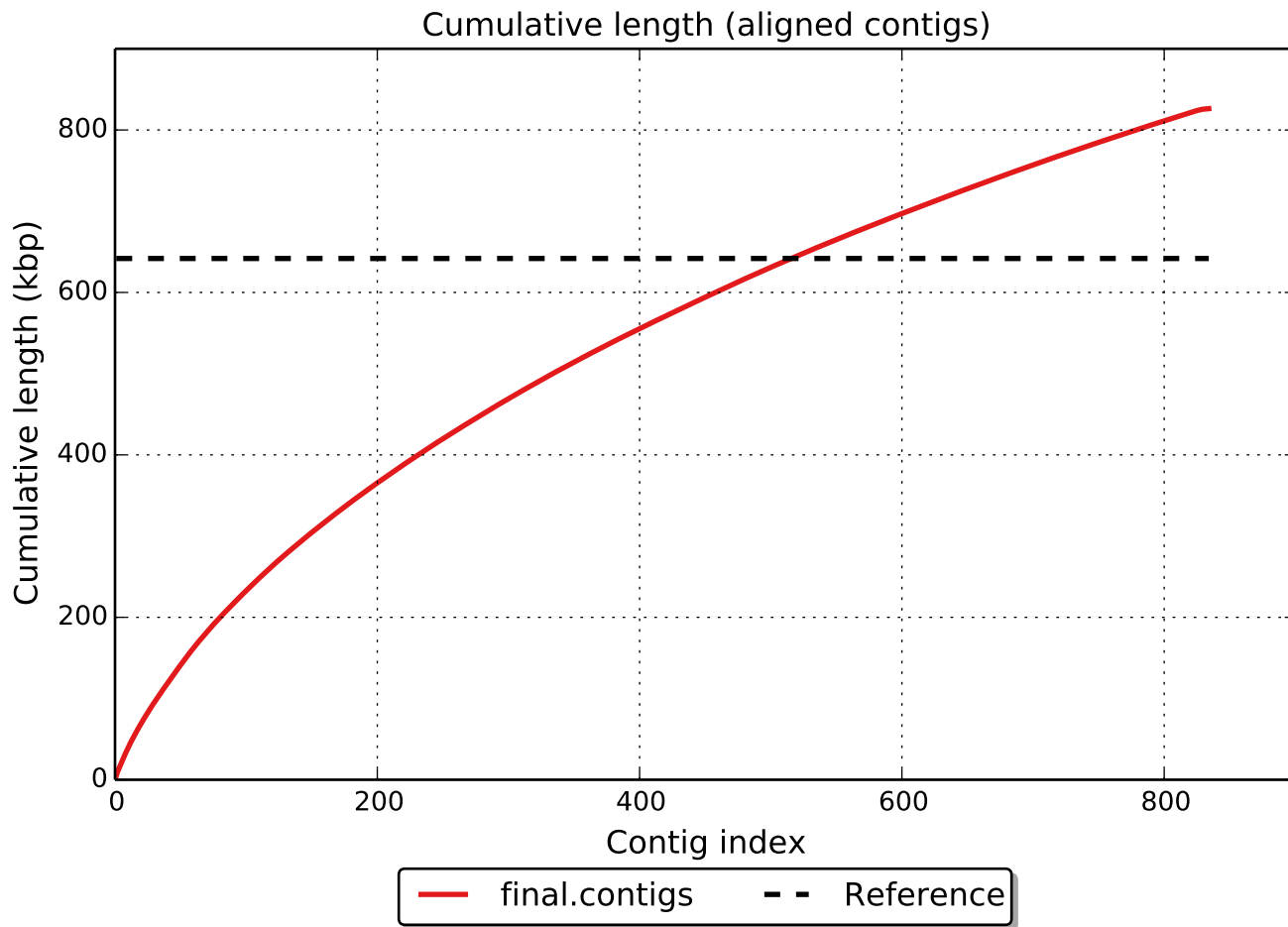


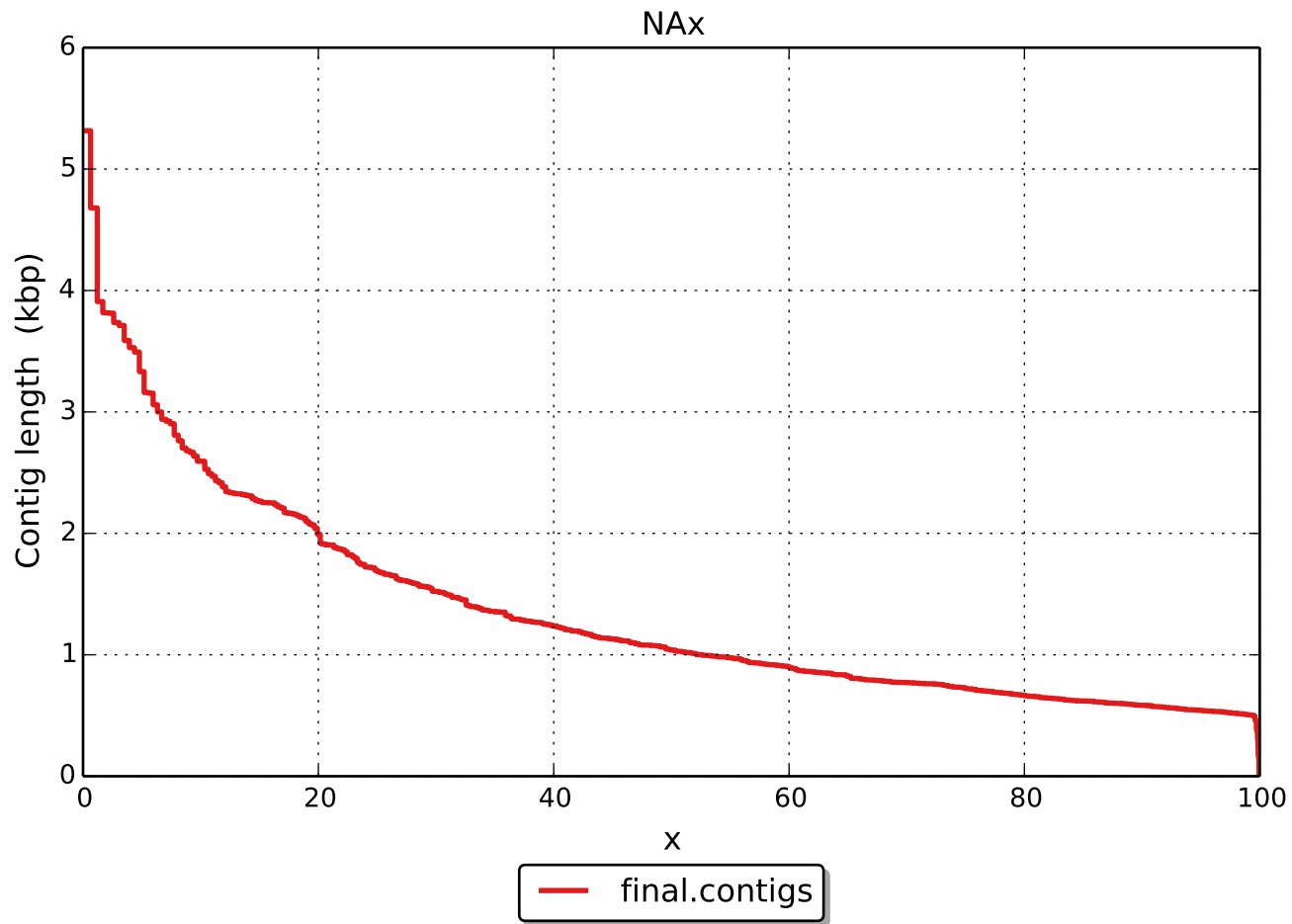












NGAx

