

## Report

	final.contigs
# contigs ( $\geq 0$ bp)	2840
# contigs ( $\geq 1000$ bp)	1466
Total length ( $\geq 0$ bp)	3502850
Total length ( $\geq 1000$ bp)	2515702
# contigs	2840
Largest contig	7759
Total length	3502850
Reference length	1892775
GC (%)	32.27
Reference GC (%)	32.26
N50	1425
NG50	2035
N75	951
NG75	1644
L50	824
LG50	347
L75	1581
LG75	608
# misassemblies	76
# misassembled contigs	75
Misassembled contigs length	124917
# local misassemblies	0
# unaligned contigs	2 + 3 part
Unaligned length	2977
Genome fraction (%)	92.772
Duplication ratio	1.993
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1733.53
# indels per 100 kbp	1.25
Largest alignment	7759
NA50	1388
NGA50	1991
NA75	909
NGA75	1603
LA50	840
LGA50	352
LA75	1618
LGA75	618

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

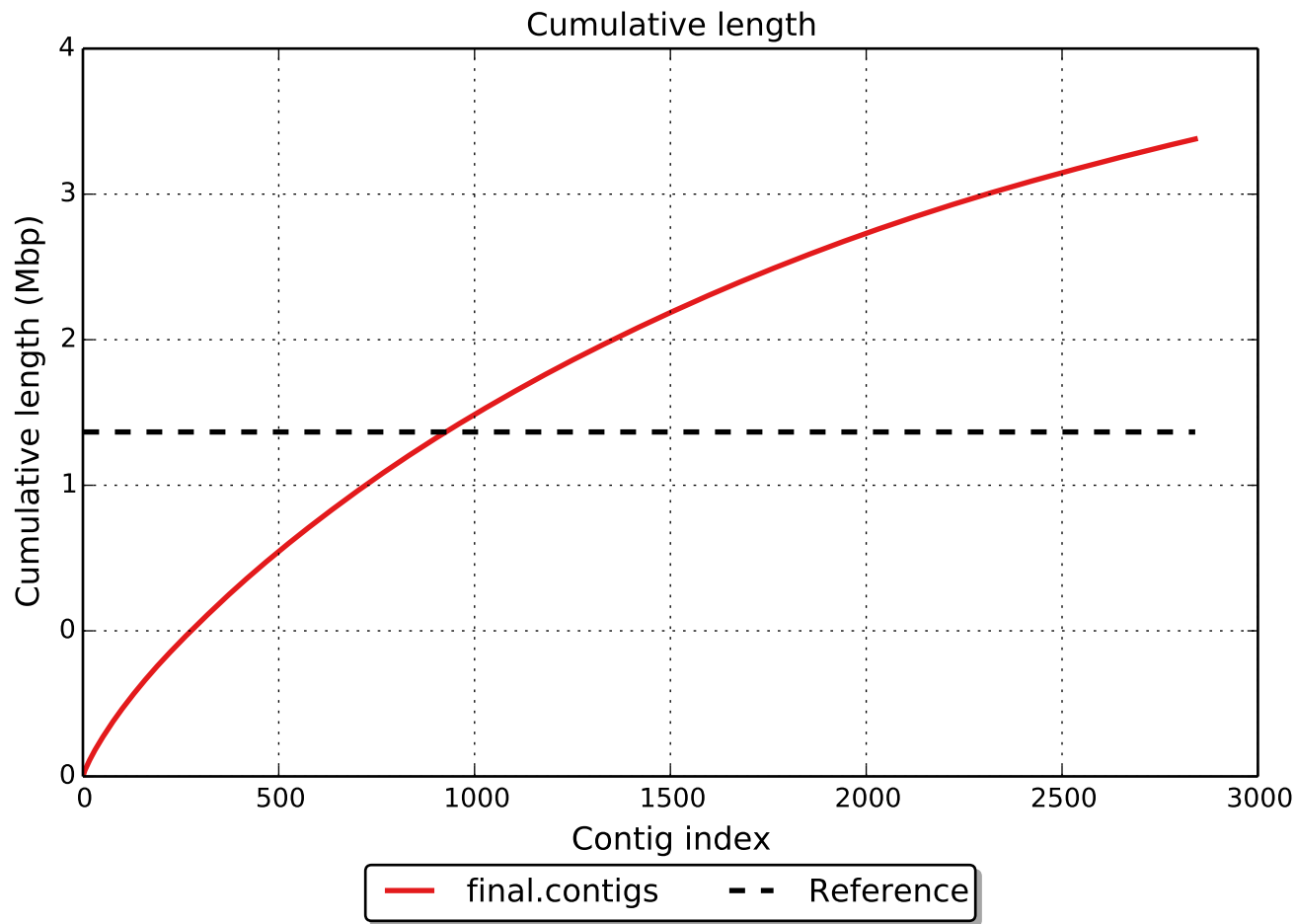
	final.contigs
# misassemblies	76
# relocations	76
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	75
Misassembled contigs length	124917
# local misassemblies	0
# mismatches	30440
# indels	22
# short indels	22
# long indels	0
Indels length	22

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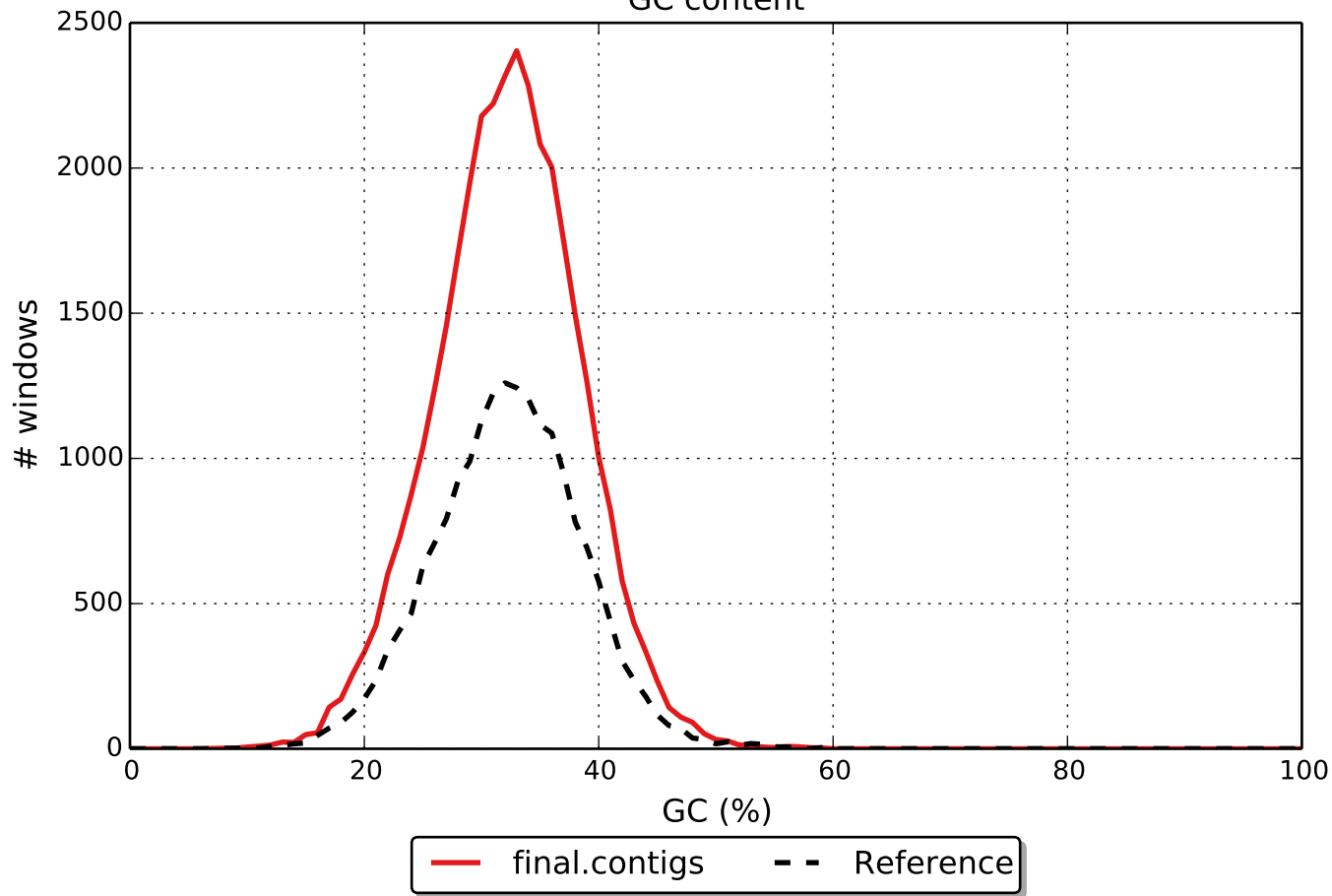
## Unaligned report

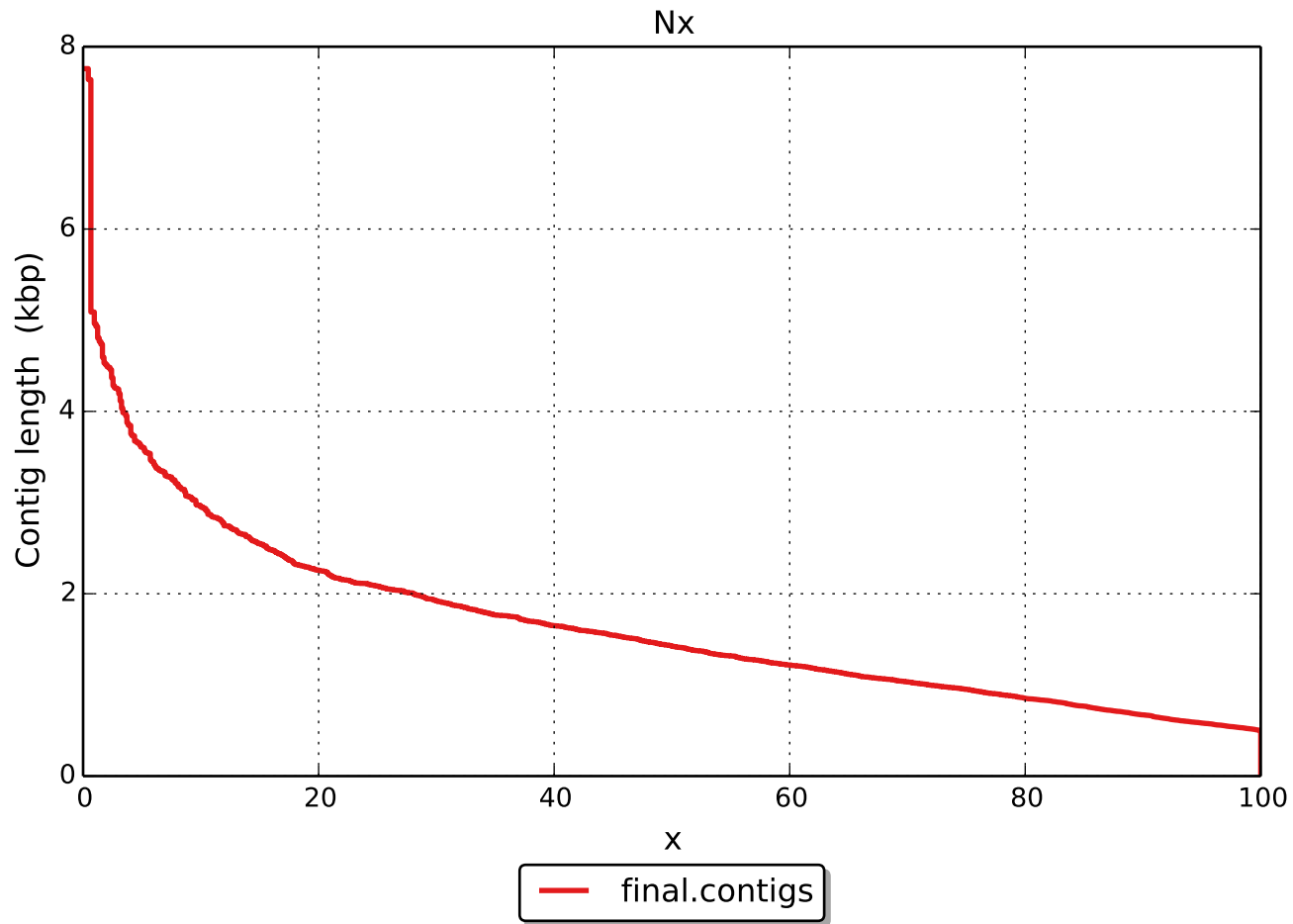
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	2263
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	714
# N's	0

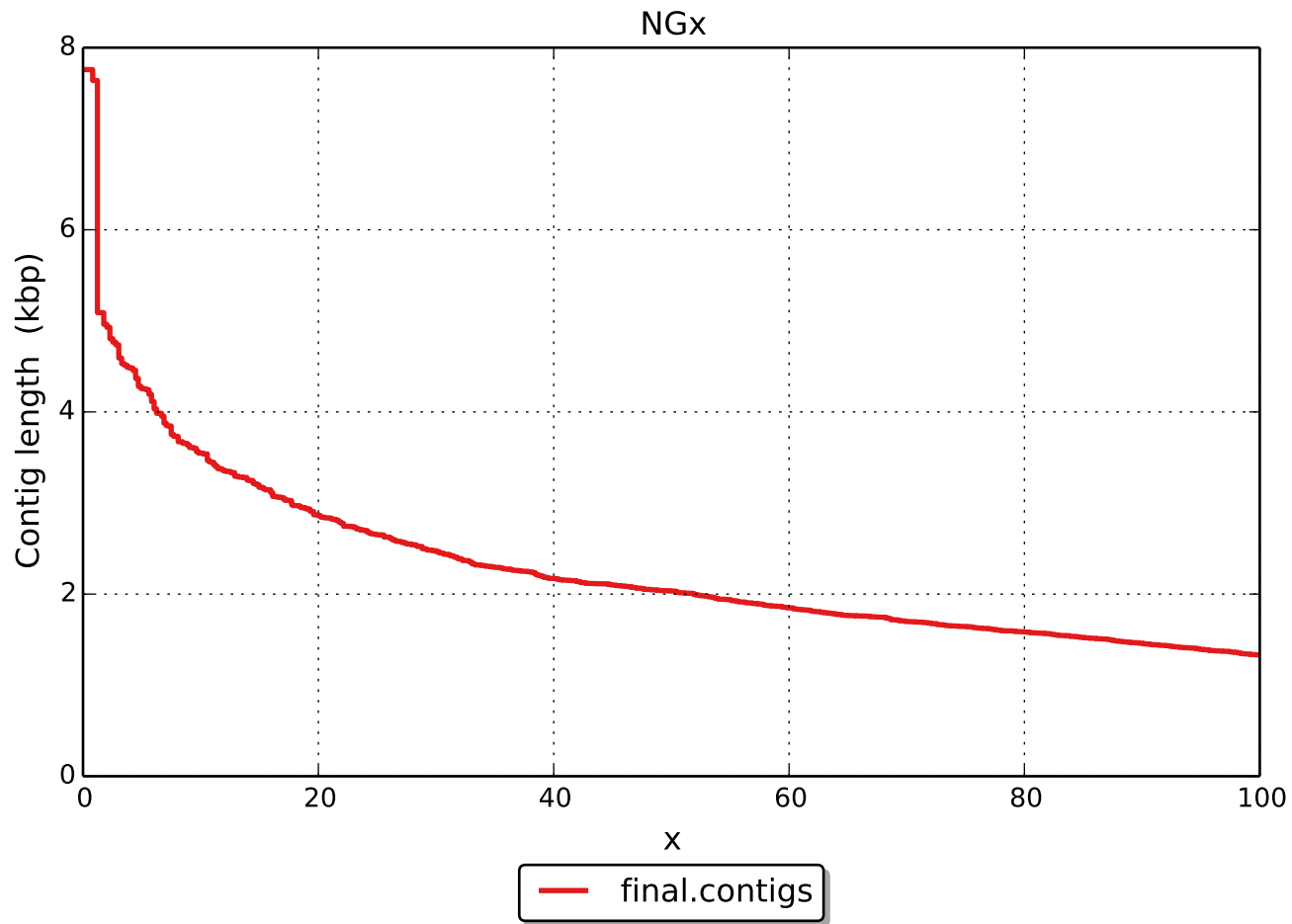
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



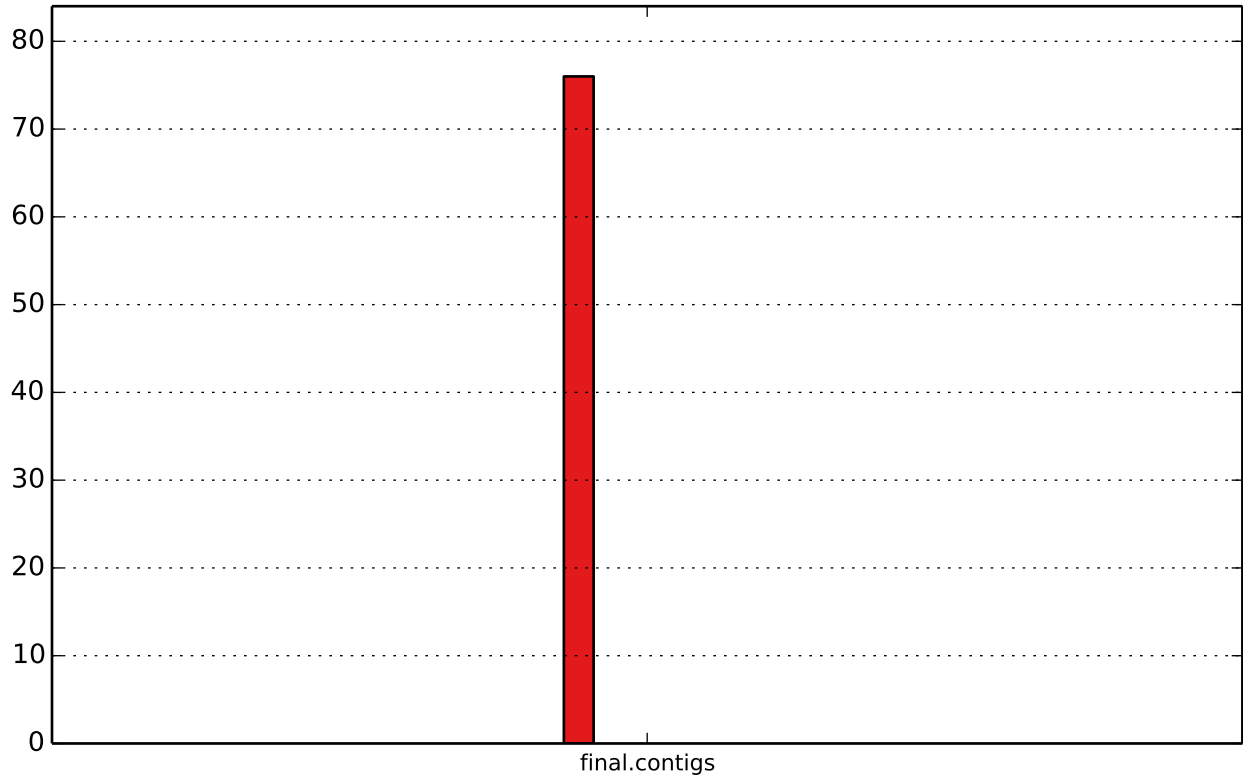
GC content



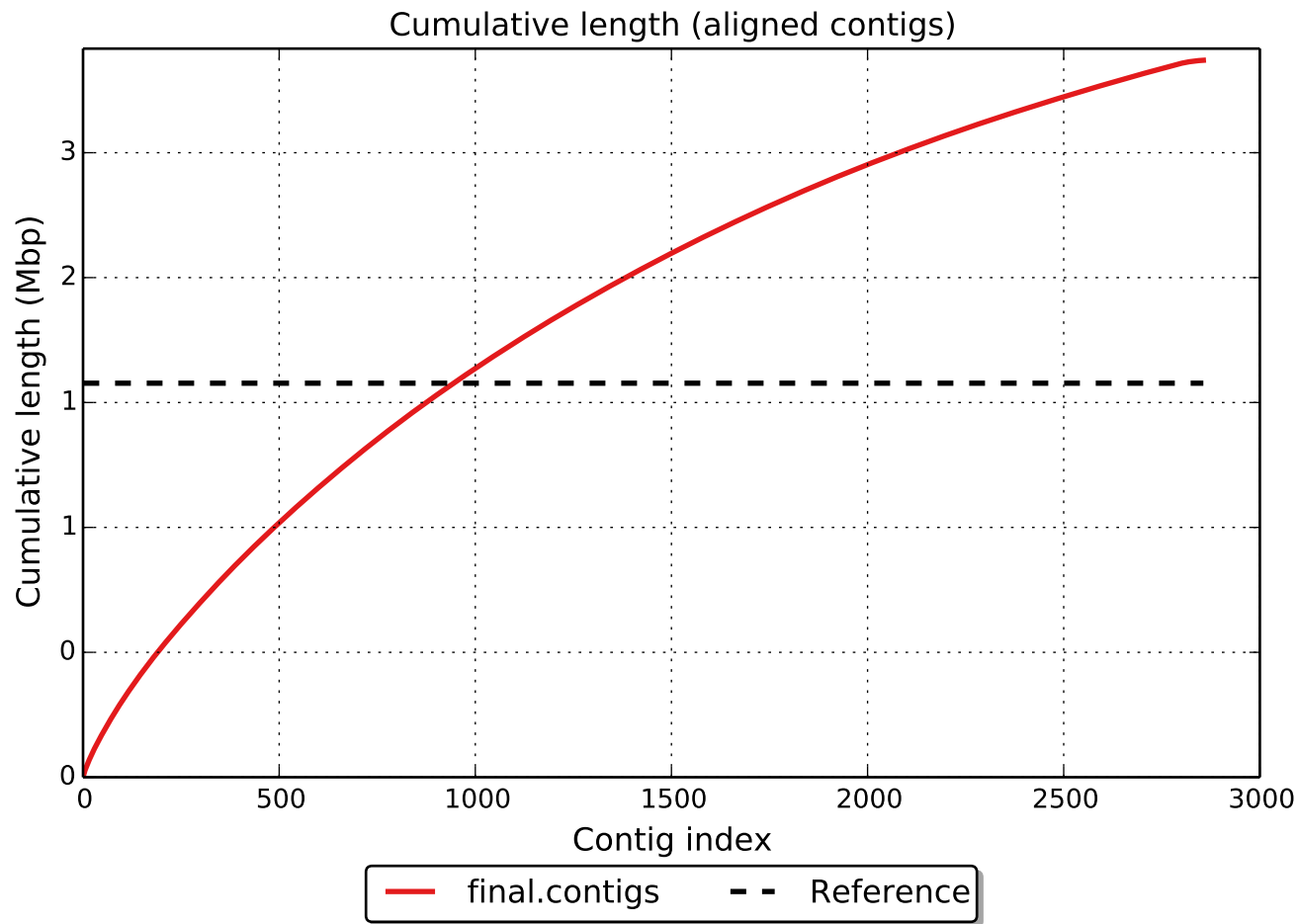


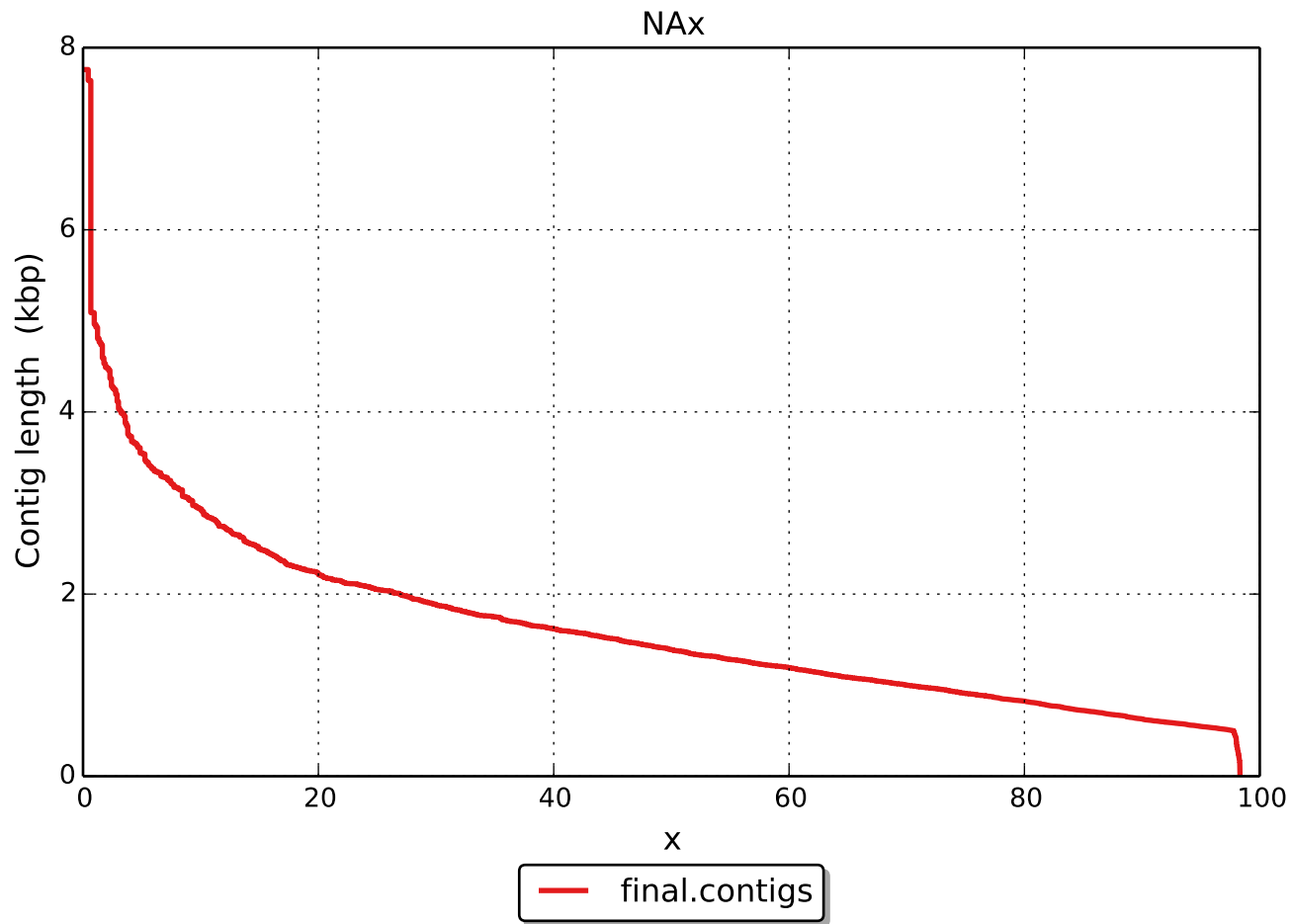


# Misassemblies









# NGAx

