

Report

	final.contigs
# contigs (≥ 0 bp)	4413
# contigs (≥ 1000 bp)	710
Total length (≥ 0 bp)	3045287
Total length (≥ 1000 bp)	1130041
# contigs	2457
Largest contig	5291
Total length	2345482
Reference length	3785550
GC (%)	32.30
Reference GC (%)	32.26
N50	984
NG50	647
N75	701
L50	754
LG50	1661
L75	1462
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	79.296
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	457.19
# indels per 100 kbp	0.07
Largest alignment	5291
NA50	984
NGA50	647
NA75	701
LA50	754
LGA50	1661
LA75	1462

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

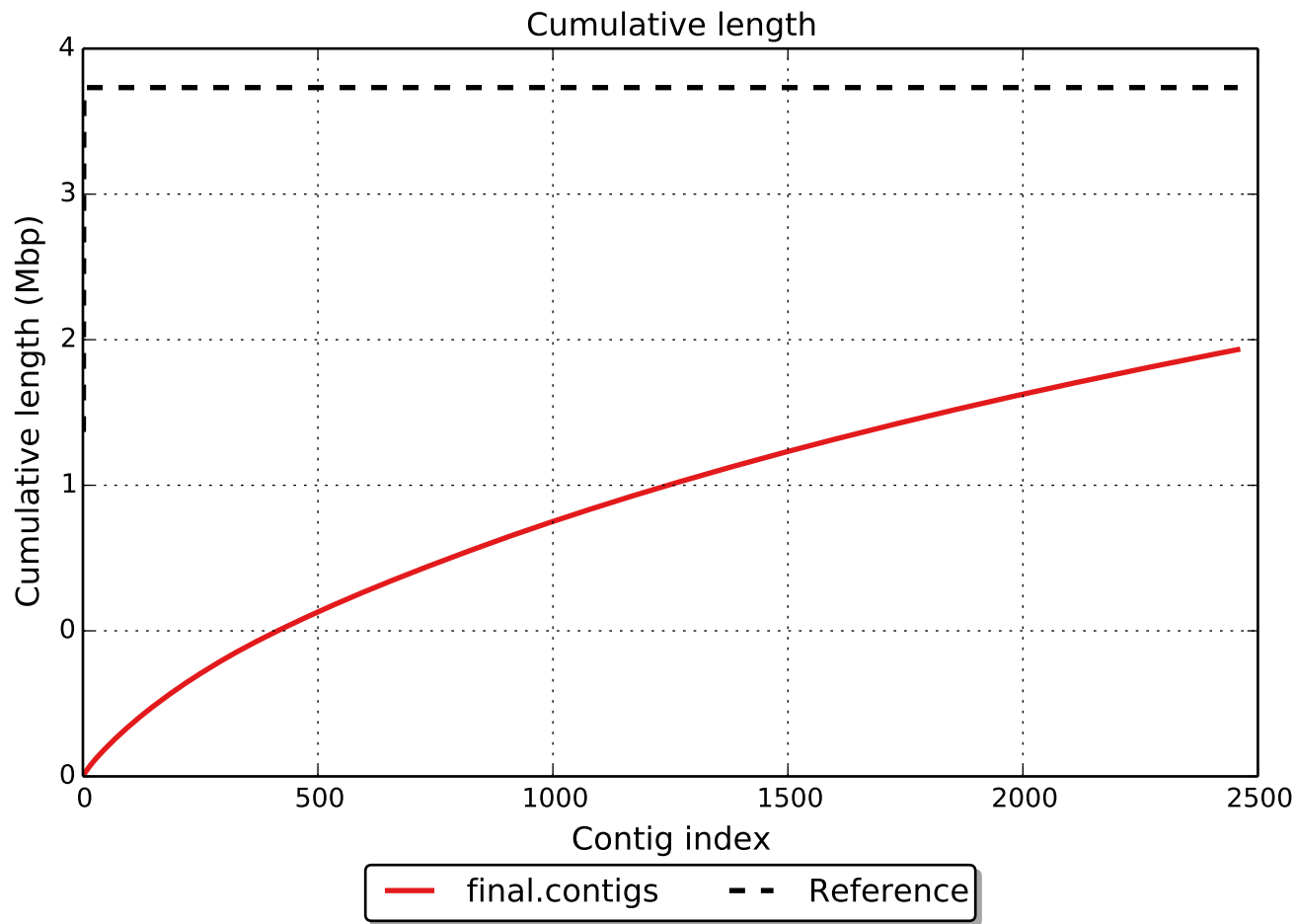
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	13724
# indels	2
# short indels	0
# long indels	2
Indels length	27

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).

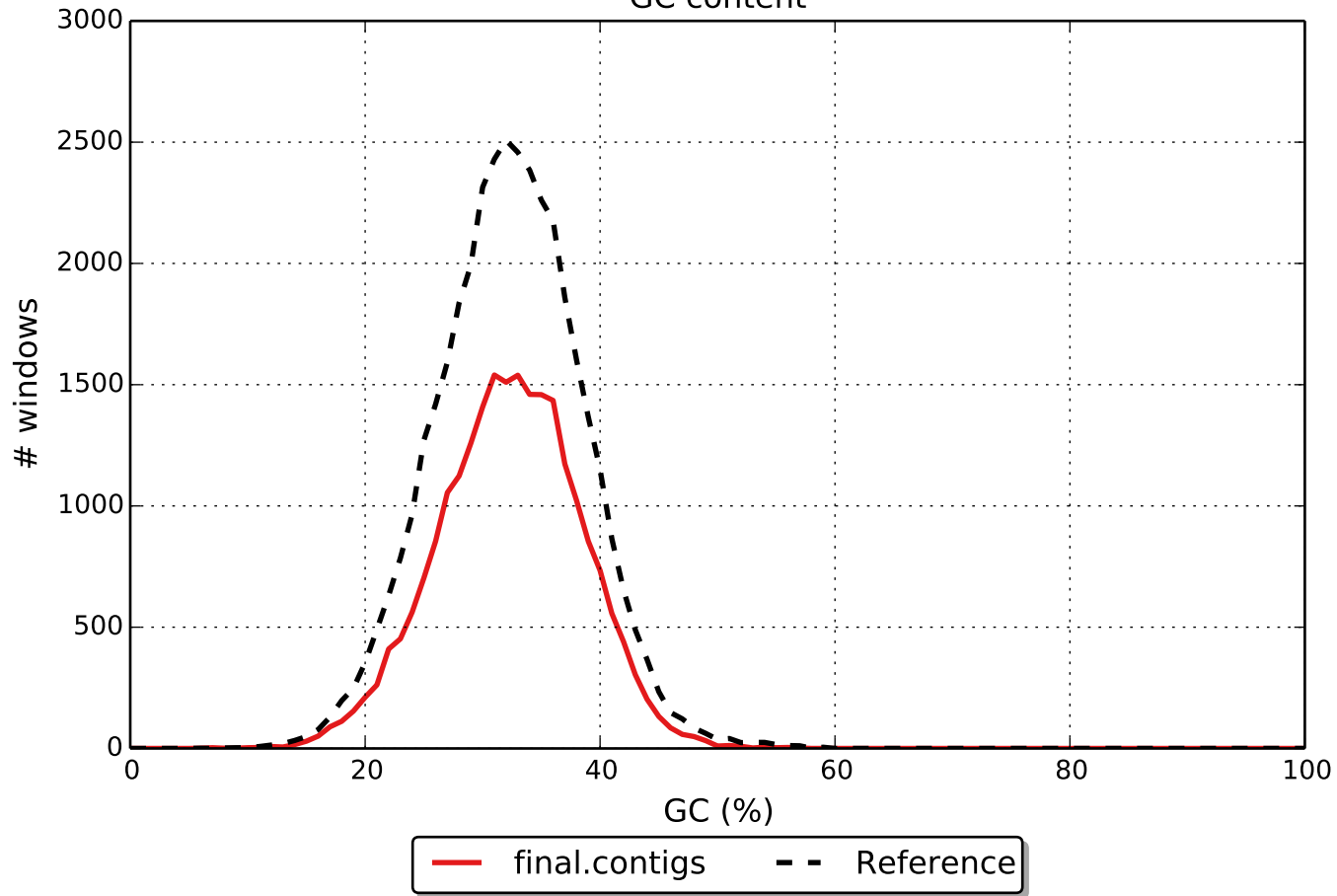
Unaligned report

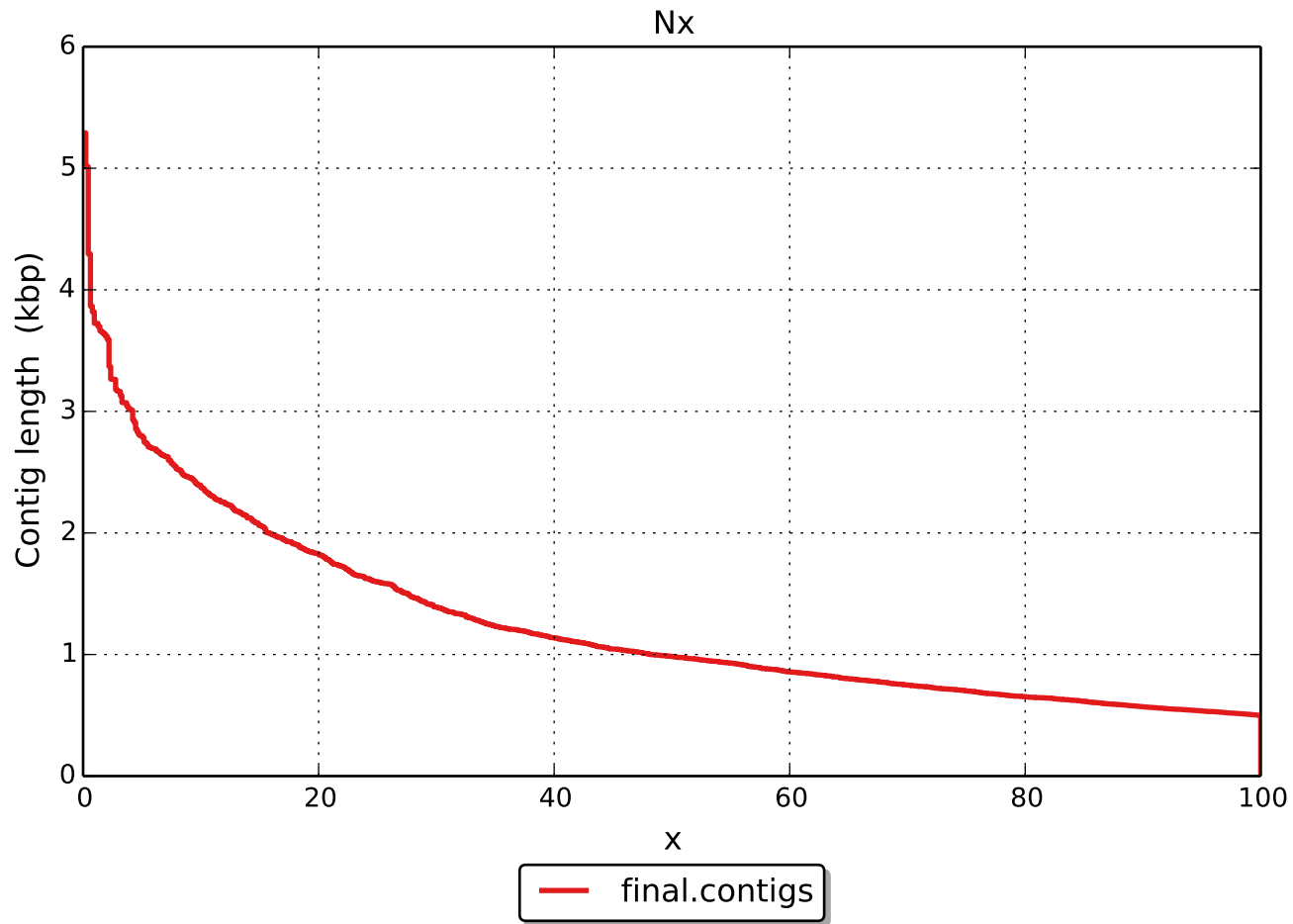
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

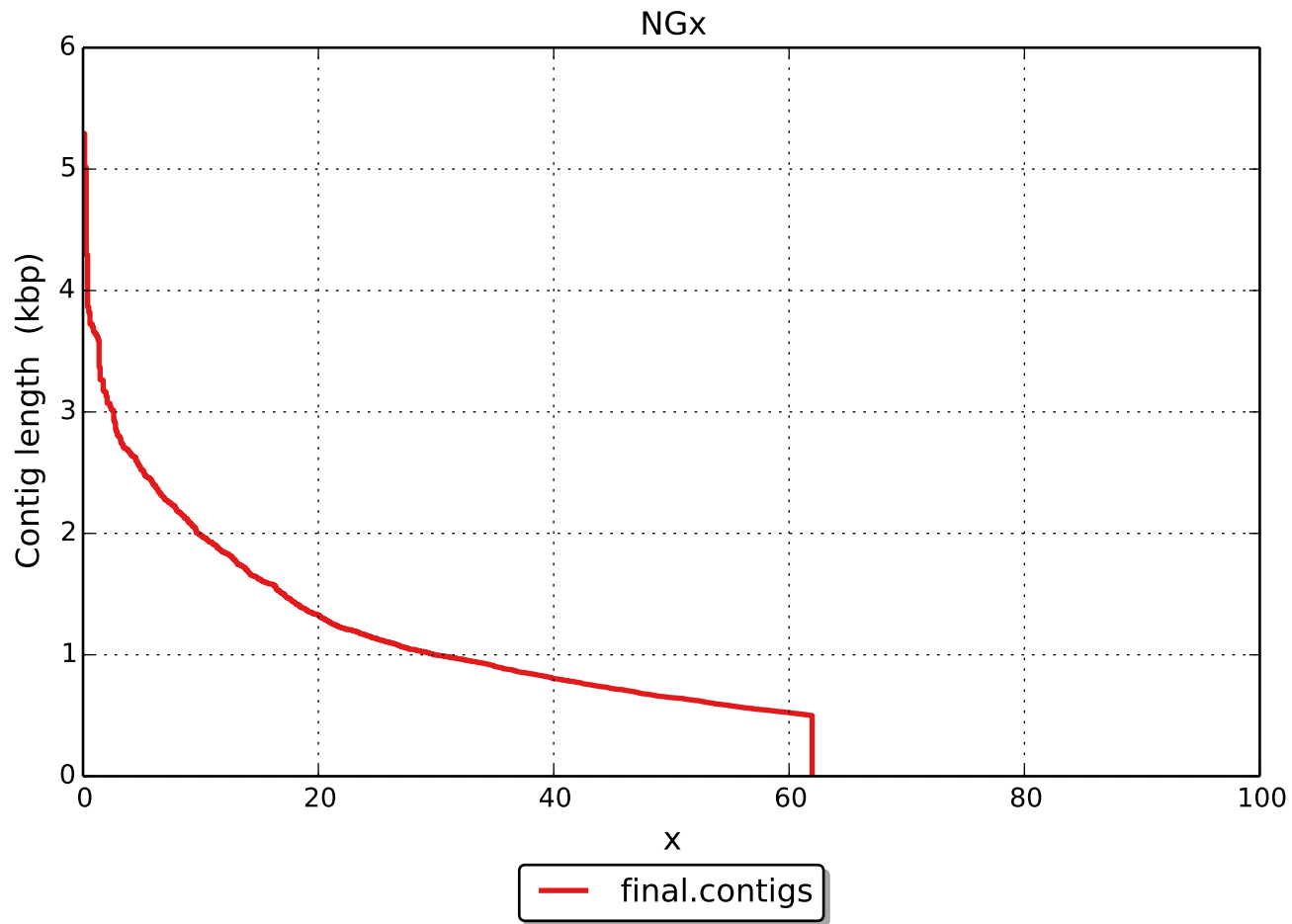
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

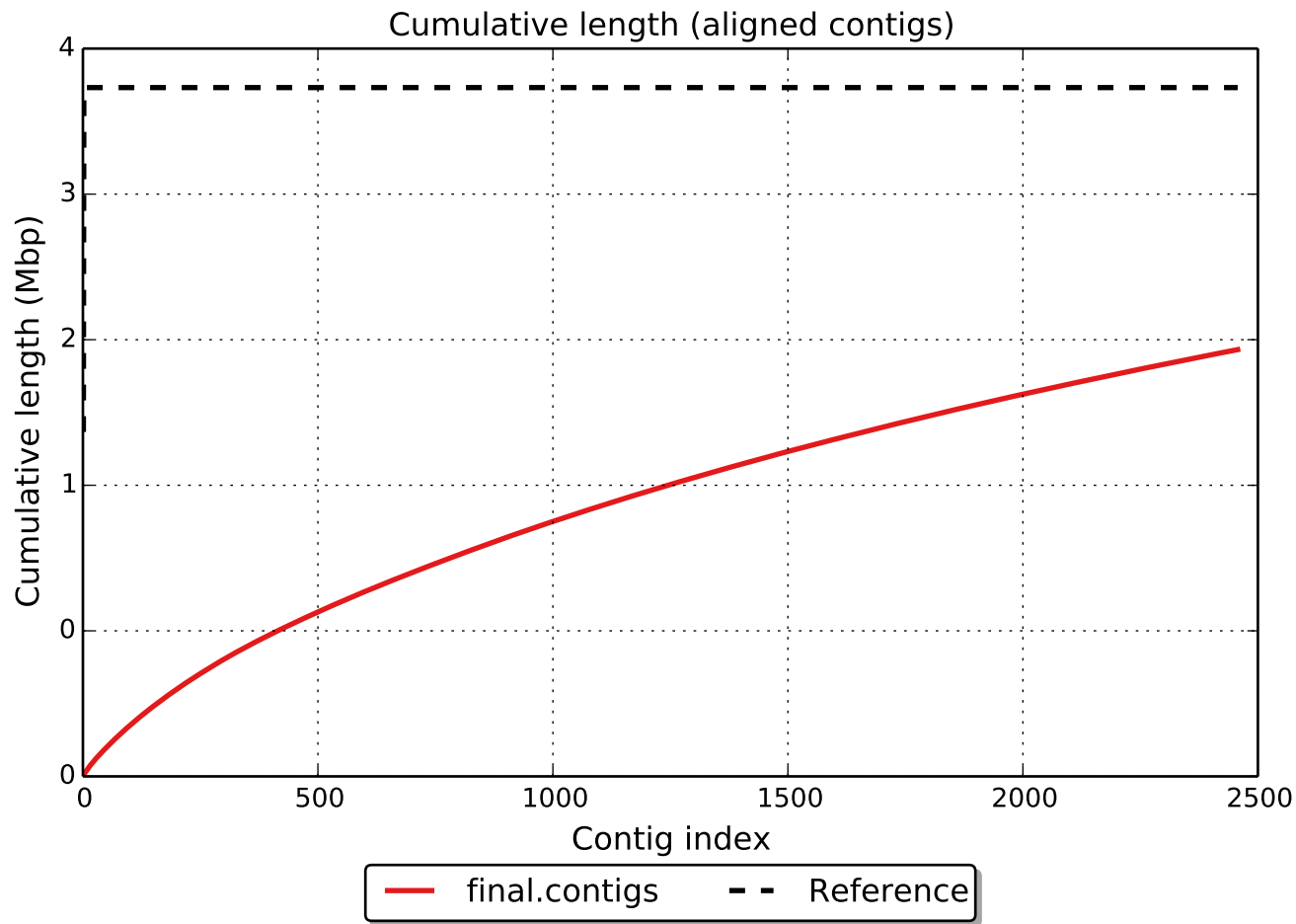


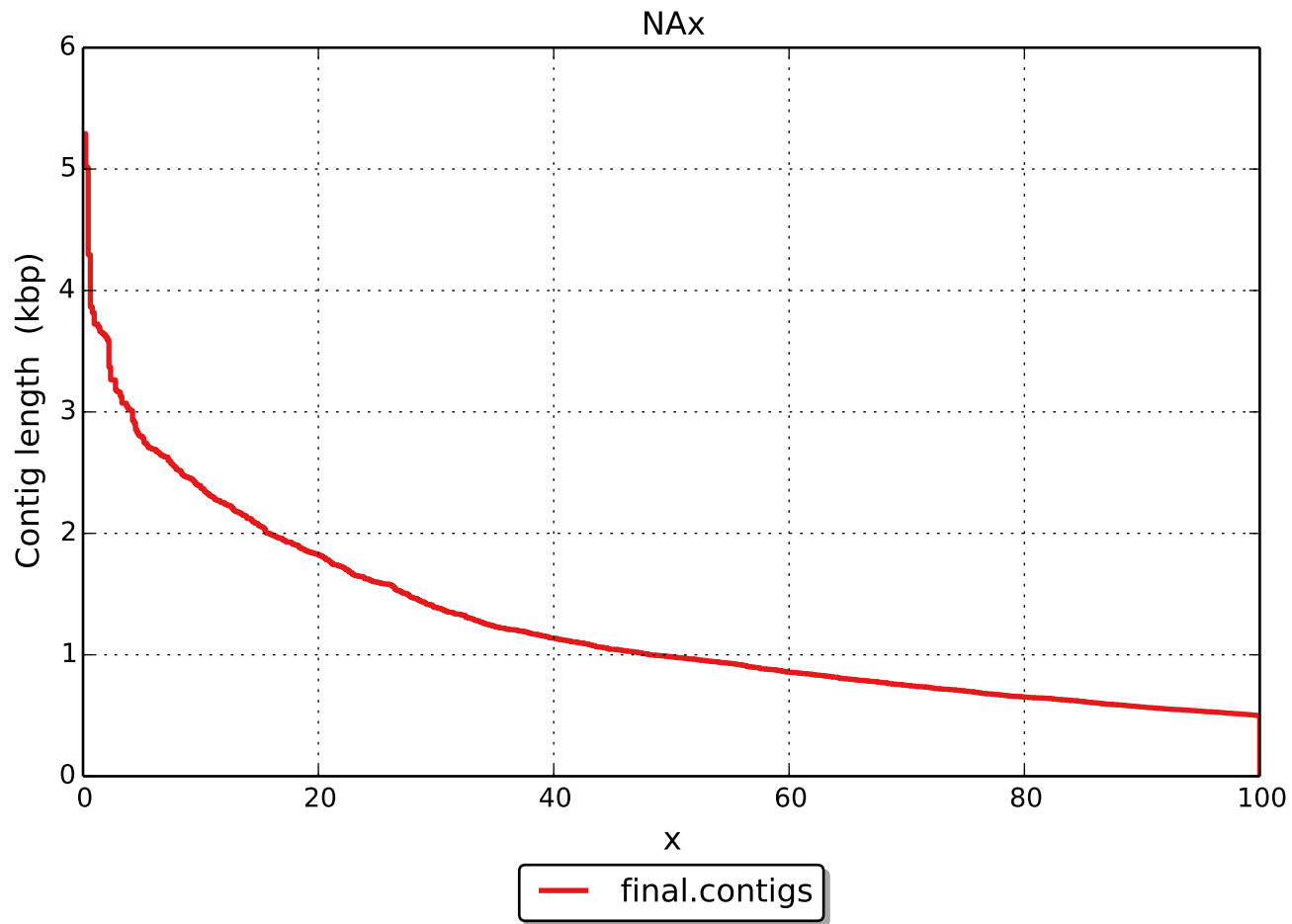




Misassemblies







NGAx

