

Report

	final.contigs
# contigs (≥ 0 bp)	10661
# contigs (≥ 1000 bp)	4193
Total length (≥ 0 bp)	11268331
Total length (≥ 1000 bp)	7683180
# contigs	7739
Largest contig	7826
Total length	10246908
Reference length	11094646
GC (%)	50.38
Reference GC (%)	50.48
N50	1562
NG50	1453
N75	999
NG75	877
L50	2129
LG50	2411
L75	4196
LG75	4877
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.690
Duplication ratio	1.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	71.01
# indels per 100 kbp	0.20
Largest alignment	7826
NA50	1562
NGA50	1453
NA75	999
NGA75	877
LA50	2129
LGA50	2411
LA75	4196
LGA75	4877

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

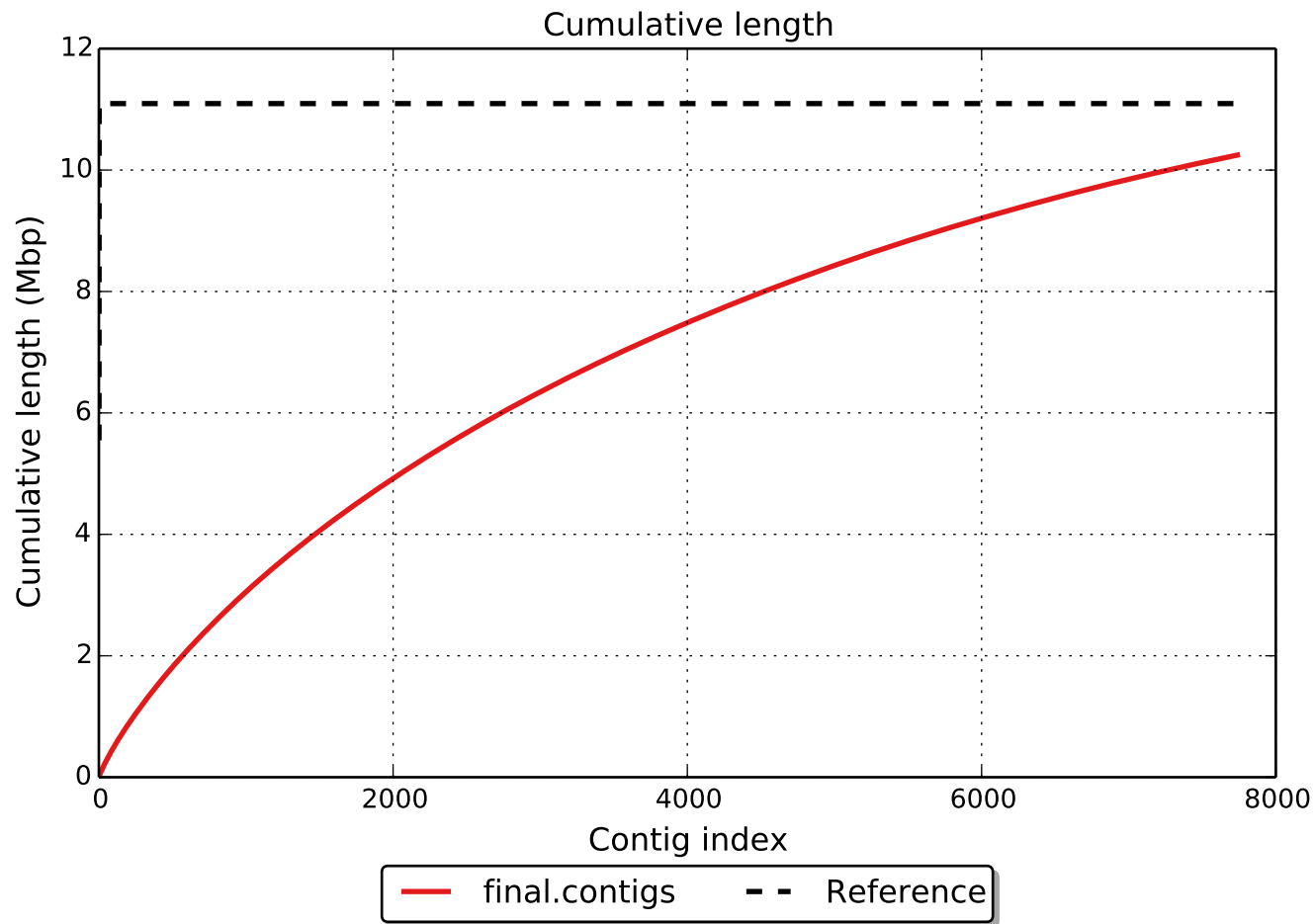
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	7066
# indels	20
# short indels	17
# long indels	3
Indels length	45

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).

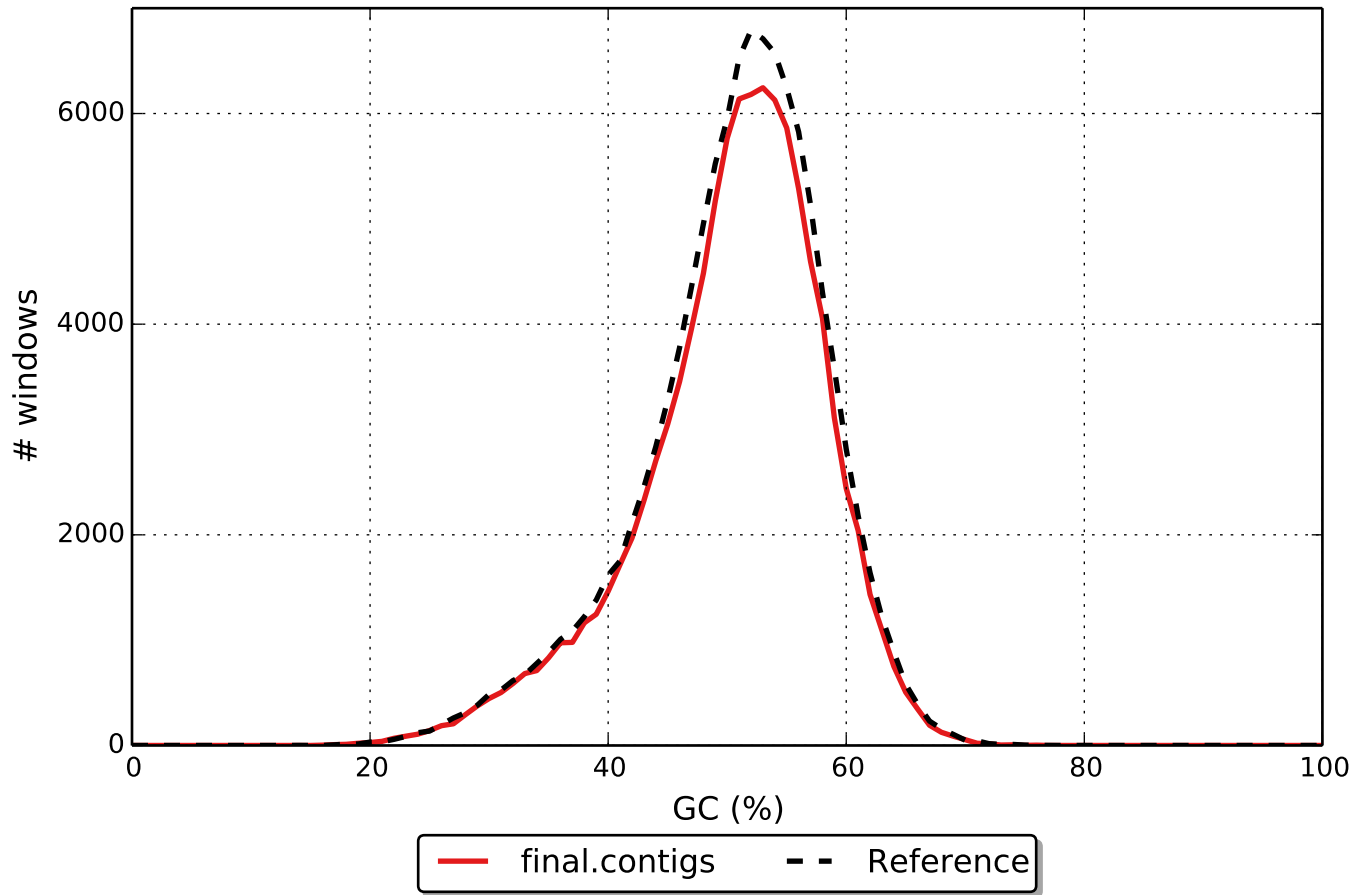
Unaligned report

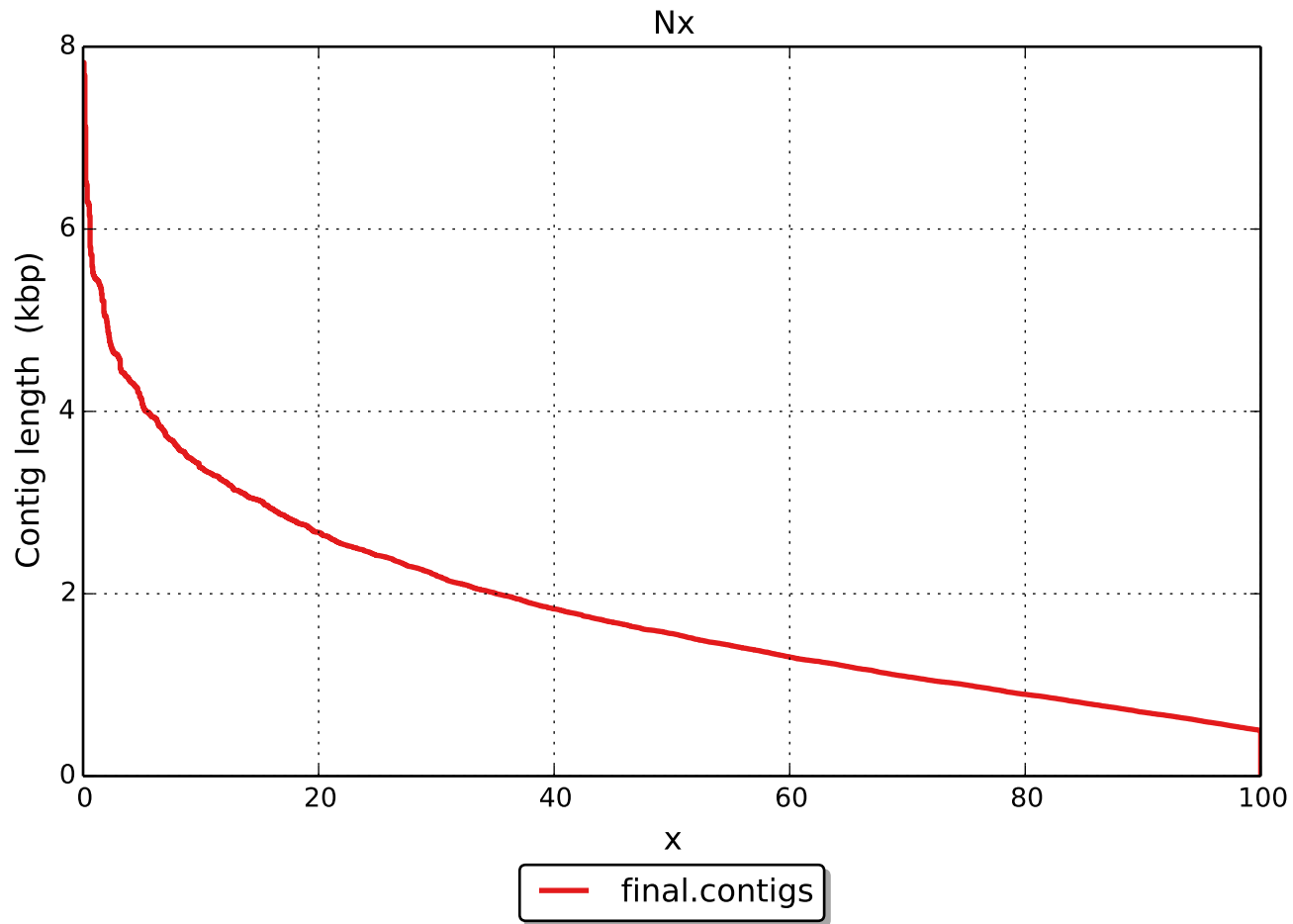
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

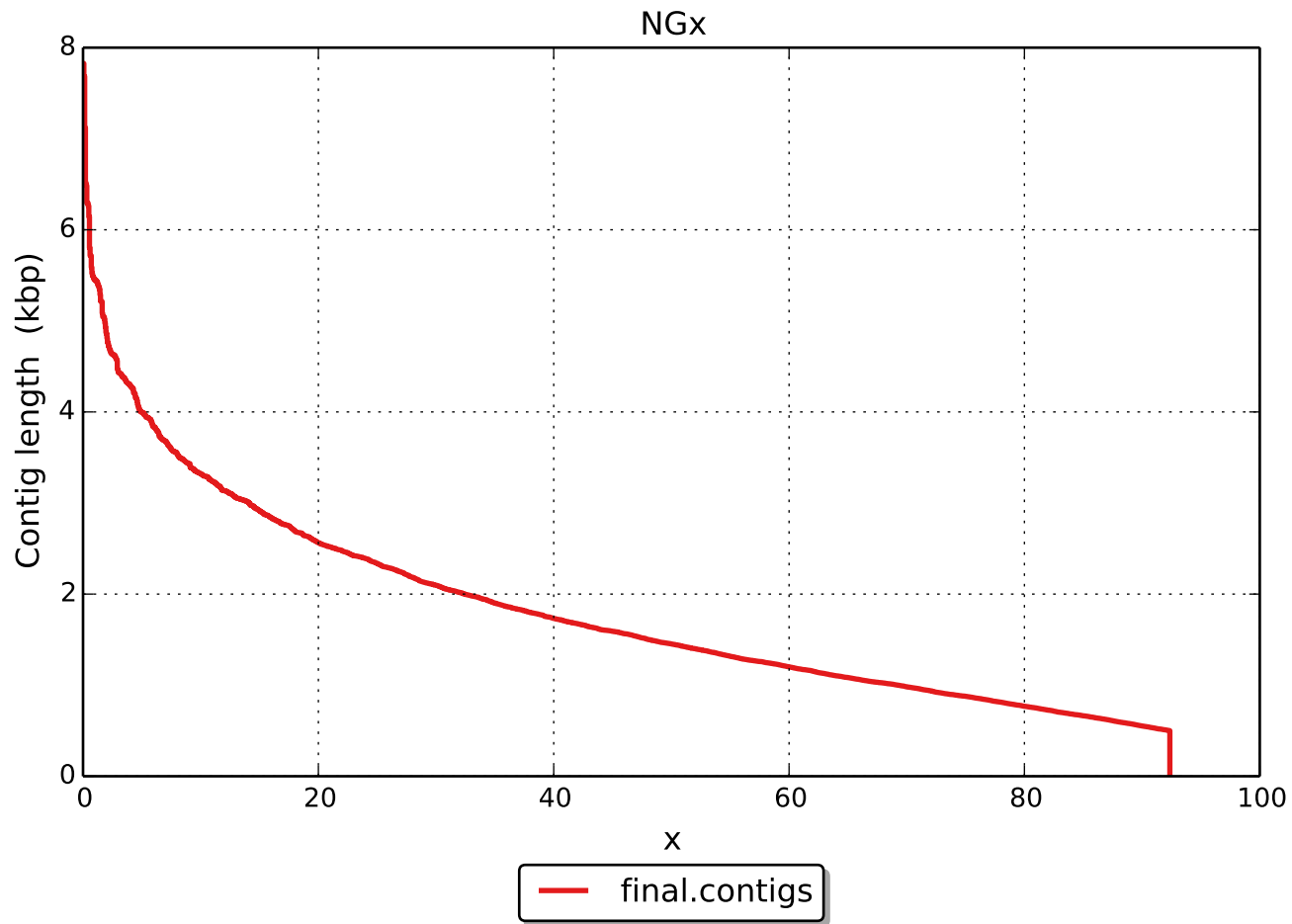
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

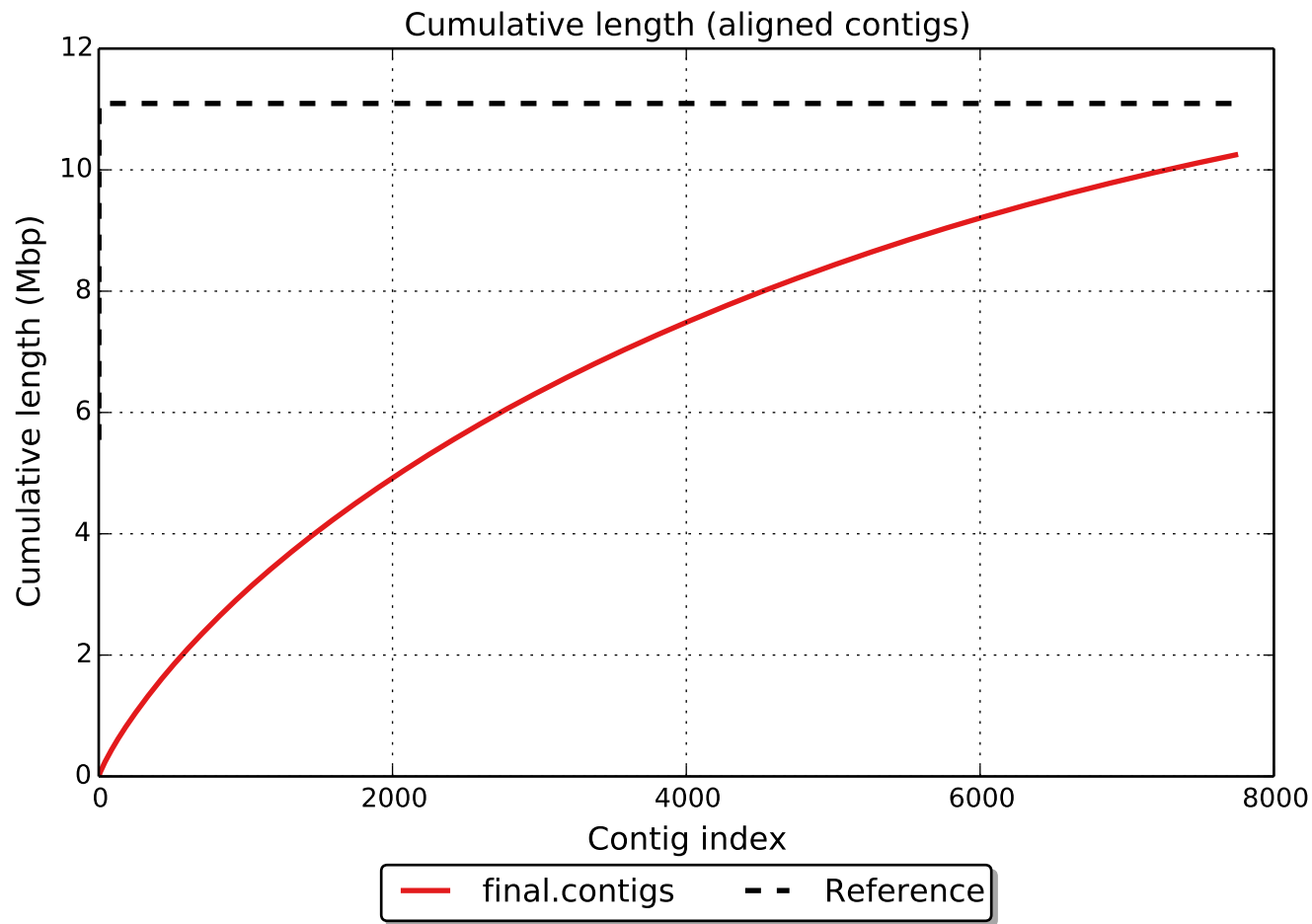


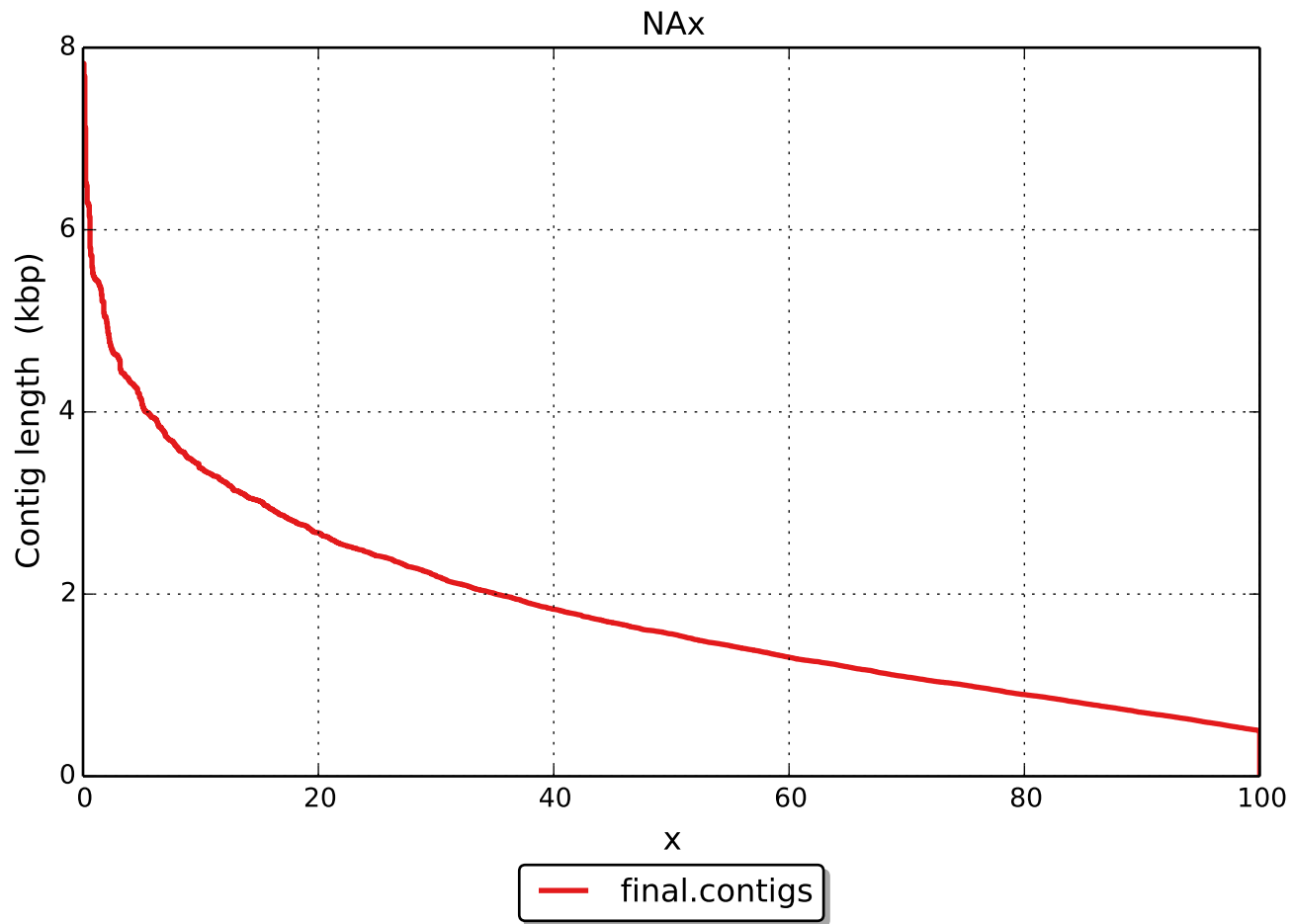




Misassemblies







NGAx

