

Report

	final.contigs
# contigs (≥ 0 bp)	3671
# contigs (≥ 1000 bp)	1549
Total length (≥ 0 bp)	4709380
Total length (≥ 1000 bp)	3246884
# contigs	3671
Largest contig	10039
Total length	4709380
Reference length	5547323
GC (%)	50.28
Reference GC (%)	50.48
N50	1635
NG50	1288
N75	866
NG75	647
L50	838
LG50	1129
L75	1857
LG75	2704
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.327
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	553.84
# indels per 100 kbp	0.16
Largest alignment	10039
NA50	1635
NGA50	1288
NA75	866
NGA75	647
LA50	838
LGA50	1129
LA75	1857
LGA75	2704

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

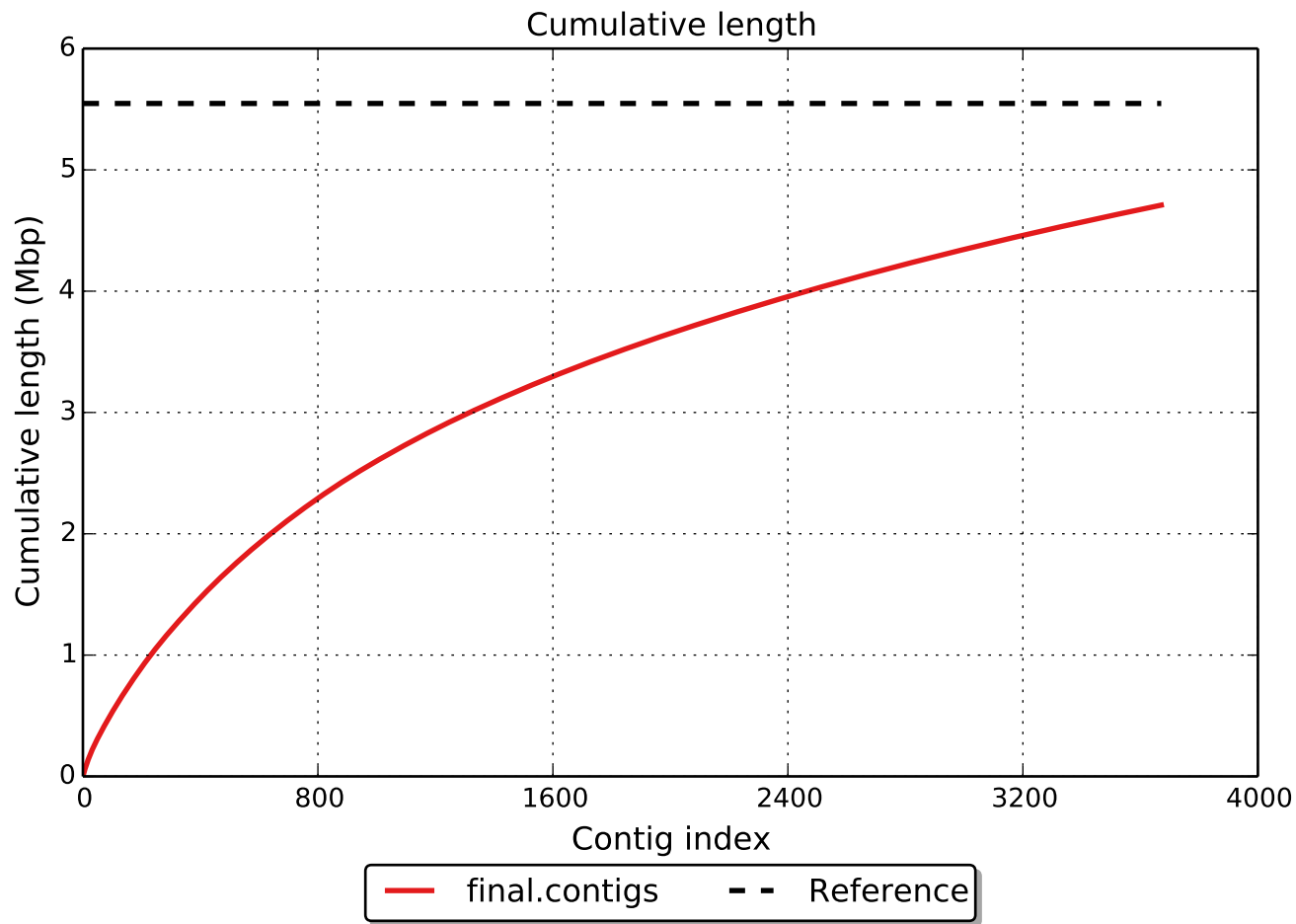
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24679
# indels	7
# short indels	6
# long indels	1
Indels length	12

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).

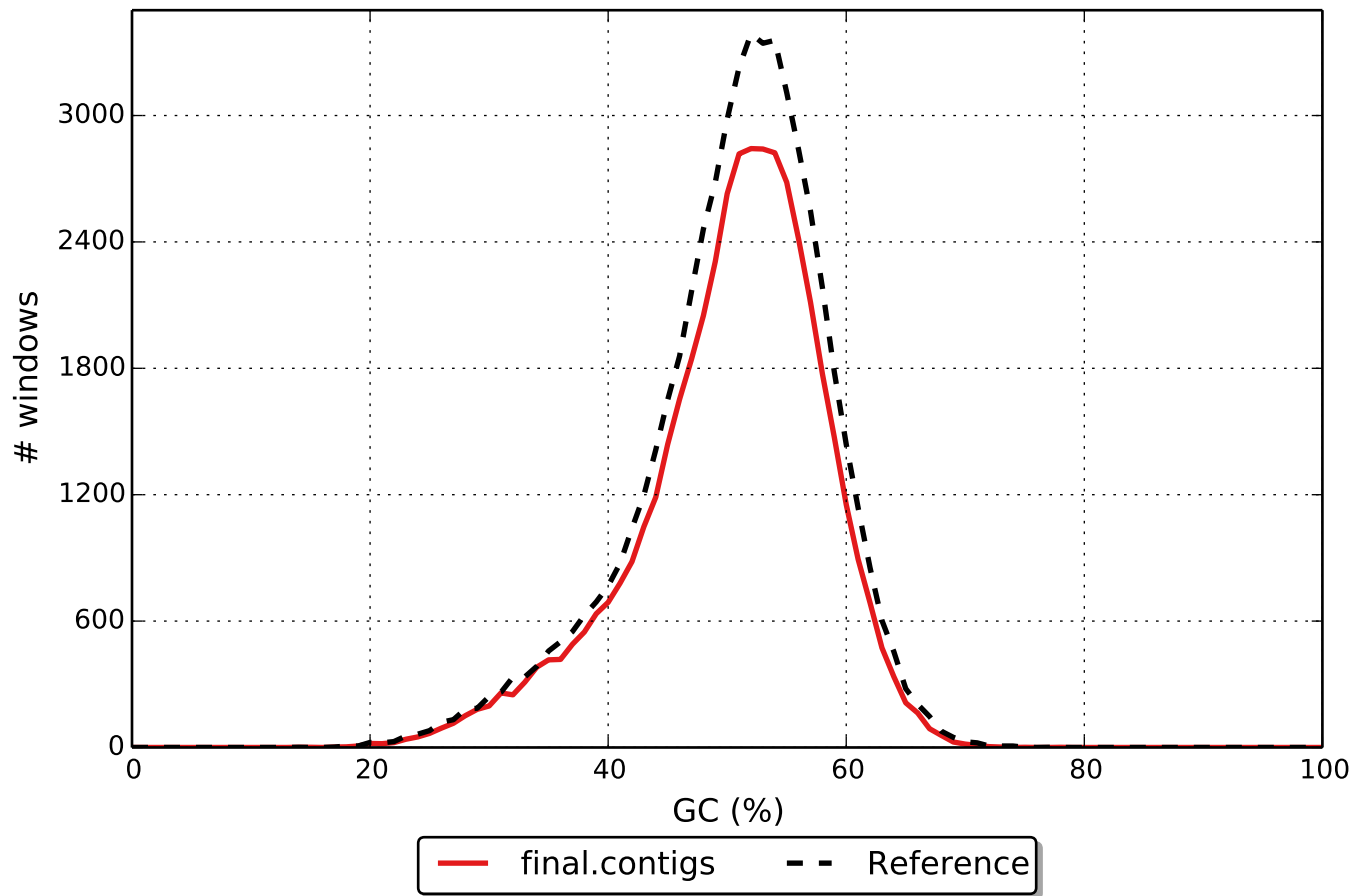
Unaligned report

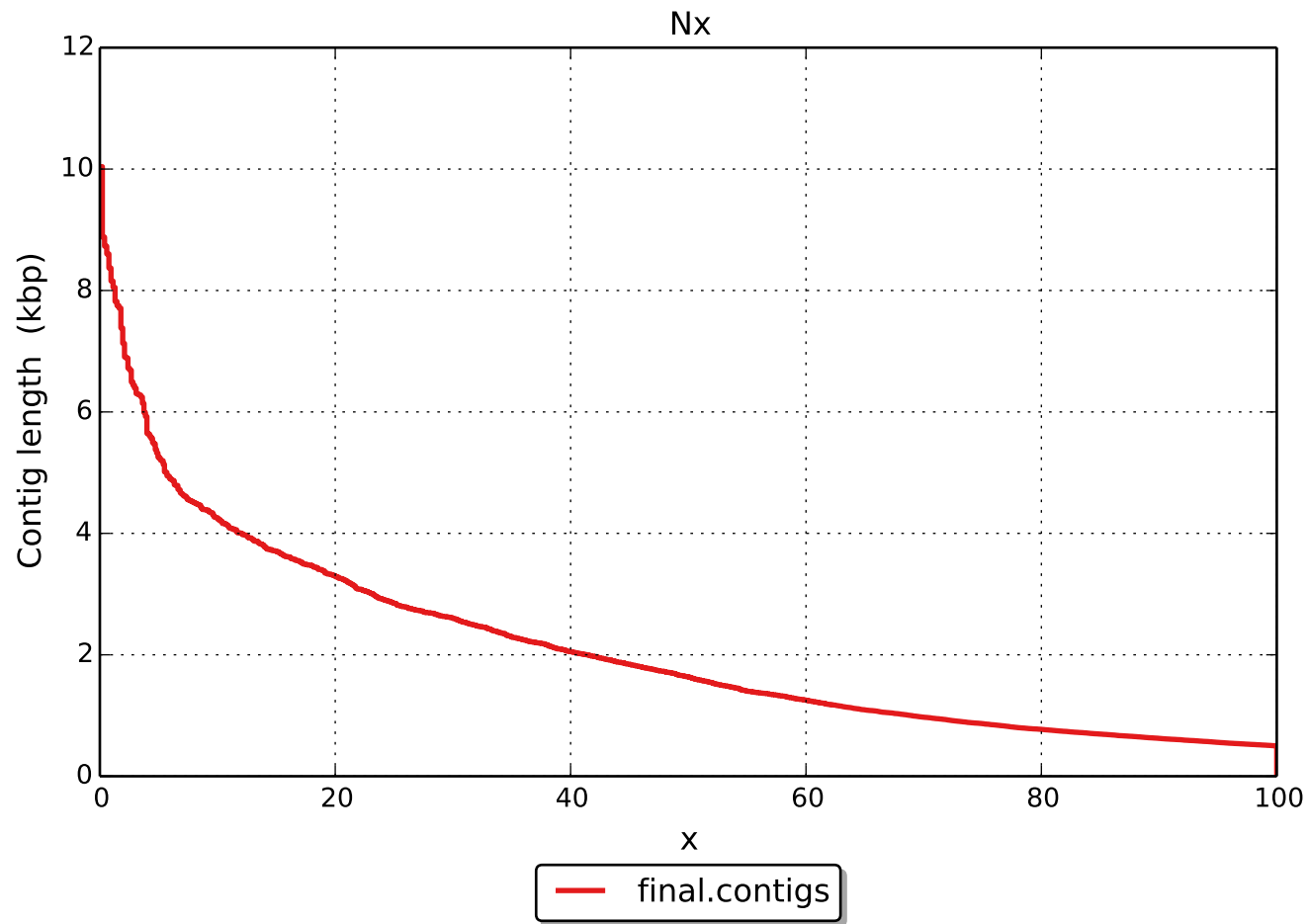
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

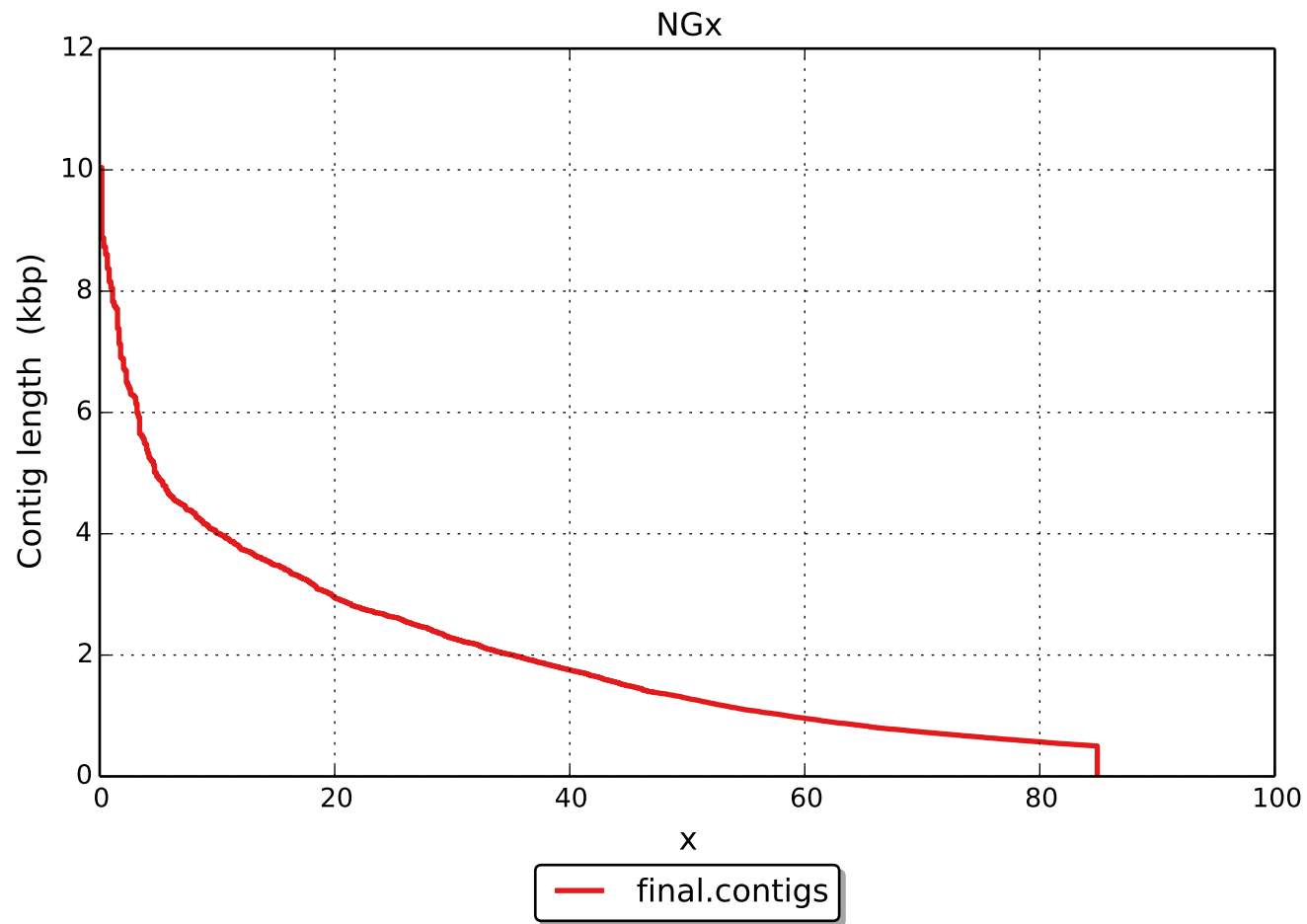
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

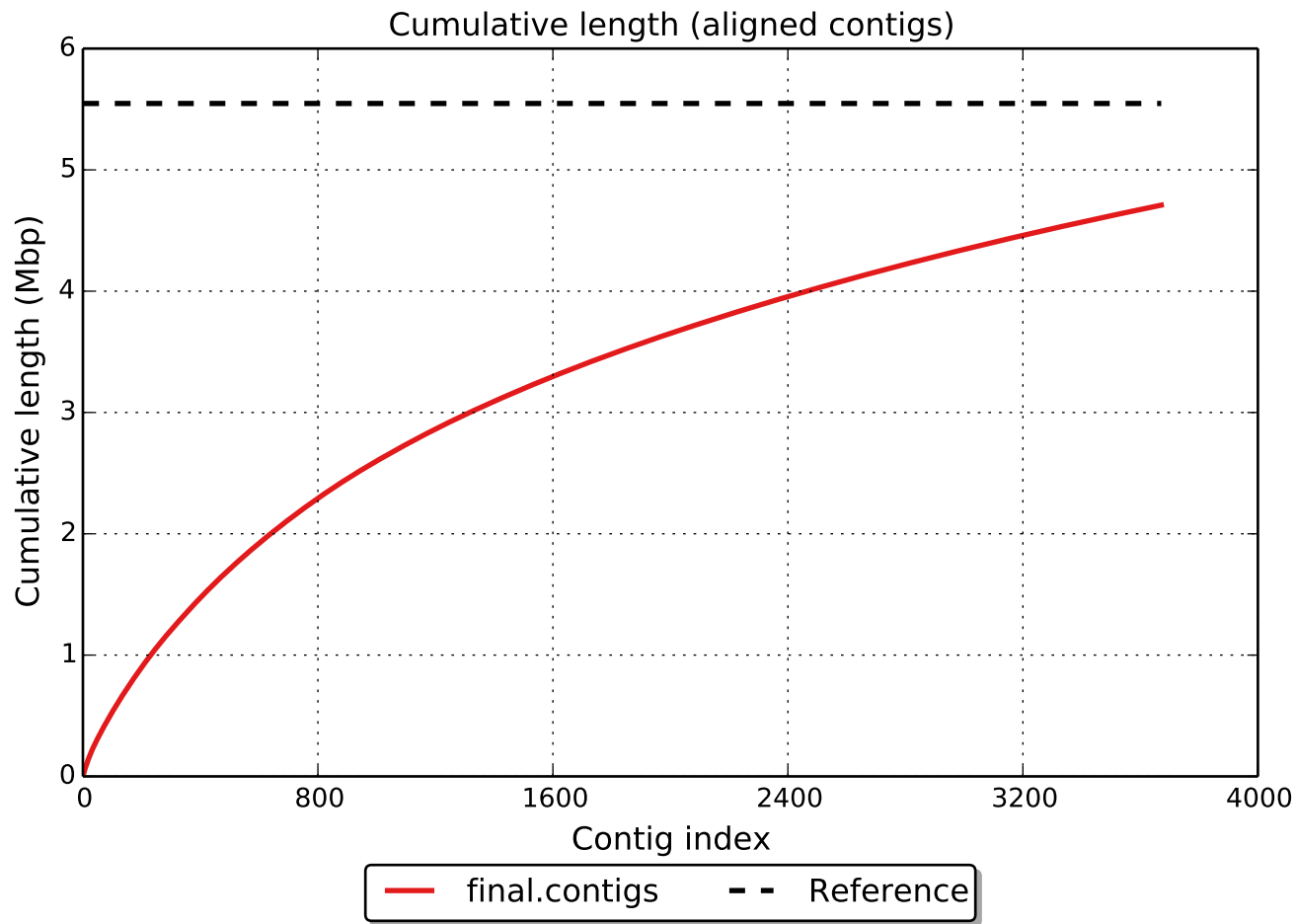


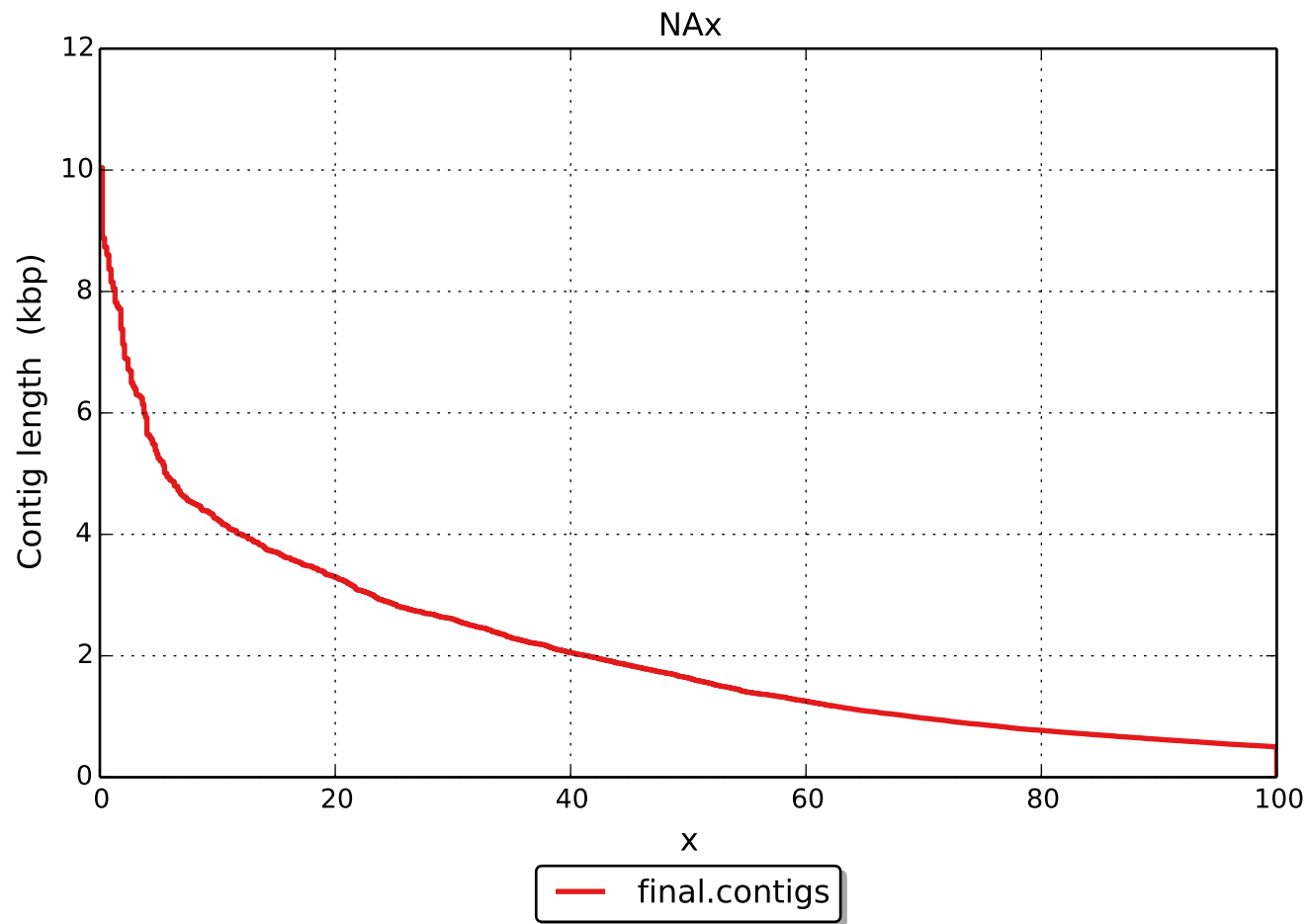




Misassemblies







NGAx

