

Report

	final.contigs
# contigs (≥ 0 bp)	1160
# contigs (≥ 1000 bp)	833
Total length (≥ 0 bp)	5078105
Total length (≥ 1000 bp)	4859127
# contigs	1160
Largest contig	39846
Total length	5078105
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	8593
NG50	7958
N75	4427
NG75	3240
L50	178
LG50	206
L75	382
LG75	475
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	90.425
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	527.57
# indels per 100 kbp	0.10
Largest alignment	39846
NA50	8593
NGA50	7958
NA75	4427
NGA75	3240
LA50	178
LGA50	206
LA75	382
LGA75	475

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

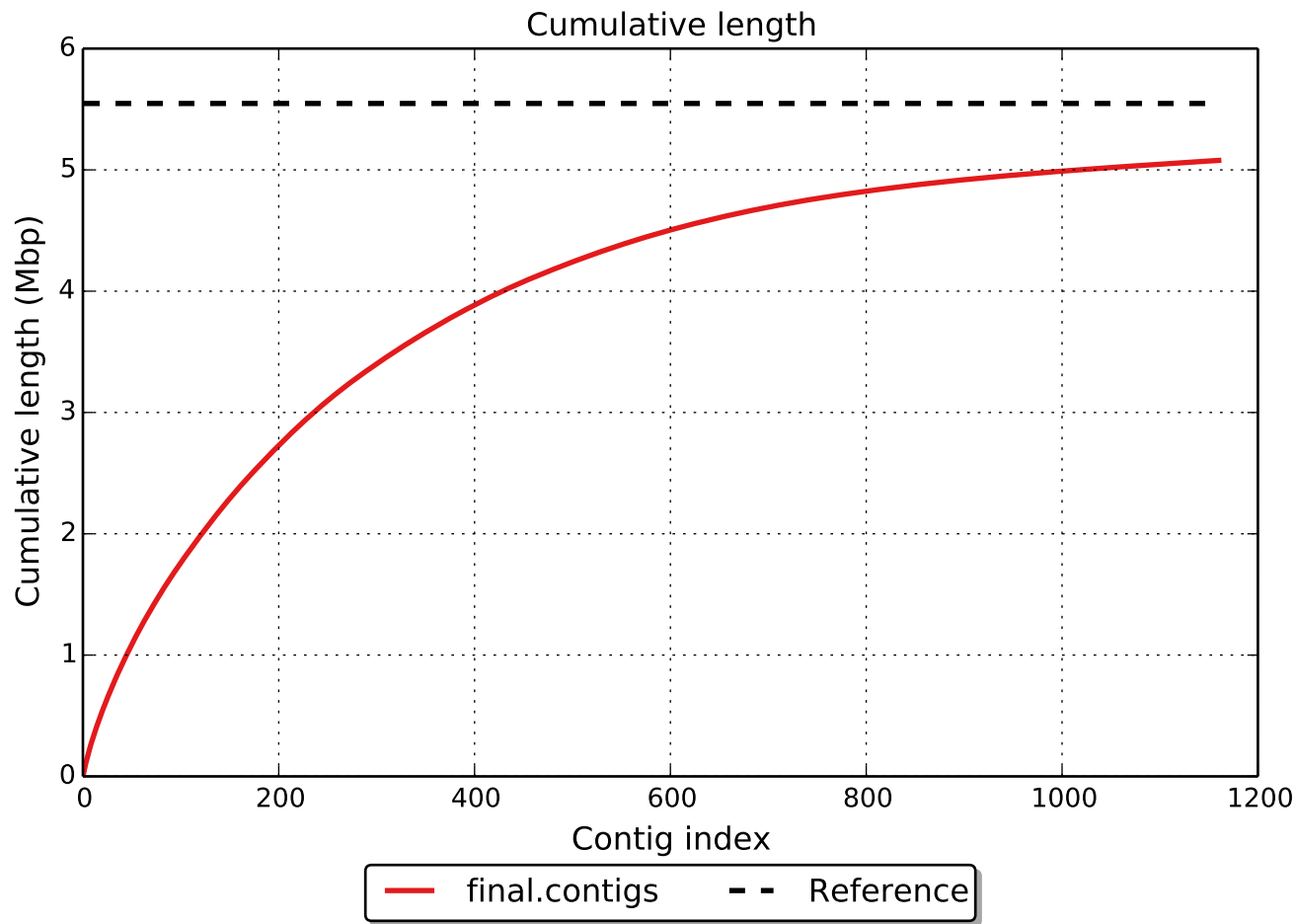
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	26464
# indels	5
# short indels	5
# long indels	0
Indels length	7

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).

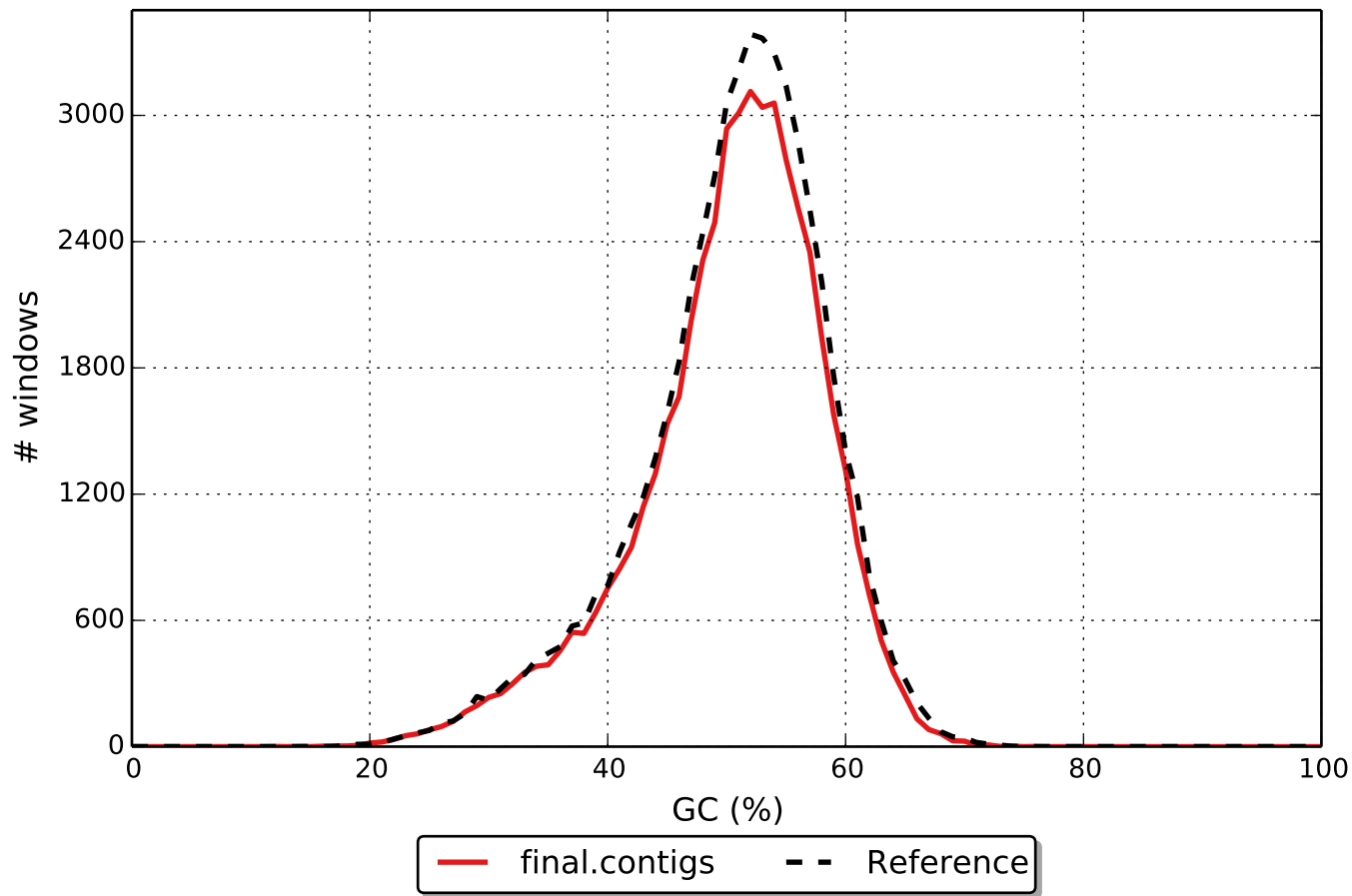
Unaligned report

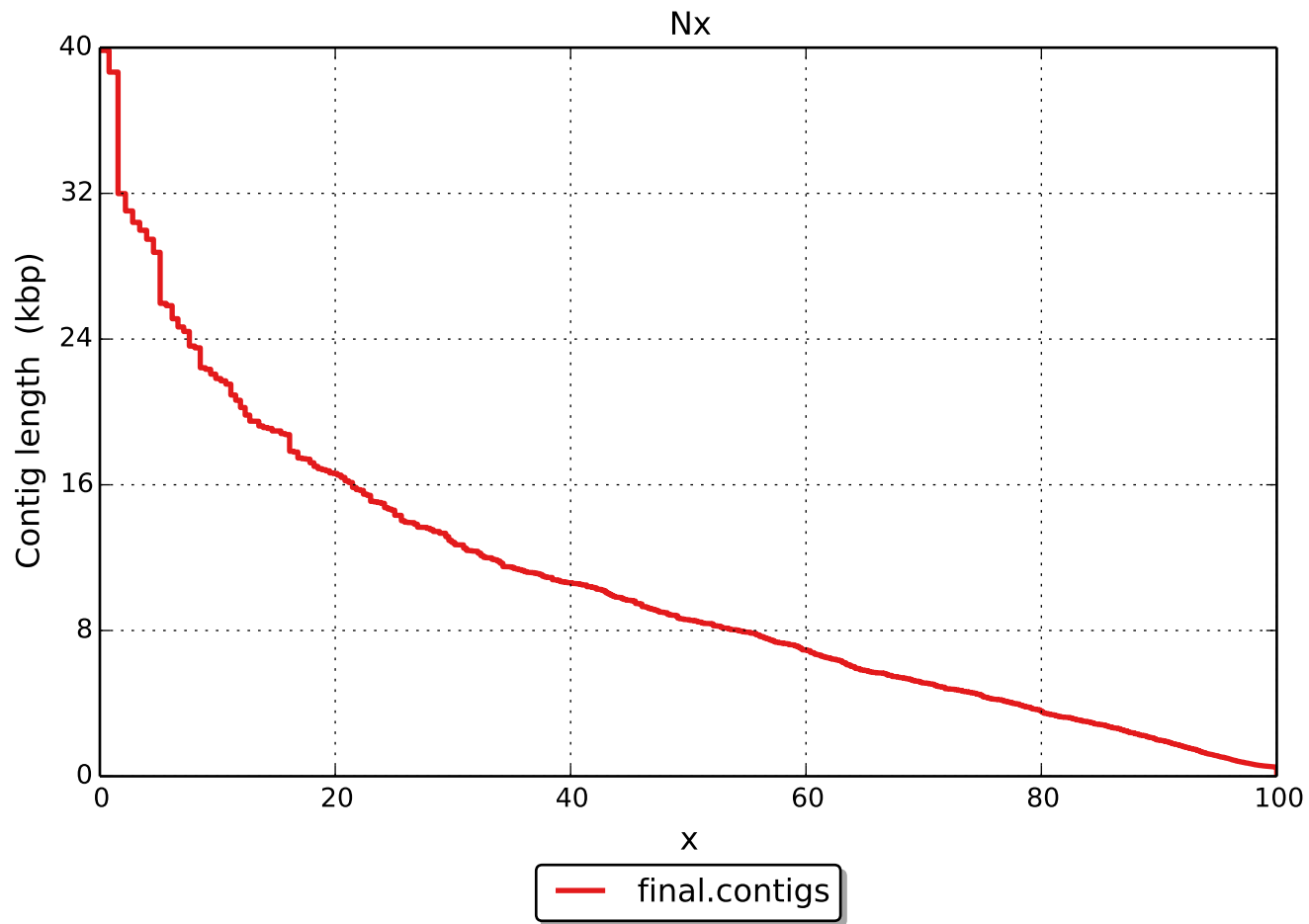
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

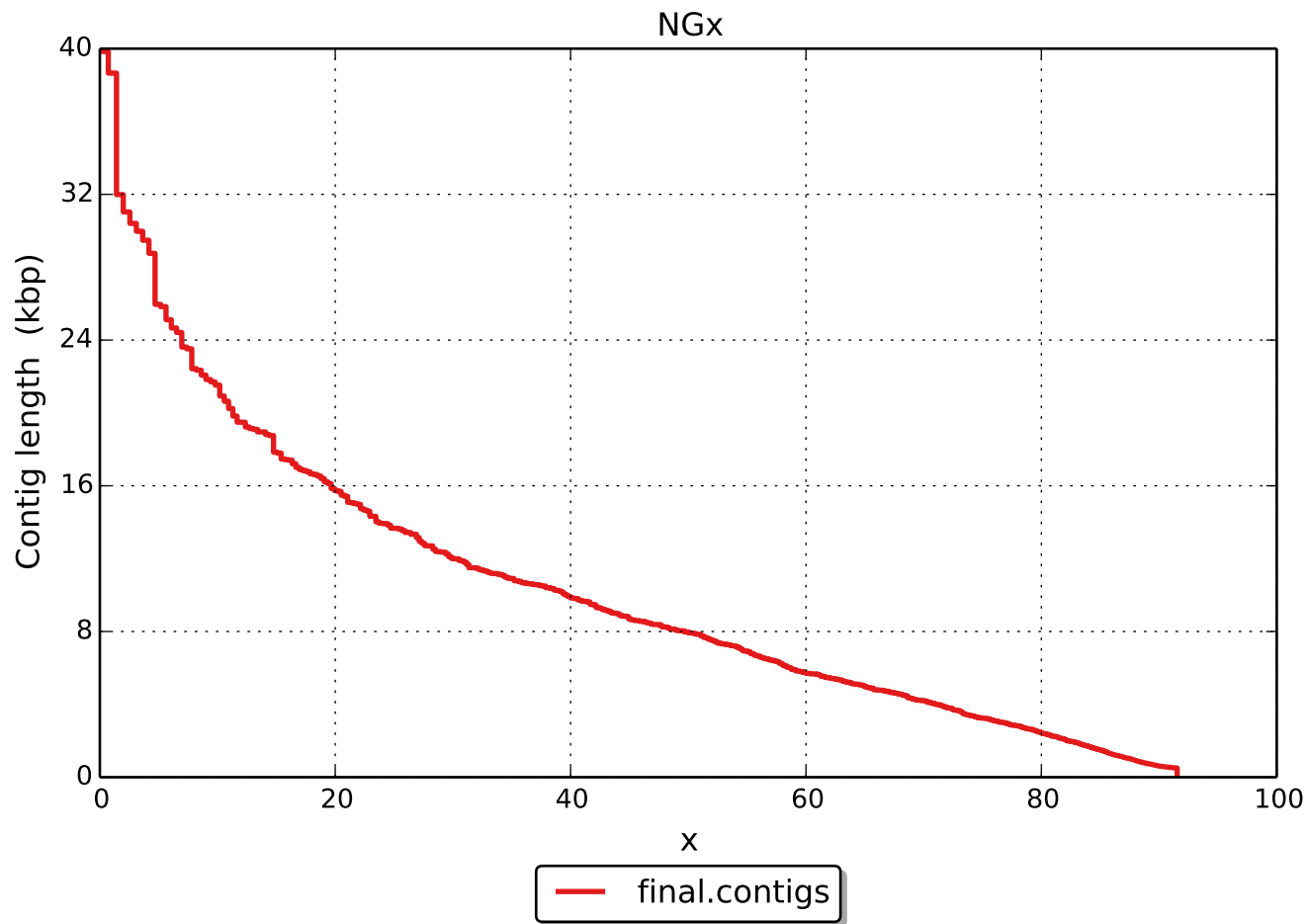
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

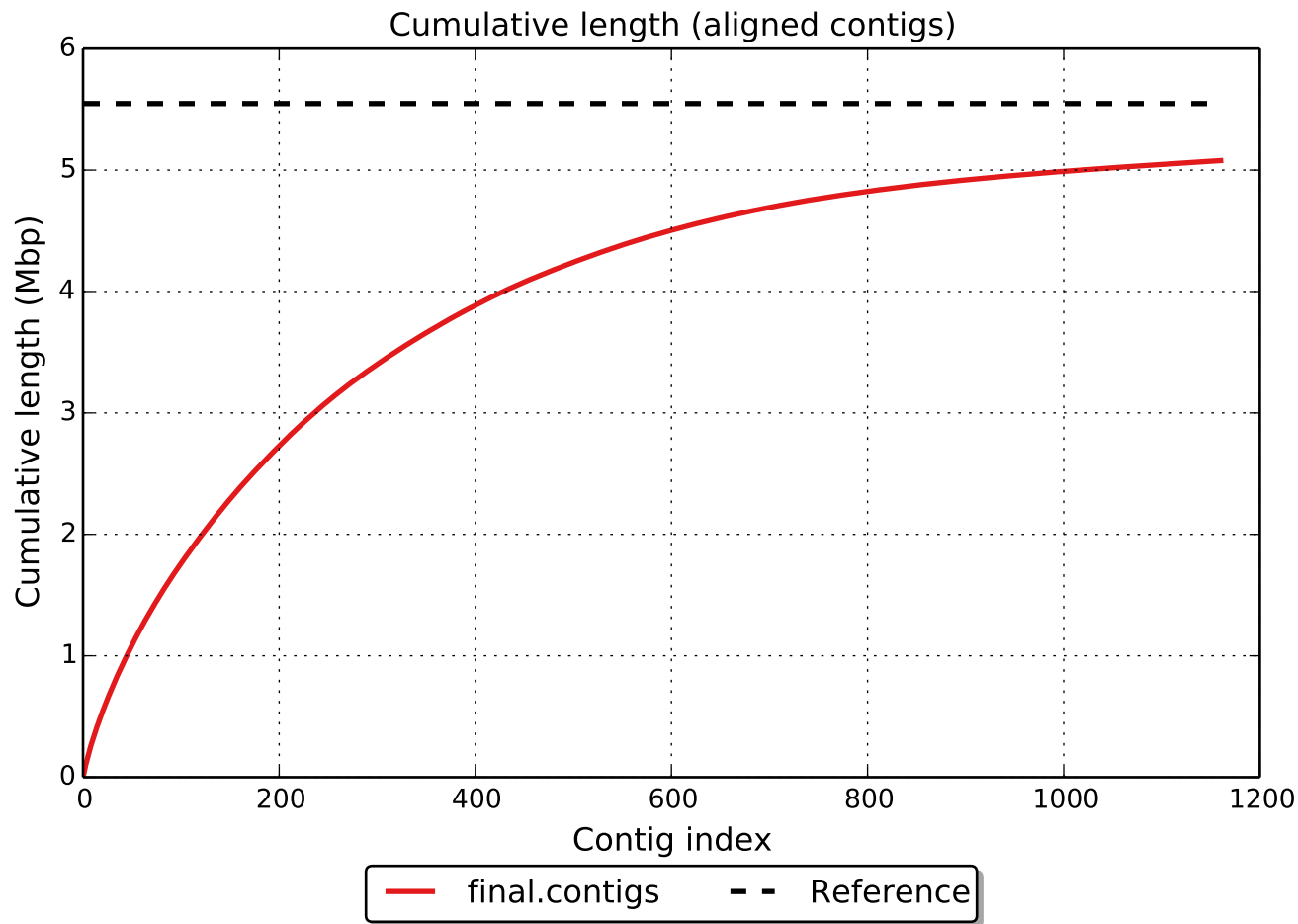


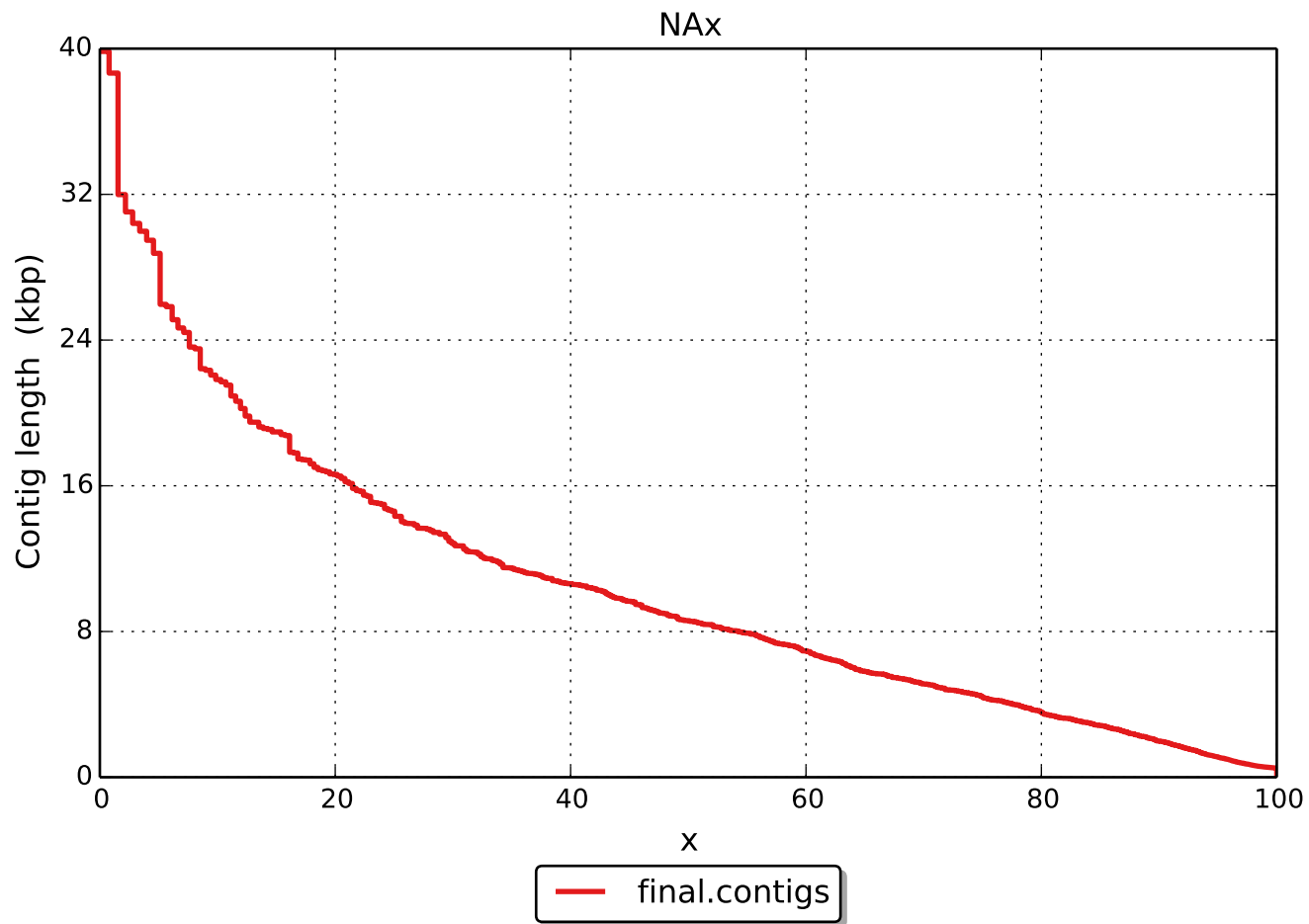




Misassemblies







NGAx

