

Report

	final.contigs
# contigs (≥ 0 bp)	3305
# contigs (≥ 1000 bp)	2110
Total length (≥ 0 bp)	5399151
Total length (≥ 1000 bp)	4519399
# contigs	3305
Largest contig	10098
Total length	5399151
Reference length	5478683
GC (%)	50.49
Reference GC (%)	50.49
N50	2025
NG50	2006
N75	1263
NG75	1224
L50	854
LG50	874
L75	1692
LG75	1740
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 2 part
Unaligned length	1351
Genome fraction (%)	94.772
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.56
# indels per 100 kbp	0.00
Largest alignment	10098
NA50	2022
NGA50	2004
NA75	1262
NGA75	1221
LA50	855
LGA50	874
LA75	1693
LGA75	1741

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

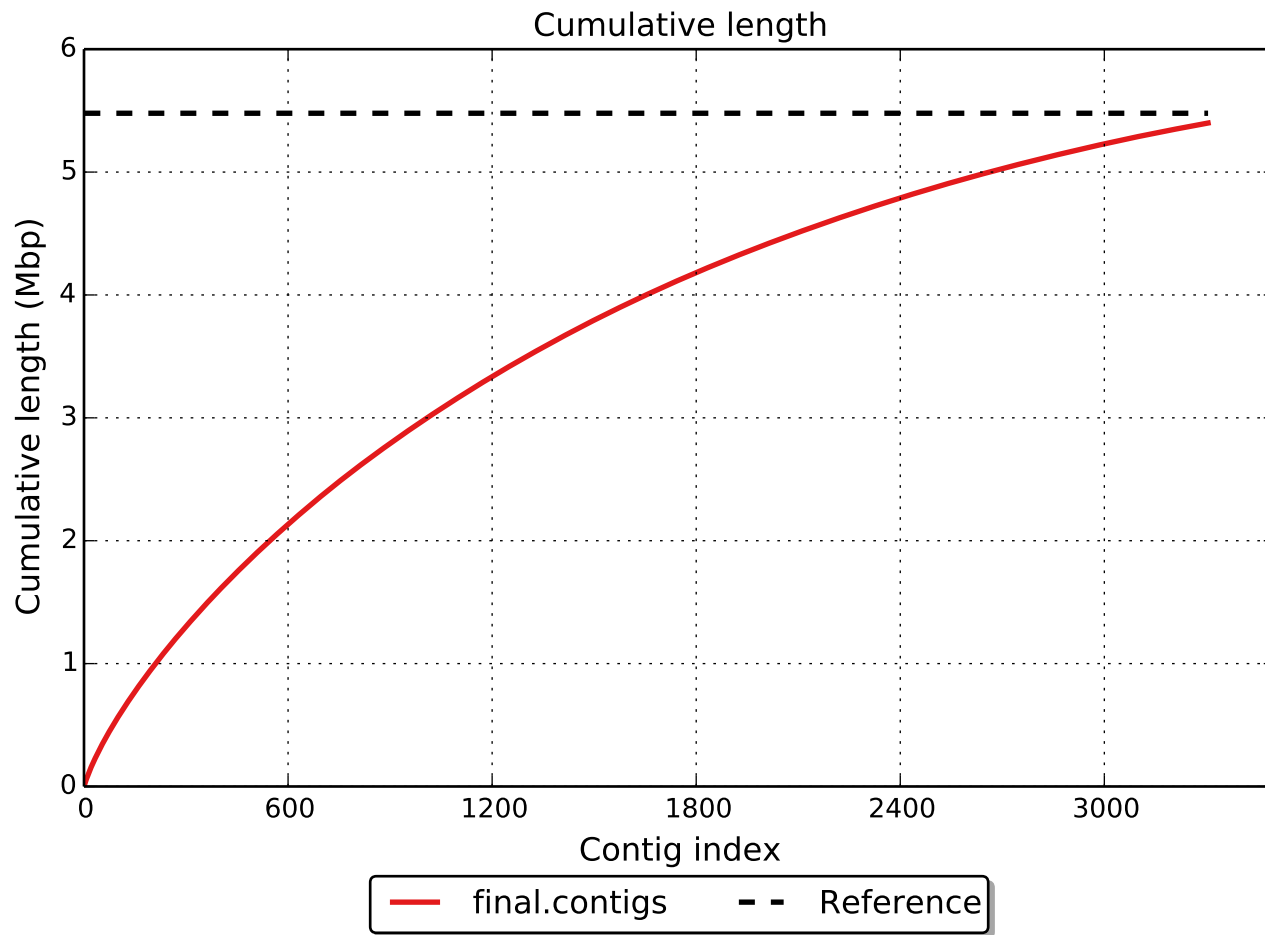
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1379
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

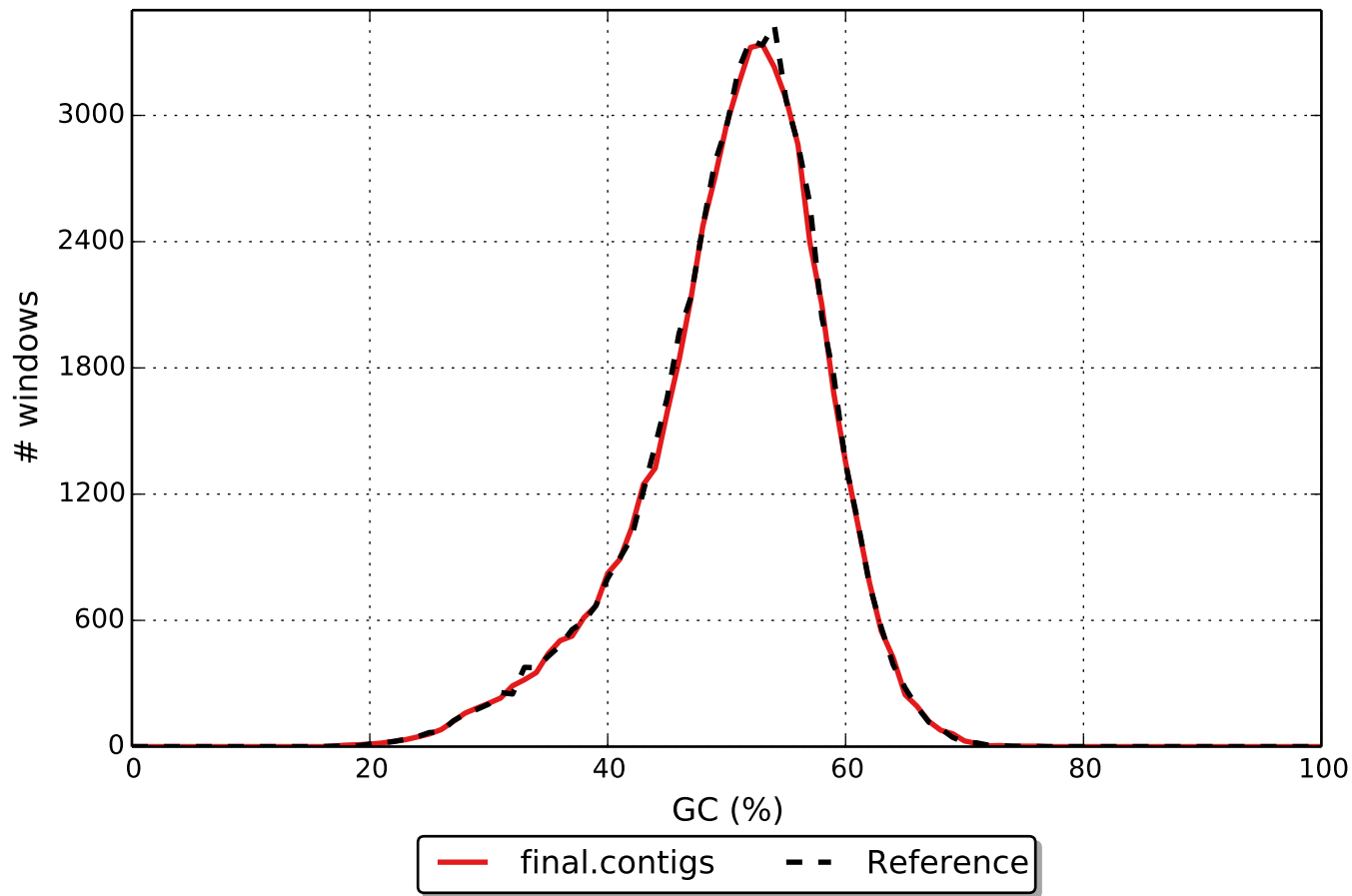
Unaligned report

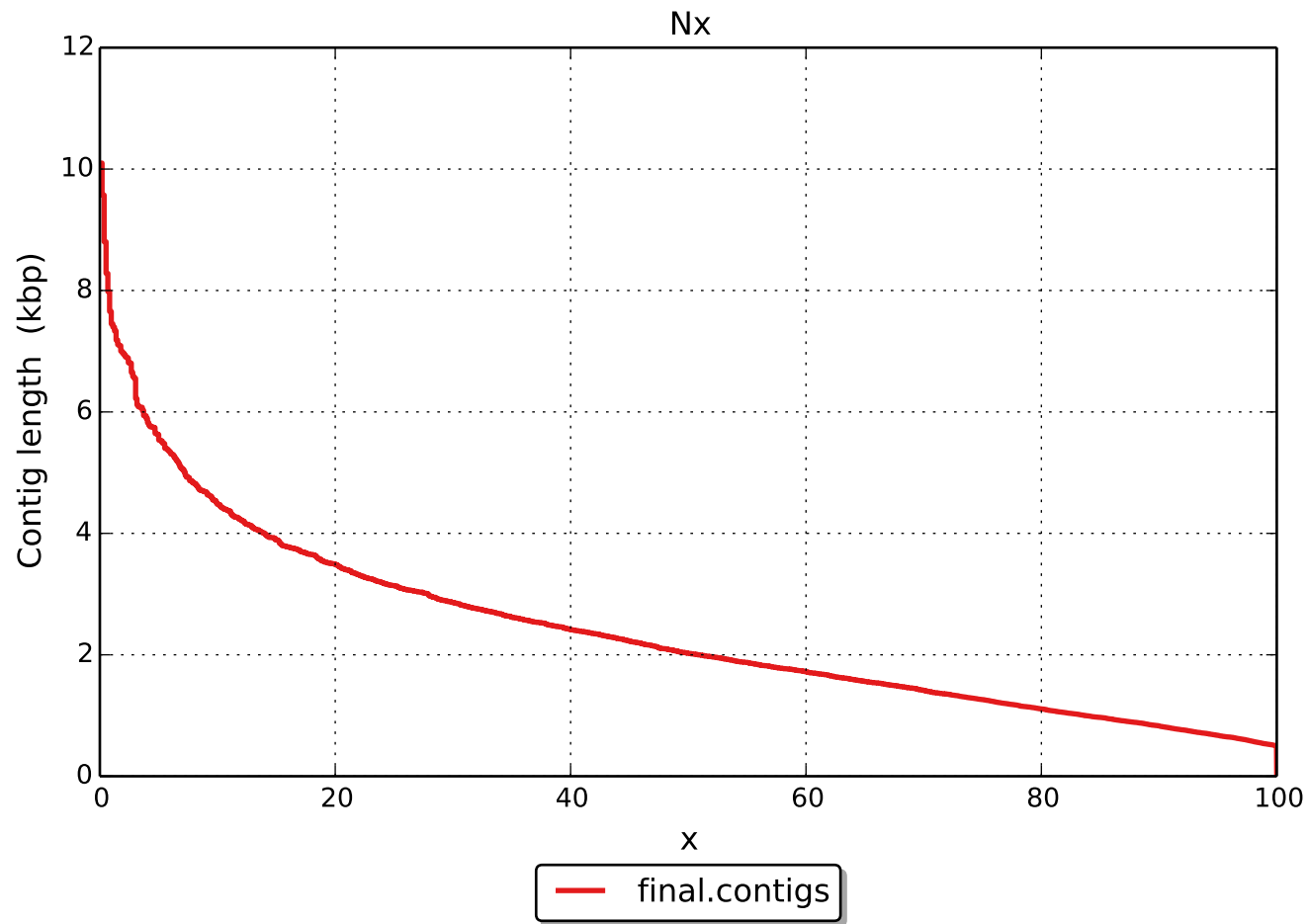
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1351
# N's	0

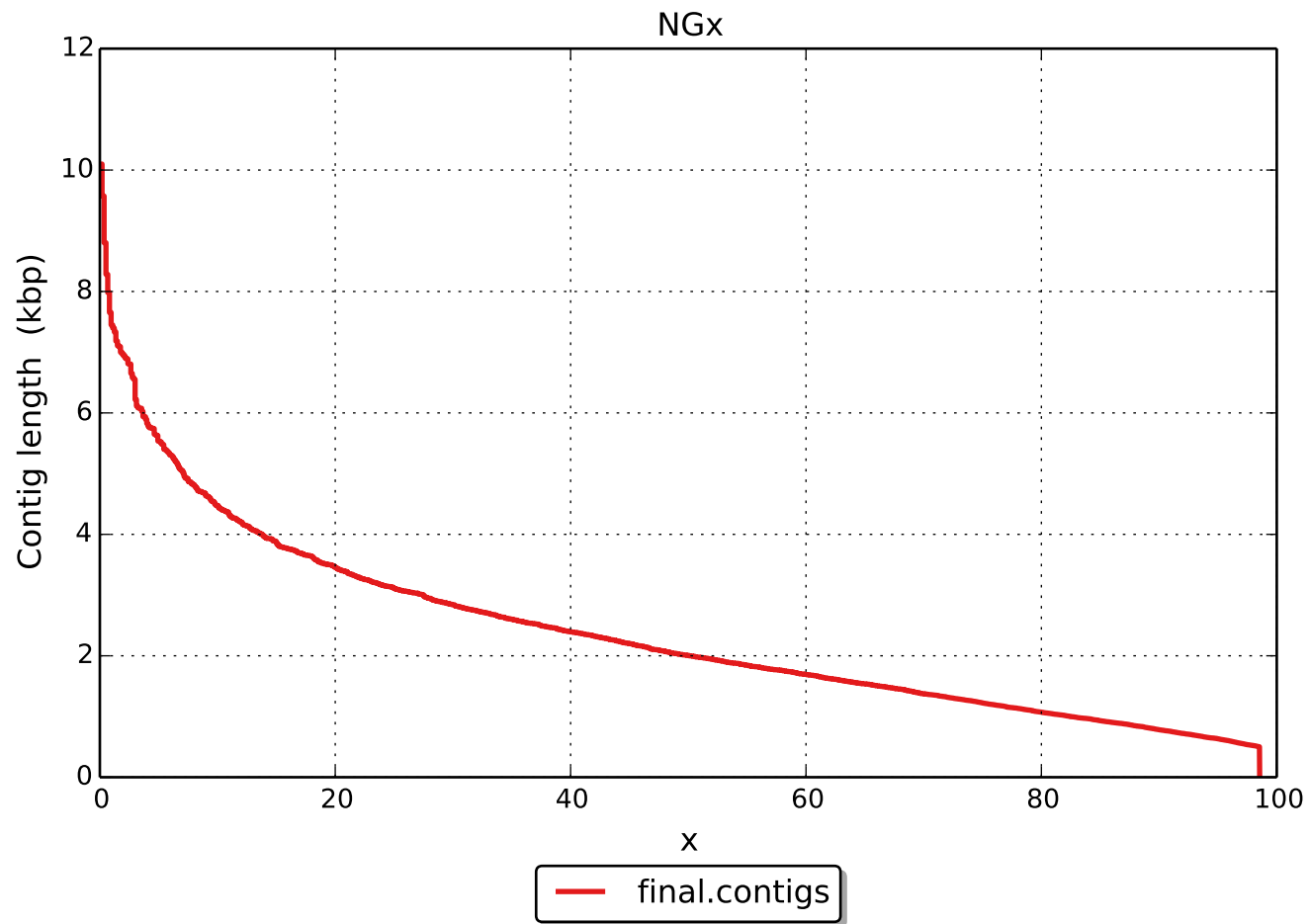
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

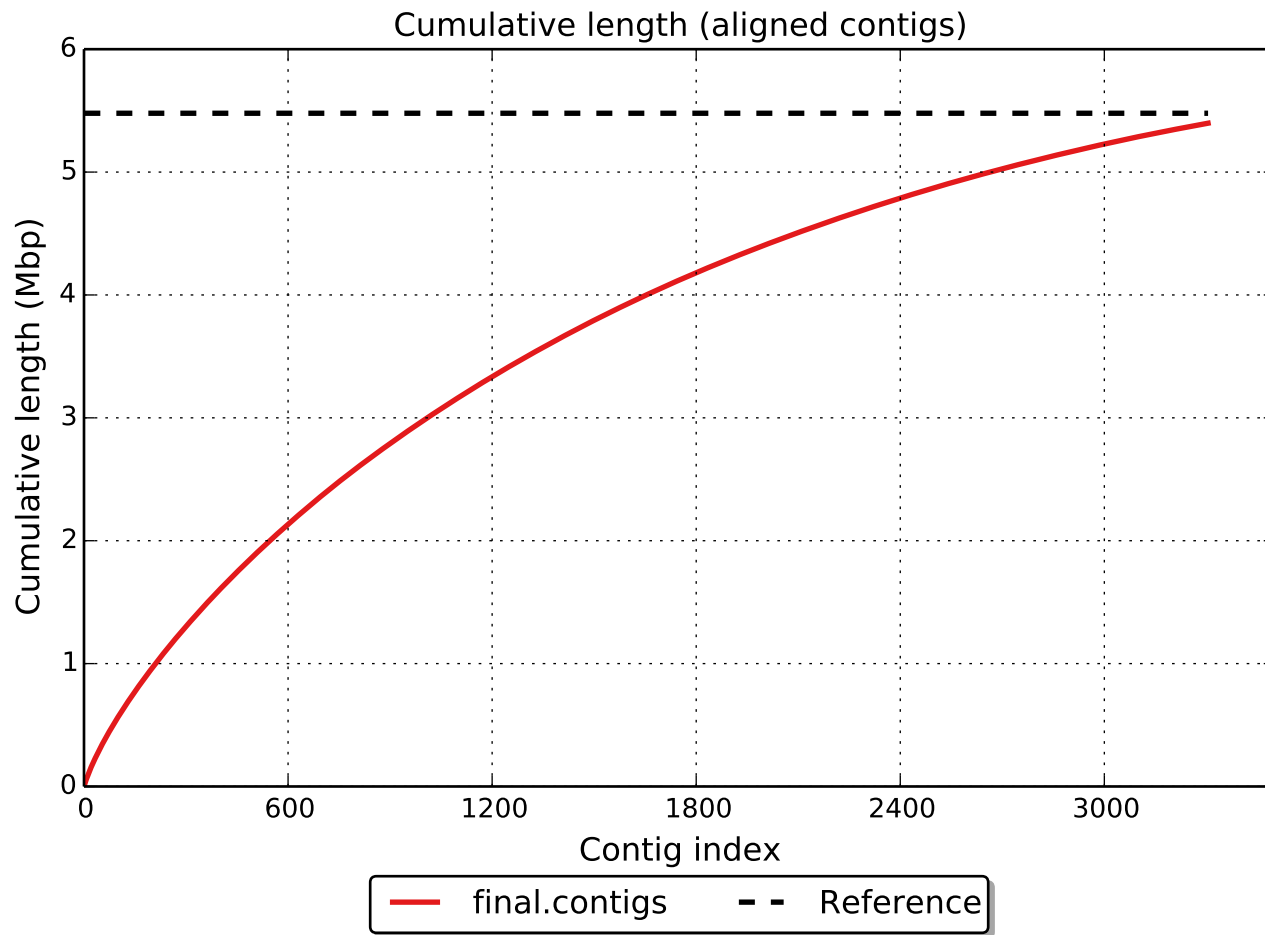


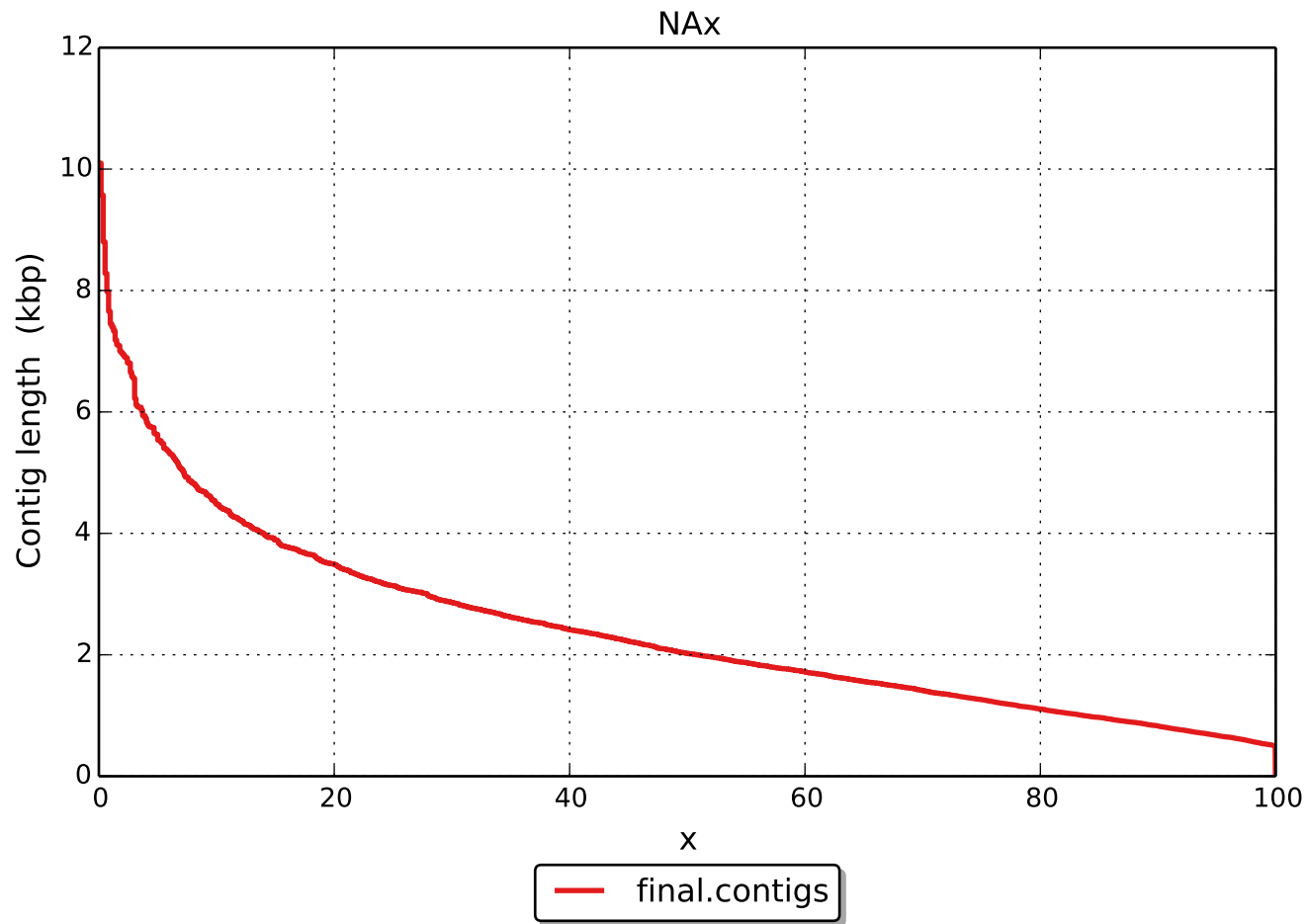




Misassemblies







NGAx

