

Report

	final.contigs
# contigs (≥ 0 bp)	3624
# contigs (≥ 1000 bp)	1606
Total length (≥ 0 bp)	4695879
Total length (≥ 1000 bp)	3300276
# contigs	3624
Largest contig	9465
Total length	4695879
Reference length	5478683
GC (%)	50.31
Reference GC (%)	50.49
N50	1648
NG50	1351
N75	885
NG75	668
L50	862
LG50	1124
L75	1842
LG75	2610
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	24
Genome fraction (%)	81.070
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	556.52
# indels per 100 kbp	0.09
Largest alignment	9465
NA50	1648
NGA50	1351
NA75	885
NGA75	668
LA50	862
LGA50	1124
LA75	1842
LGA75	2610

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

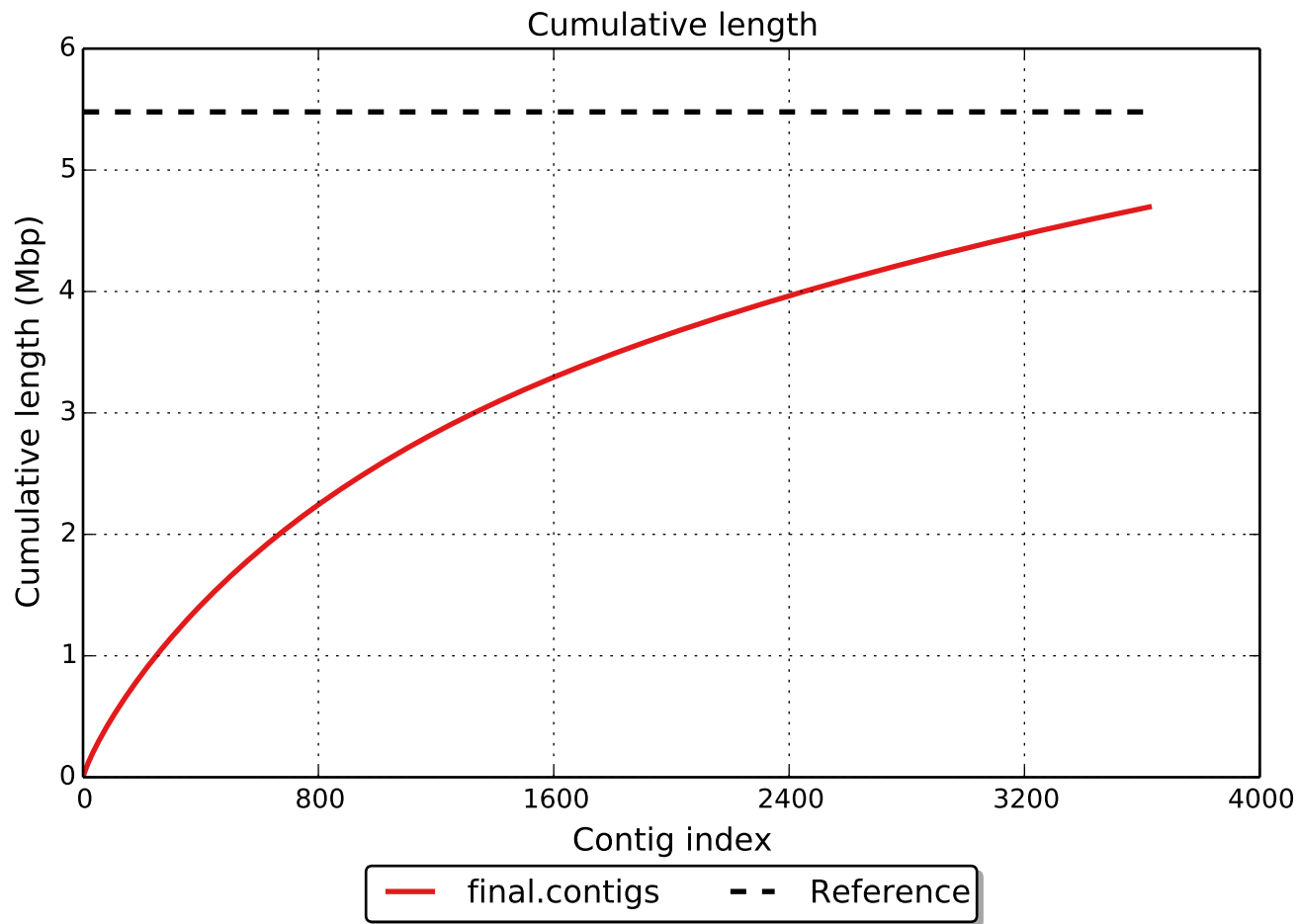
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	24718
# indels	4
# short indels	2
# long indels	2
Indels length	26

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).

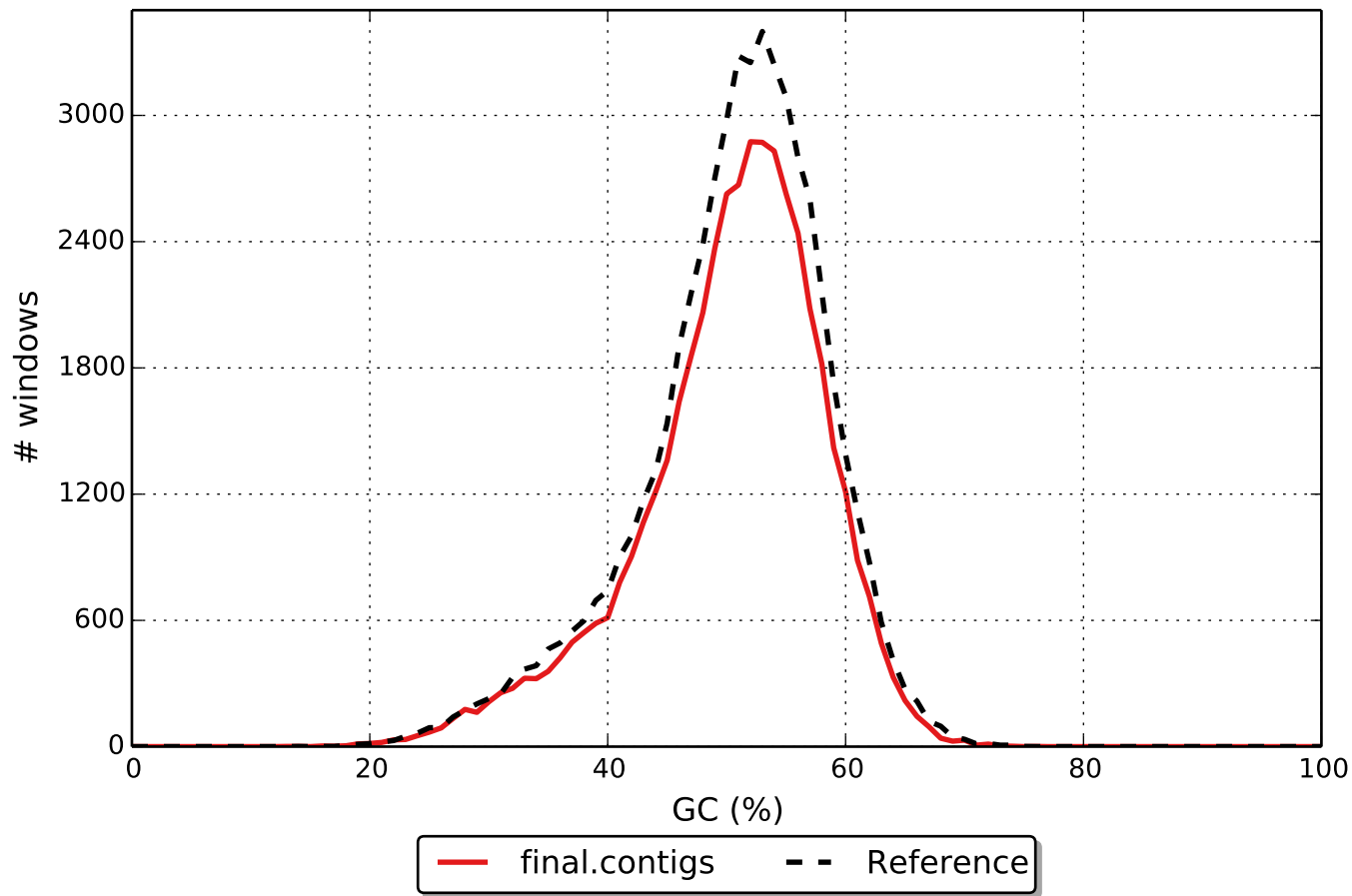
Unaligned report

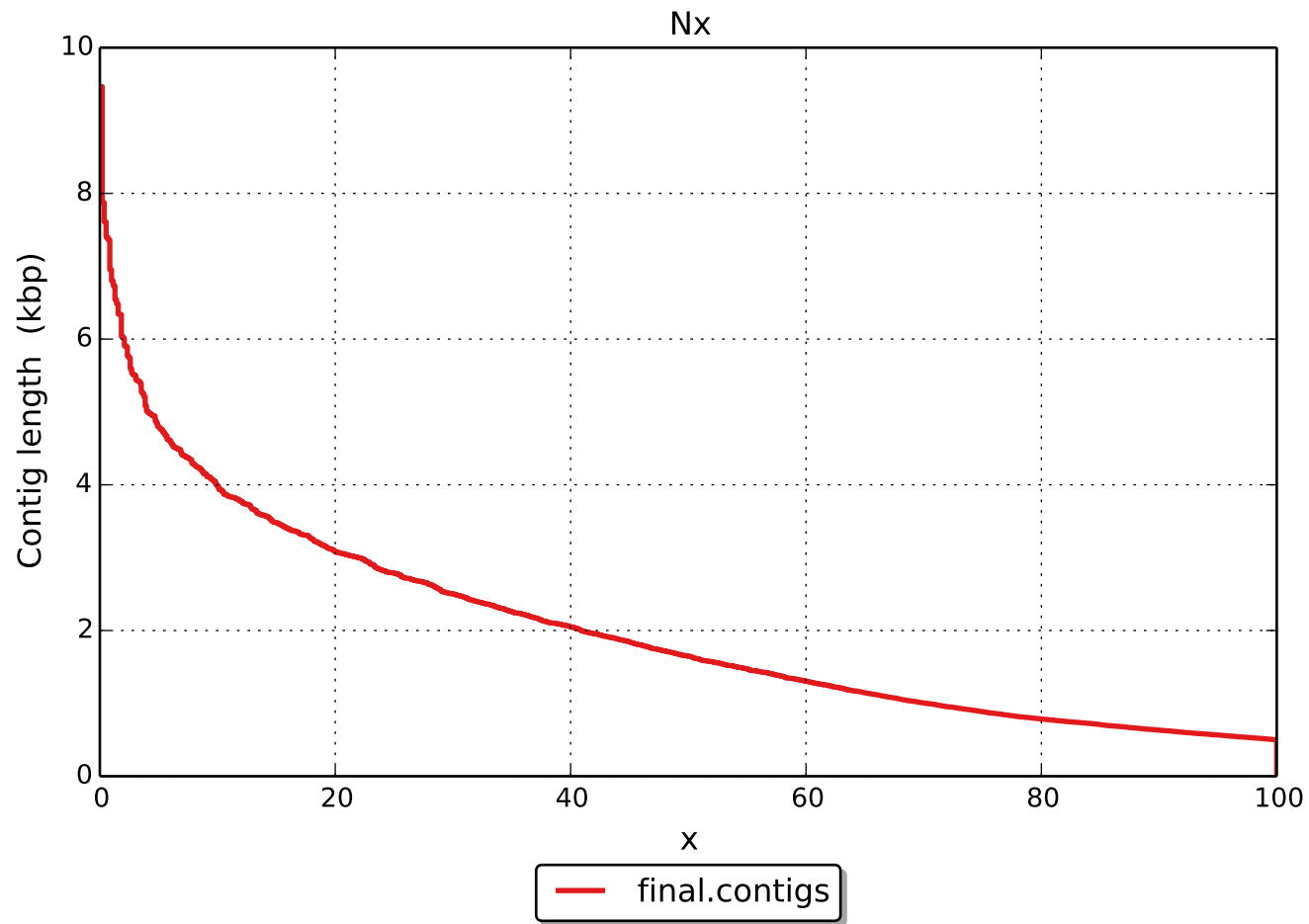
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	24
# N's	0

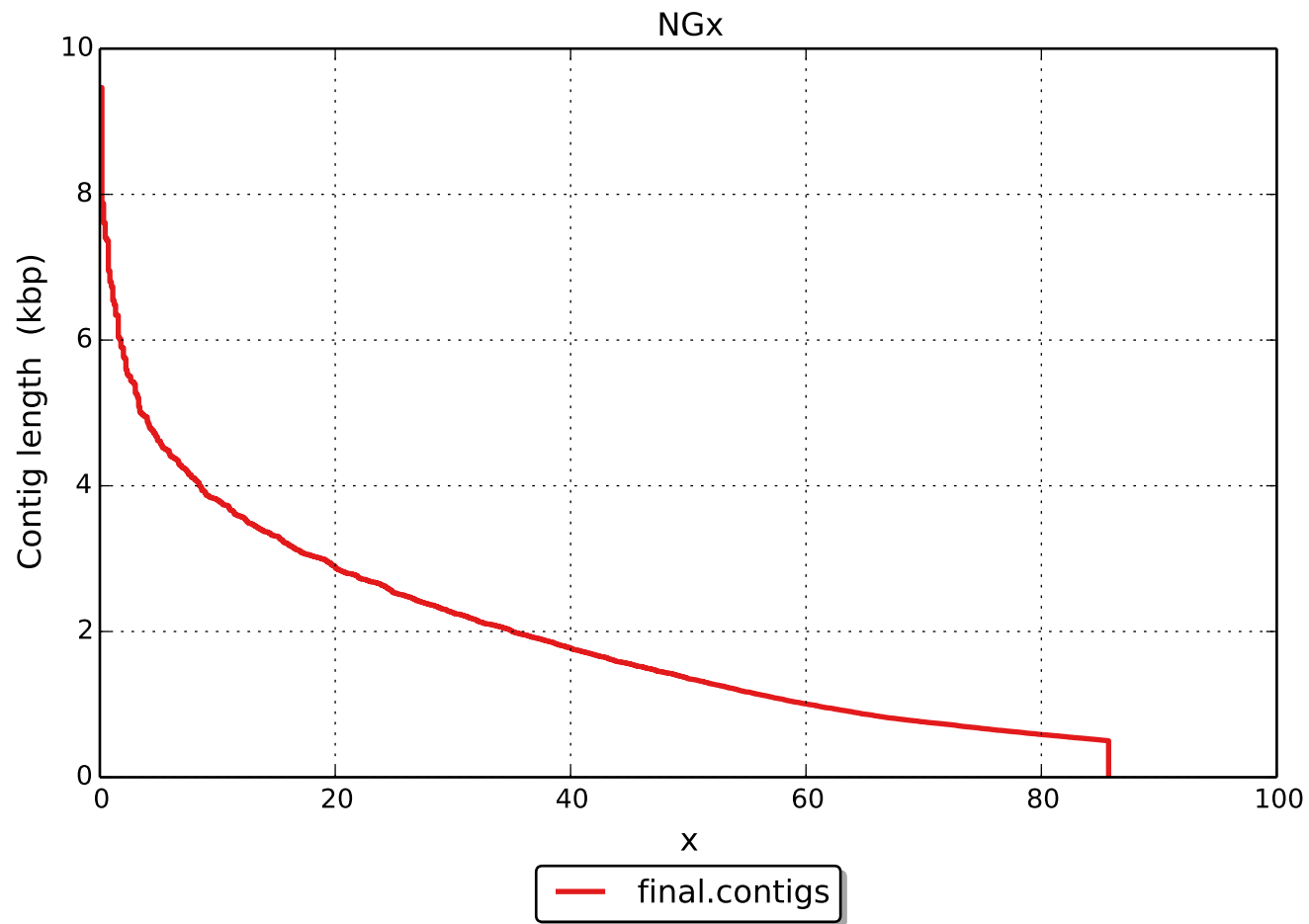
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

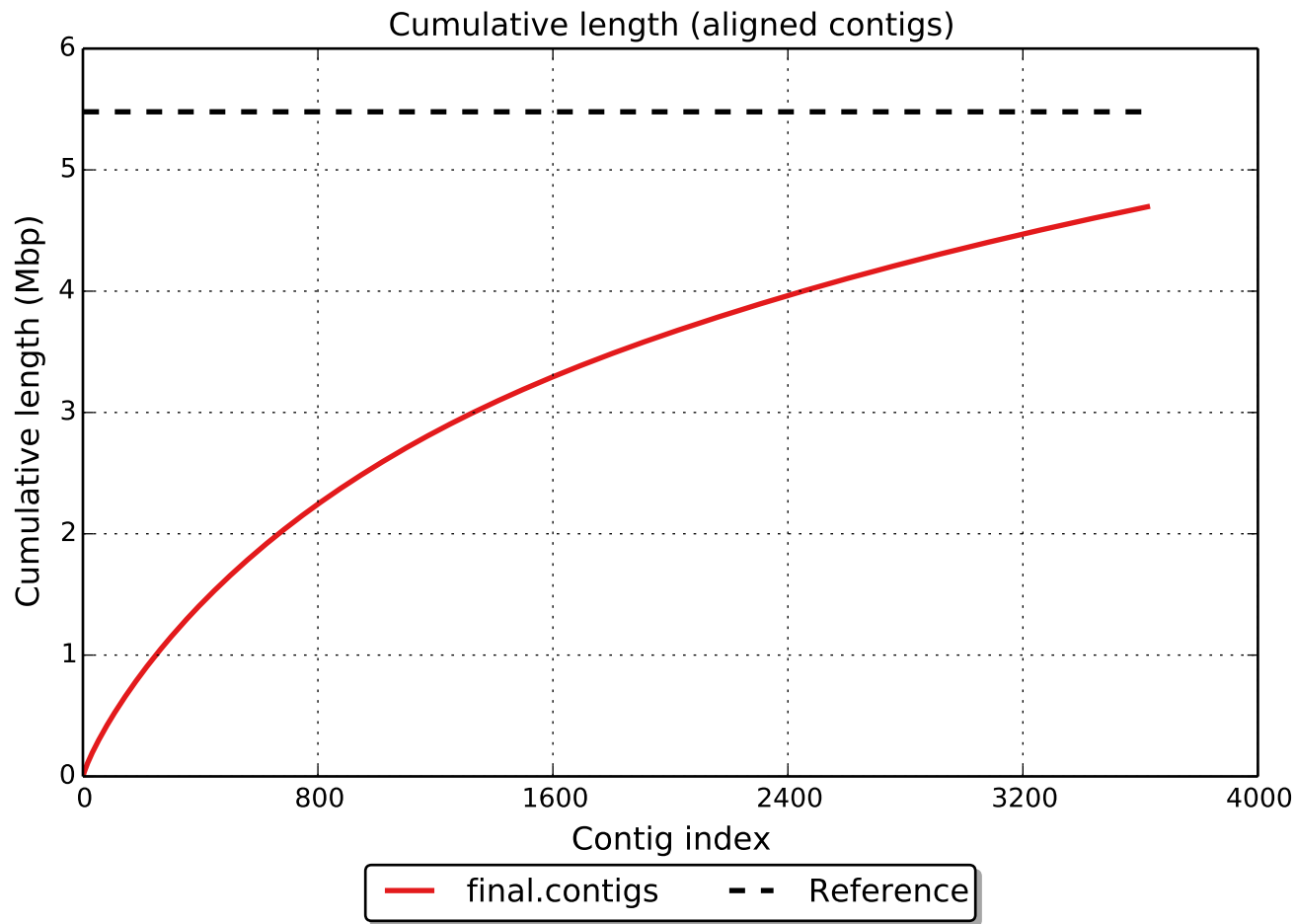


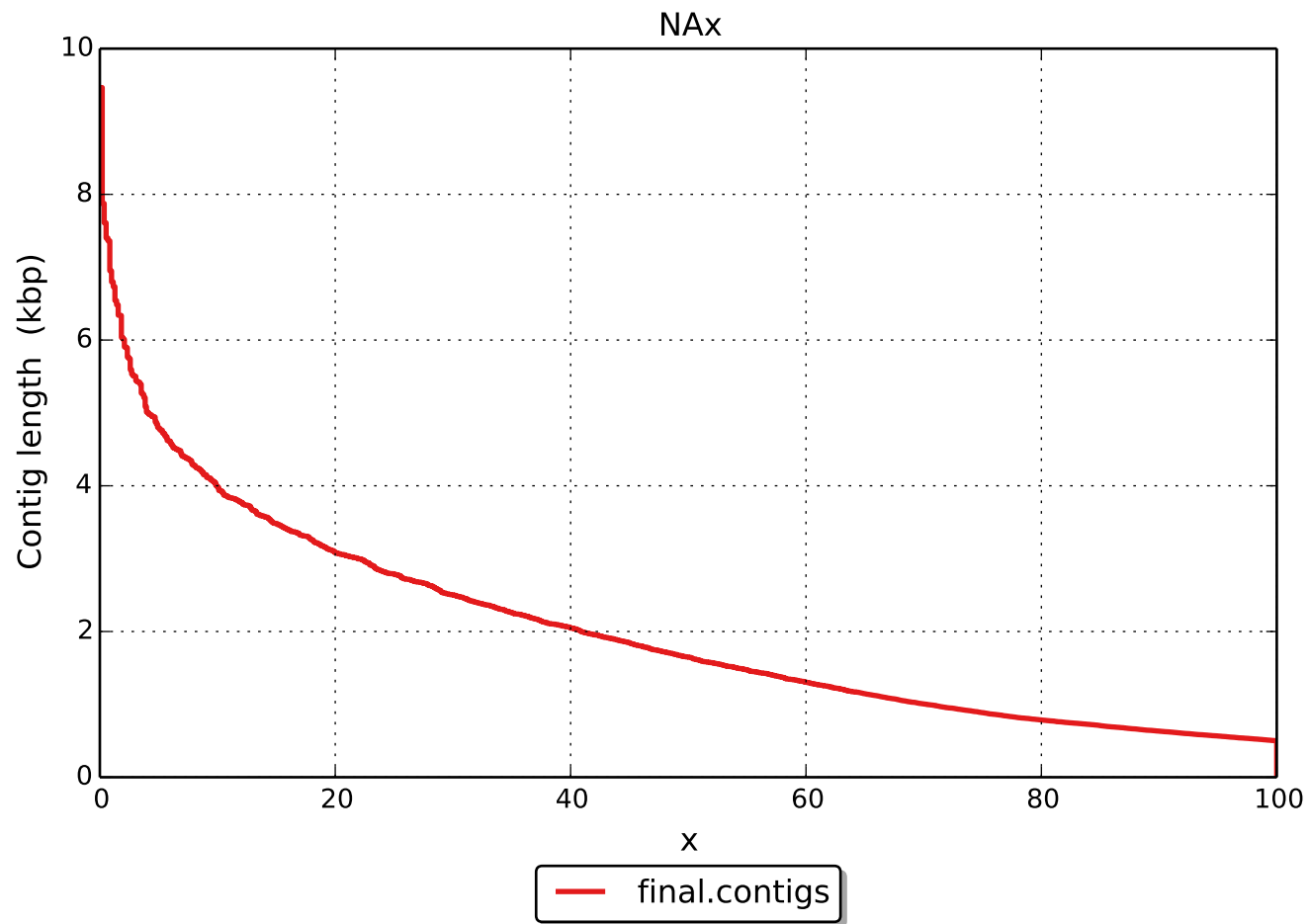




Misassemblies







NGAx

