

Report

	final.contigs
# contigs (≥ 0 bp)	3788
# contigs (≥ 1000 bp)	2019
Total length (≥ 0 bp)	4960572
Total length (≥ 1000 bp)	3683395
# contigs	3788
Largest contig	7826
Total length	4960572
Reference length	5547323
GC (%)	50.28
Reference GC (%)	50.48
N50	1543
NG50	1388
N75	983
NG75	818
L50	1040
LG50	1241
L75	2057
LG75	2547
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.311
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	68.44
# indels per 100 kbp	0.21
Largest alignment	7826
NA50	1543
NGA50	1388
NA75	983
NGA75	818
LA50	1040
LGA50	1241
LA75	2057
LGA75	2547

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

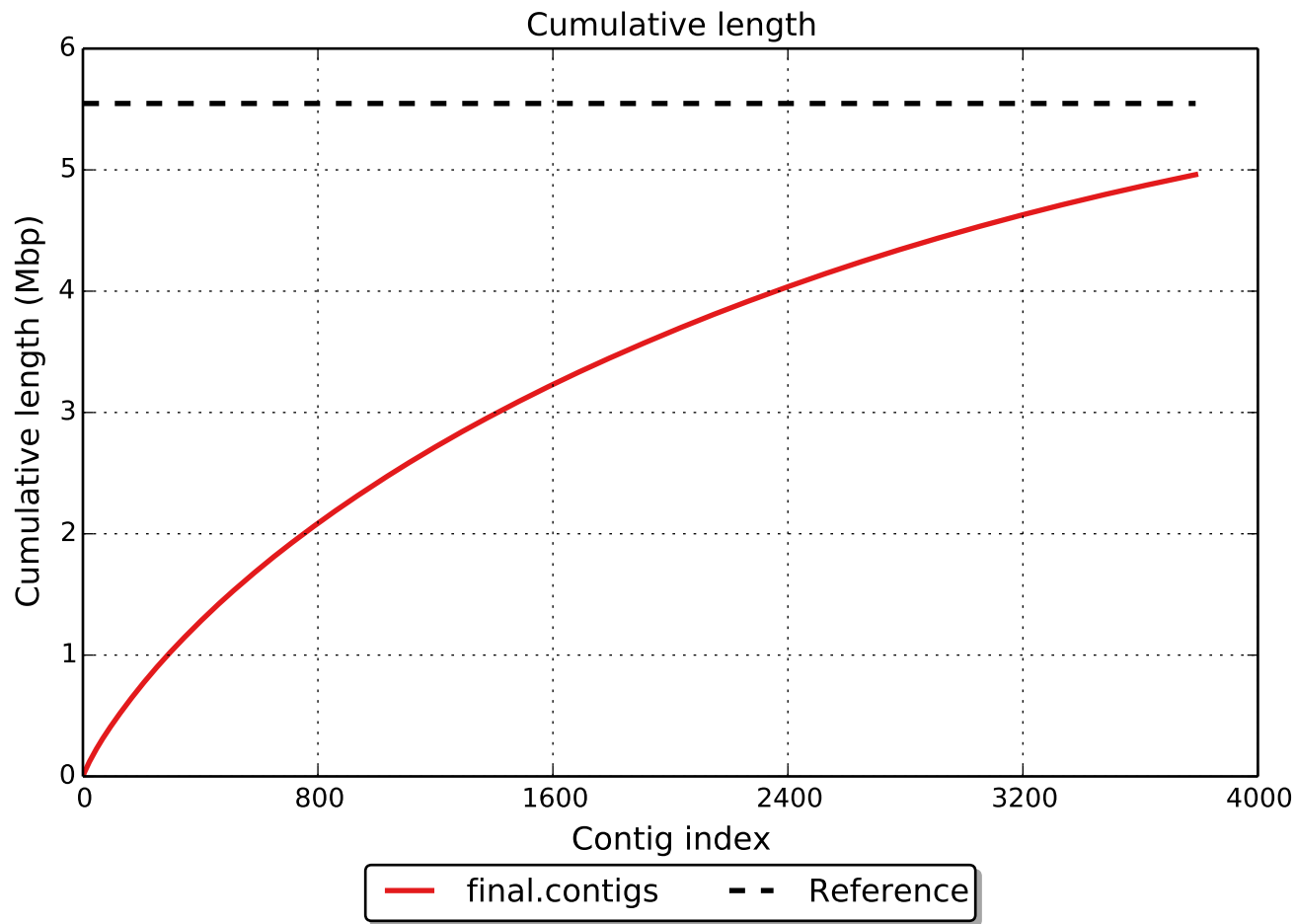
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3239
# indels	10
# short indels	8
# long indels	2
Indels length	20

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).

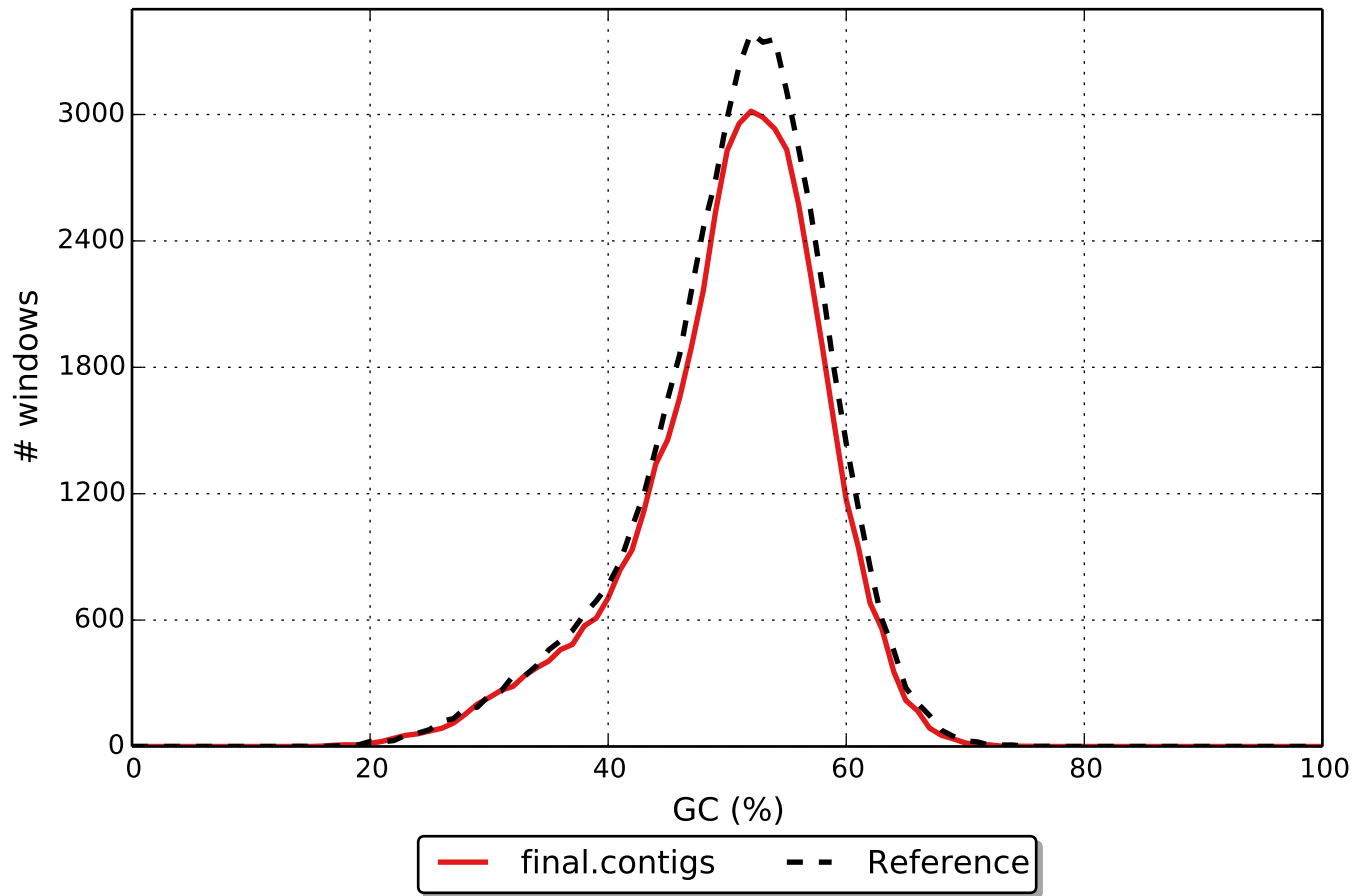
Unaligned report

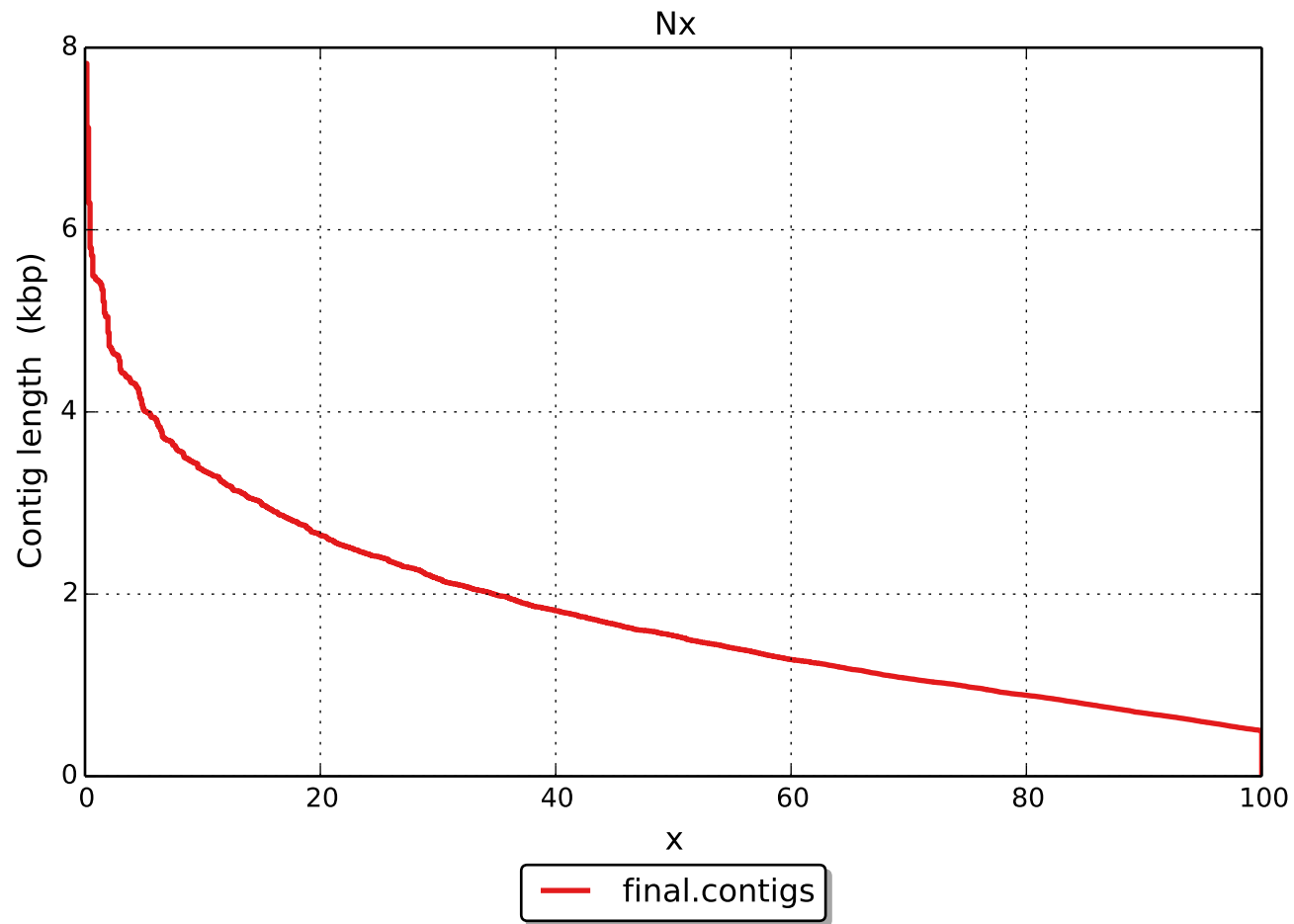
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

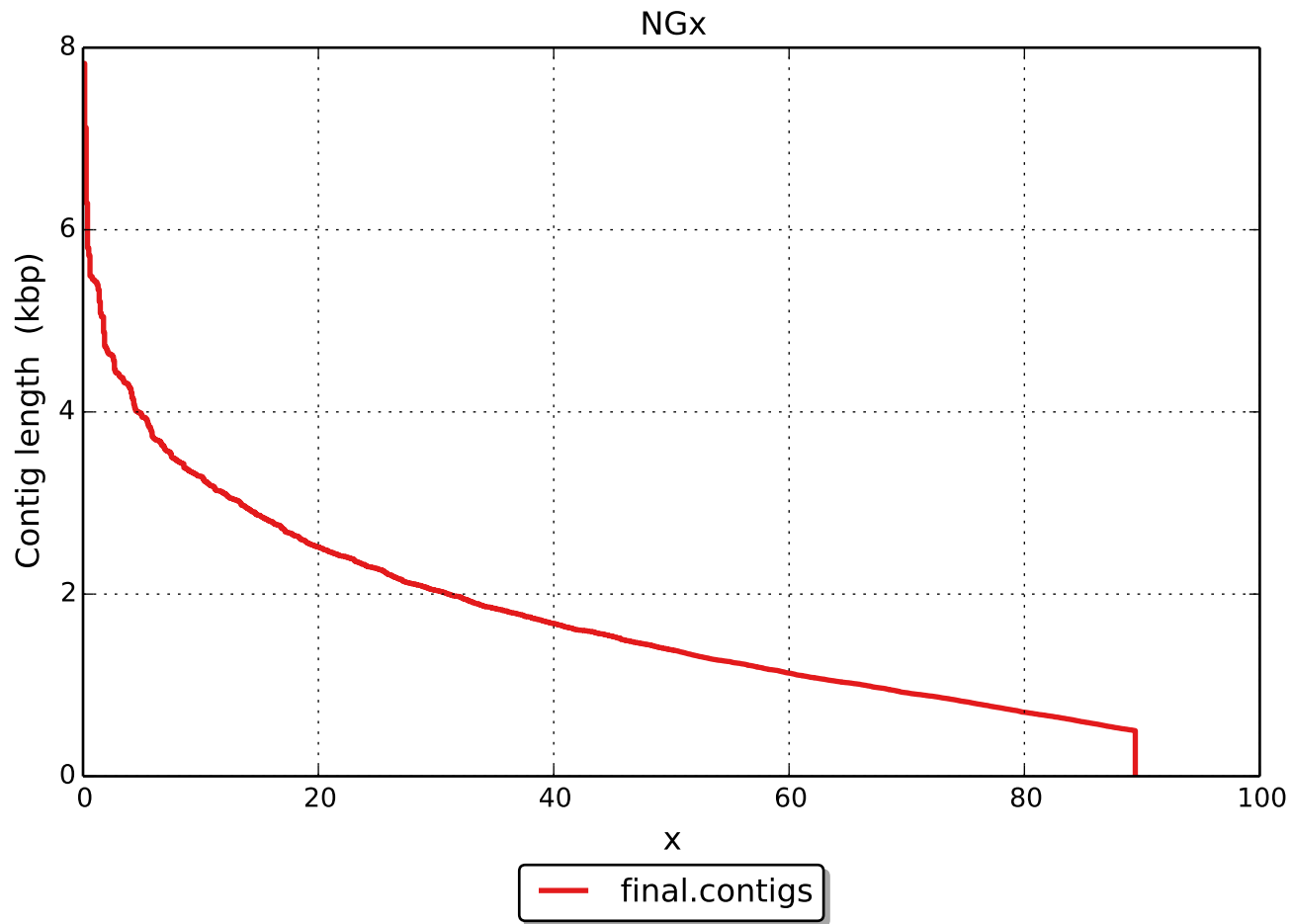
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

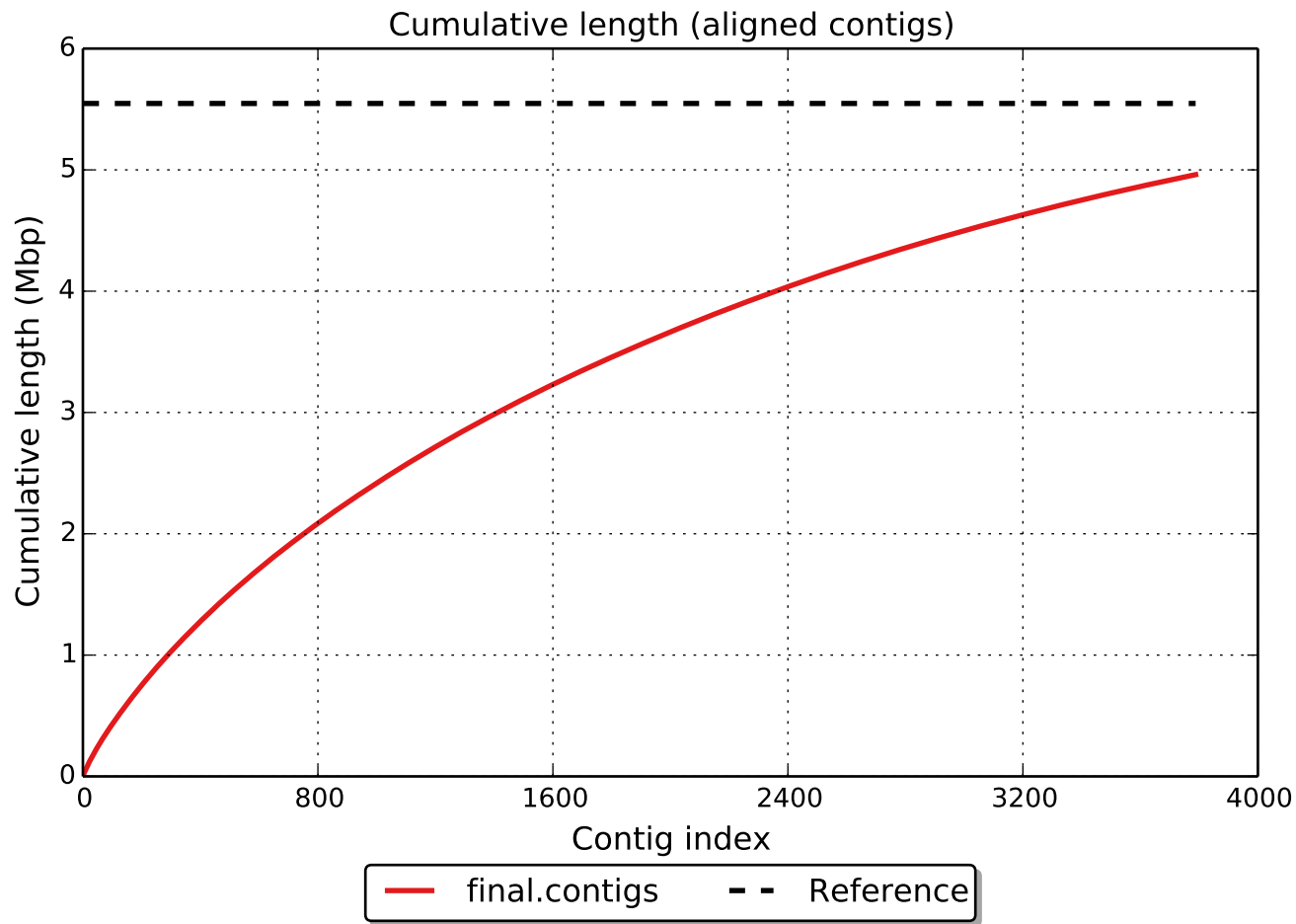


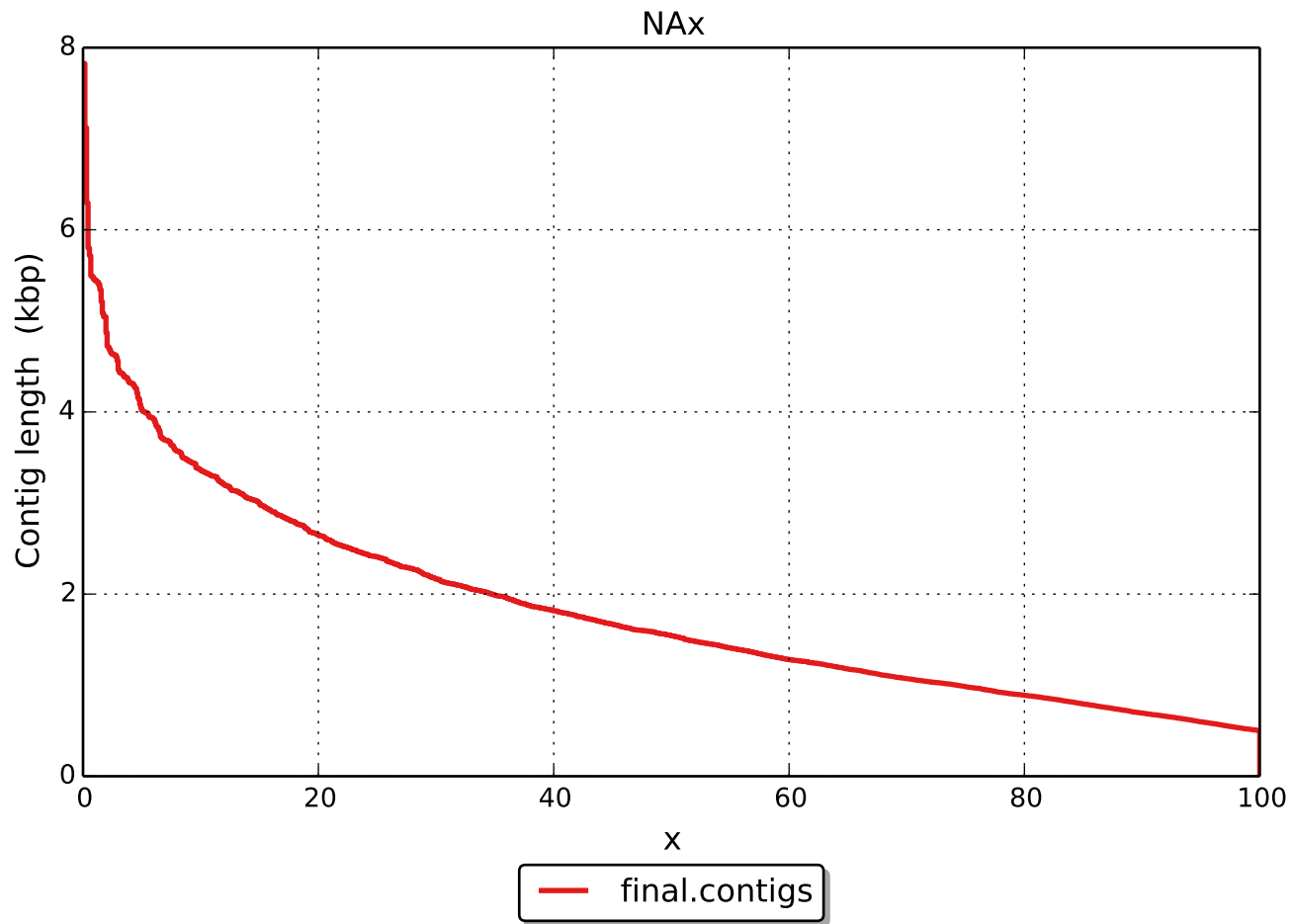




Misassemblies







NGAx

