

Report

	final.contigs
# contigs (≥ 0 bp)	3299
# contigs (≥ 1000 bp)	671
Total length (≥ 0 bp)	2629294
Total length (≥ 1000 bp)	1379814
# contigs	1697
Largest contig	8768
Total length	2074893
Reference length	3785550
GC (%)	32.31
Reference GC (%)	32.26
N50	1503
NG50	591
N75	810
L50	384
LG50	1364
L75	869
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	52.915
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	346.31
# indels per 100 kbp	0.05
Largest alignment	8768
NA50	1503
NGA50	591
NA75	810
LA50	384
LGA50	1364
LA75	869

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

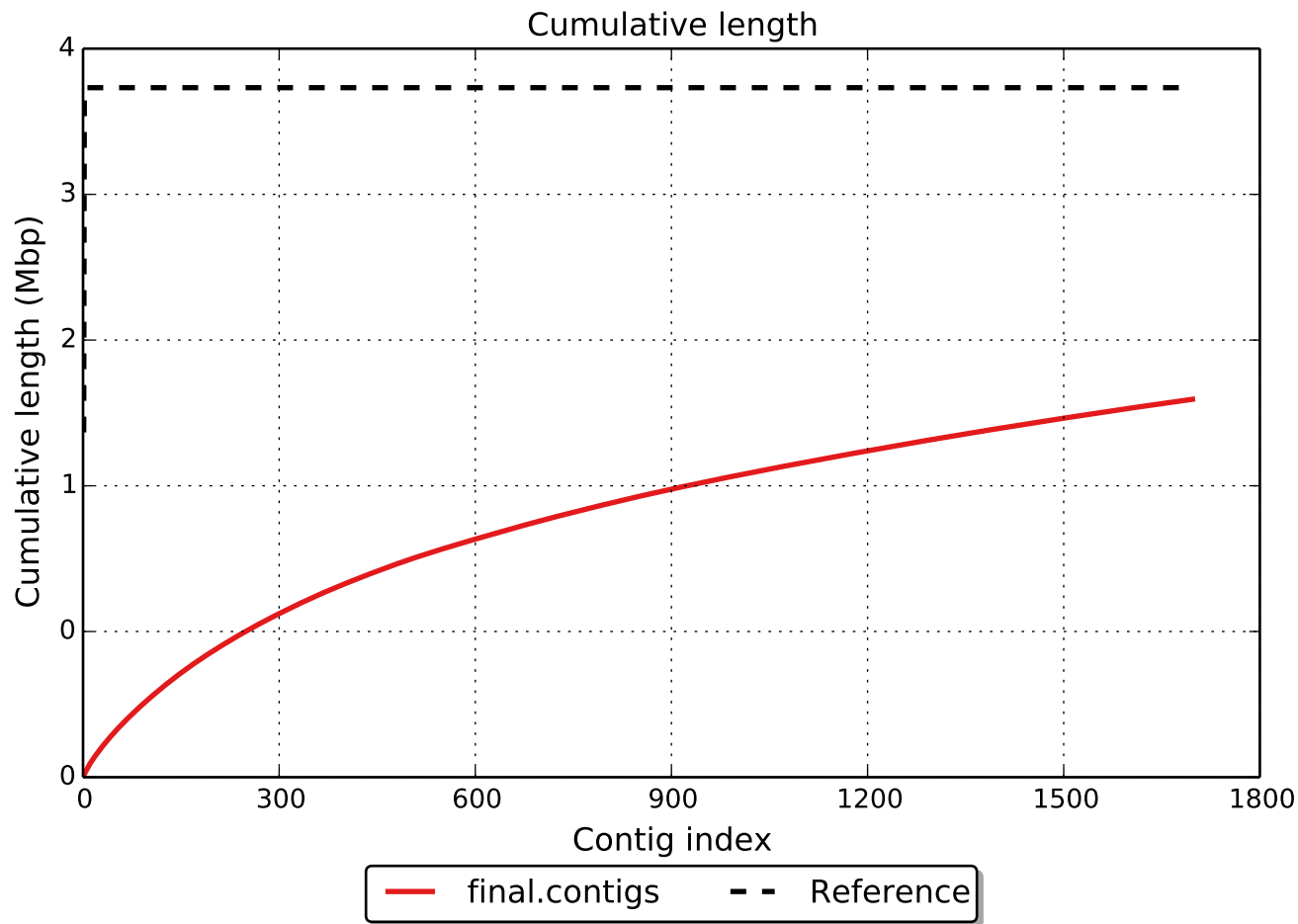
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	6937
# indels	1
# short indels	0
# long indels	1
Indels length	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).

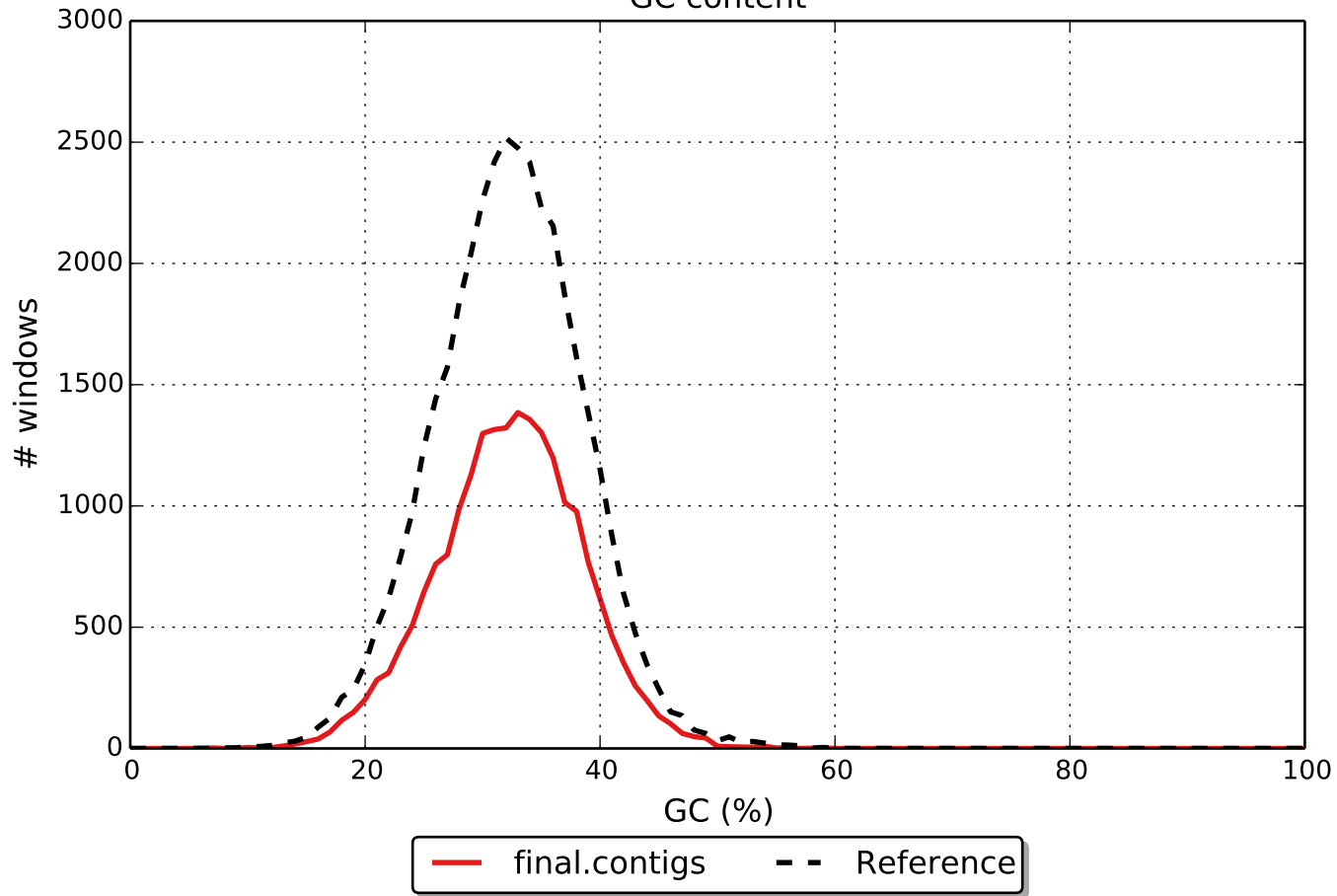
Unaligned report

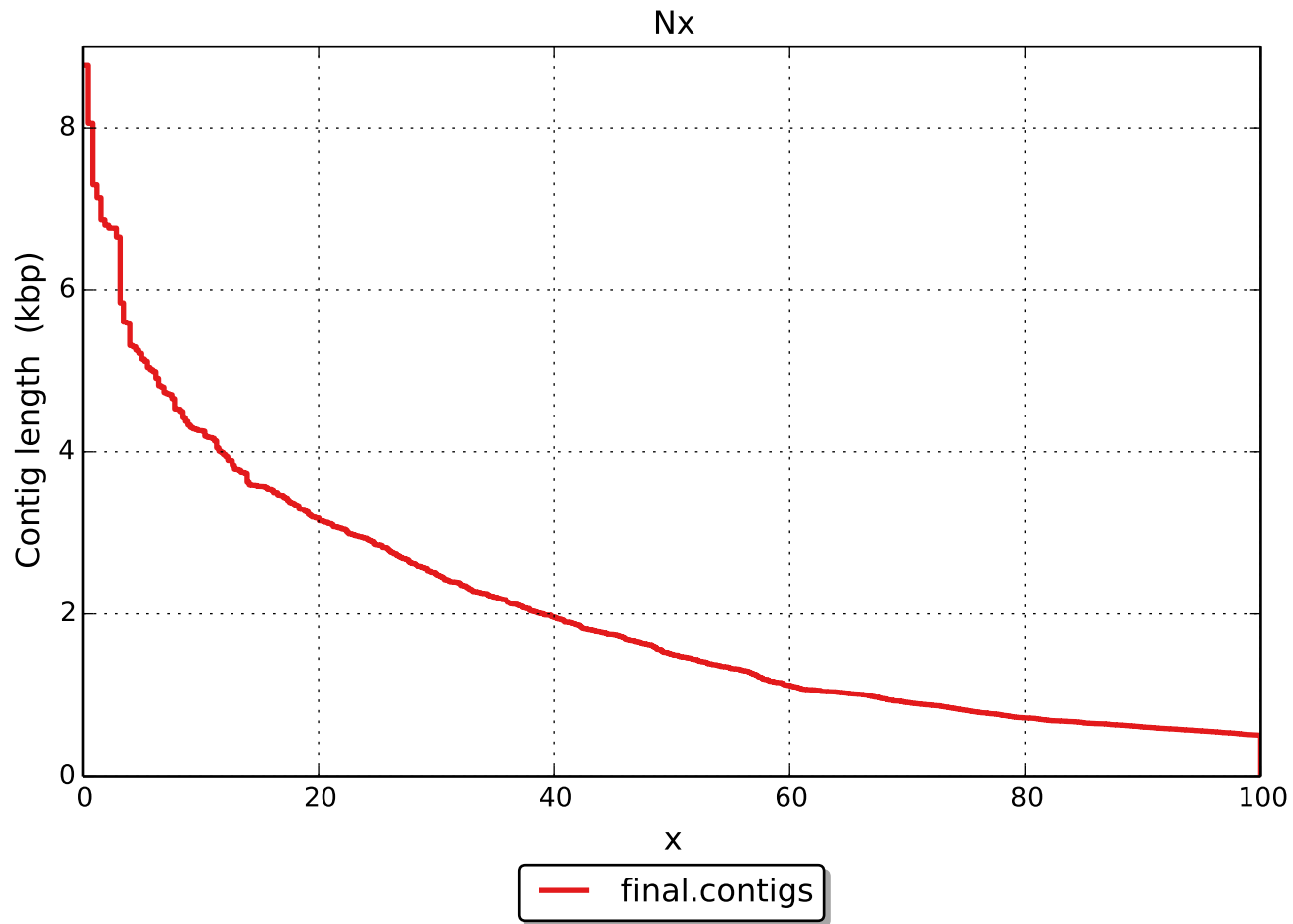
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

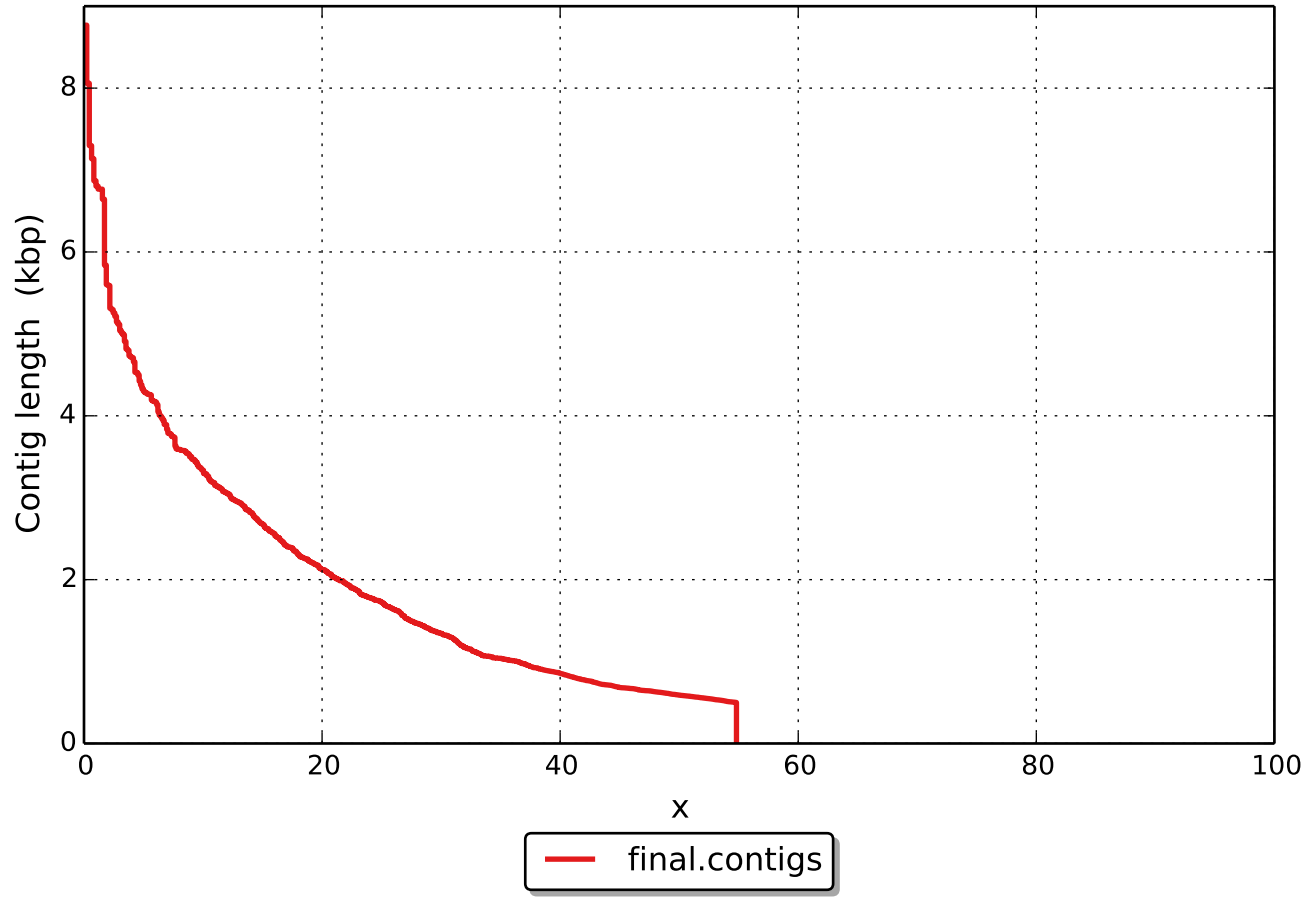


GC content



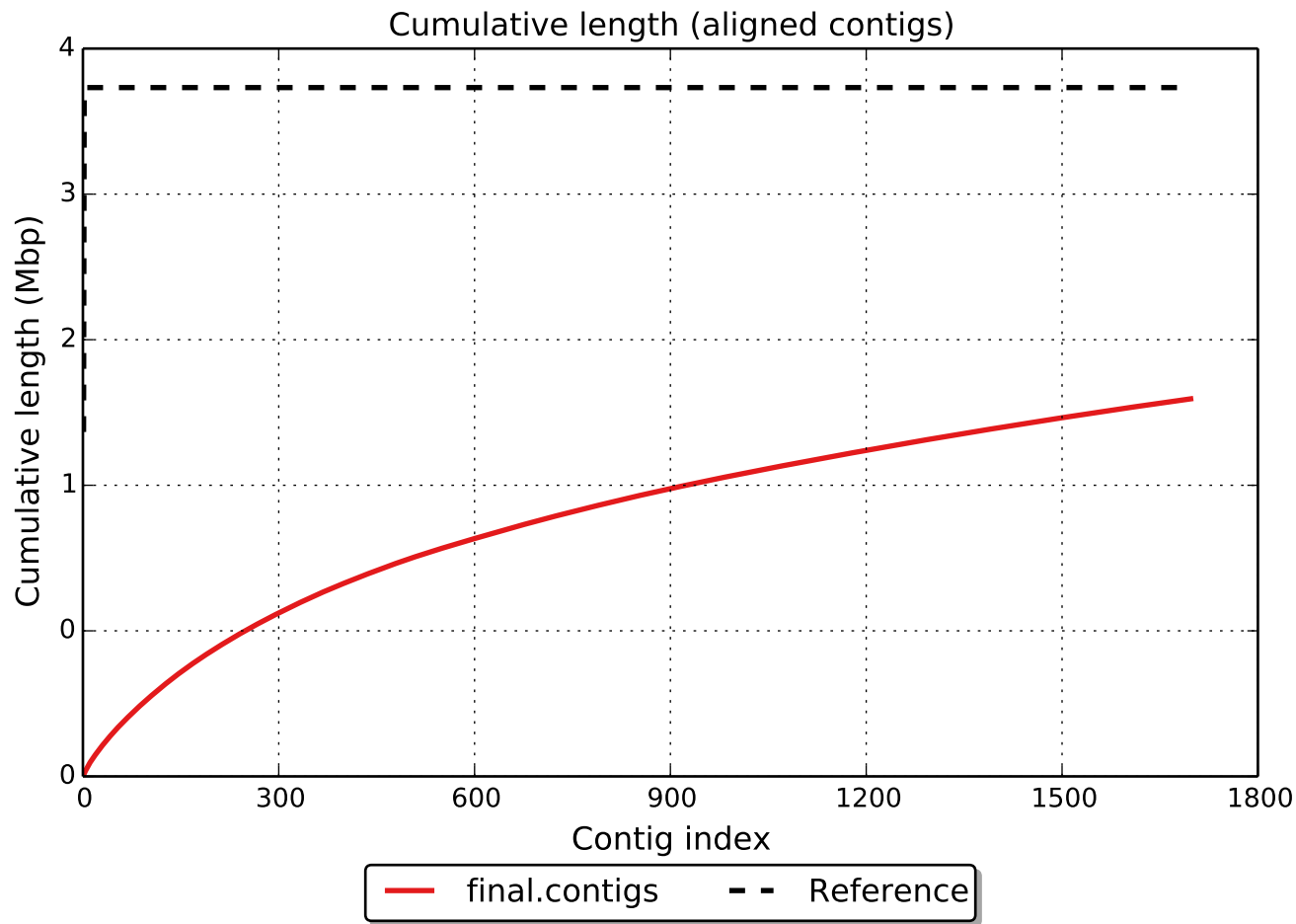


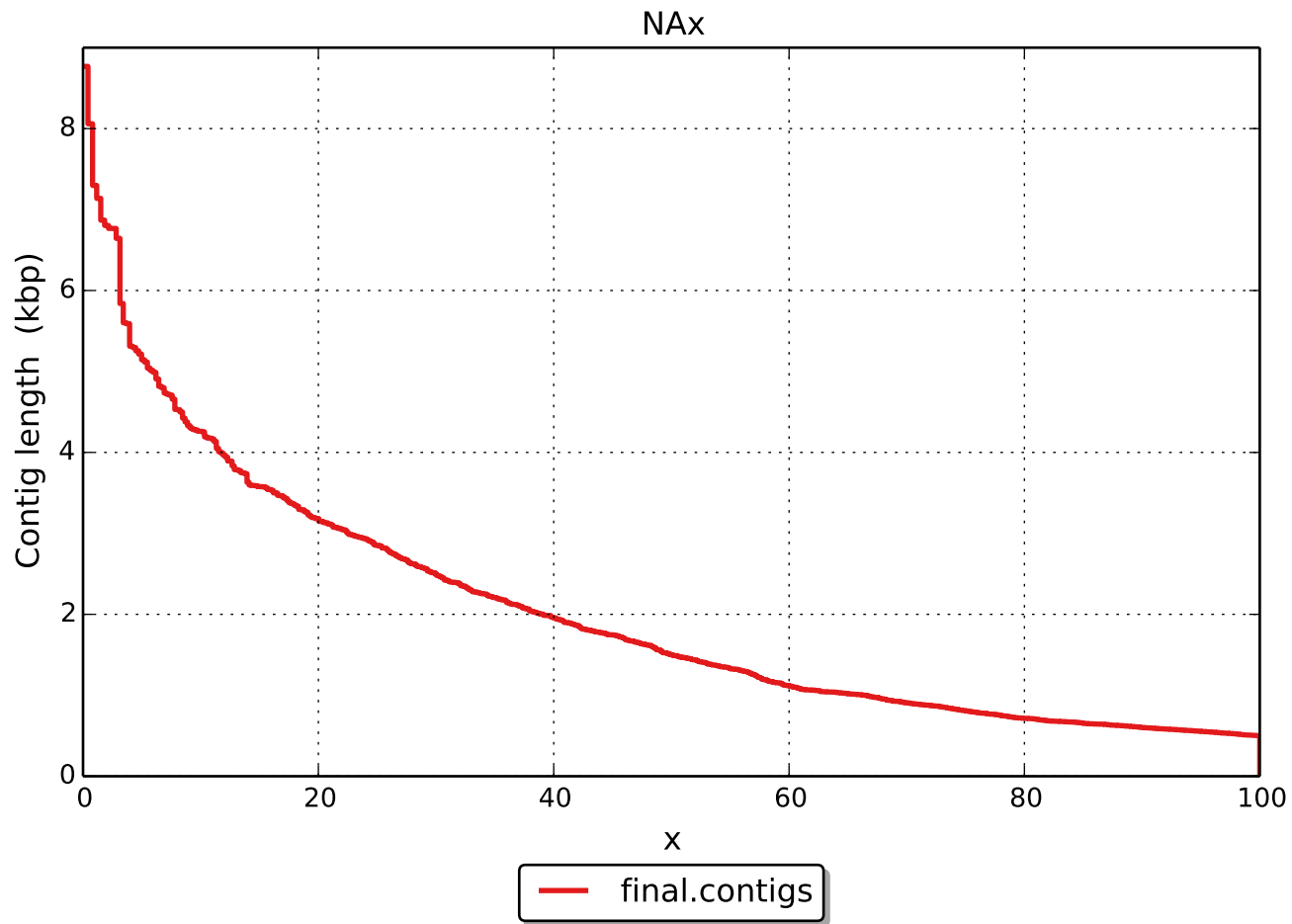
NGx



Misassemblies







NGAx

