

Report

	final.contigs
# contigs (≥ 0 bp)	111286
# contigs (≥ 1000 bp)	600
# contigs (≥ 5000 bp)	332
# contigs (≥ 10000 bp)	166
# contigs (≥ 25000 bp)	24
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	51645353
Total length (≥ 1000 bp)	4747030
Total length (≥ 5000 bp)	4110660
Total length (≥ 10000 bp)	2891295
Total length (≥ 25000 bp)	772746
Total length (≥ 50000 bp)	0
# contigs	22679
Largest contig	48373
Total length	17701067
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	617
NG50	12352
N75	546
NG75	7831
L50	6520
LG50	115
L75	14187
LG75	234
# misassemblies	17
# misassembled contigs	17
Misassembled contigs length	38518
# local misassemblies	12
# unaligned contigs	13217 + 259 part
Unaligned length	7691809
Genome fraction (%)	99.434
Duplication ratio	2.169
# N's per 100 kbp	0.00
# mismatches per 100 kbp	260.11
# indels per 100 kbp	0.48
Largest alignment	48373
NA50	532
NGA50	12352
NGA75	7809
LA50	7182
LGA50	115
LGA75	234

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

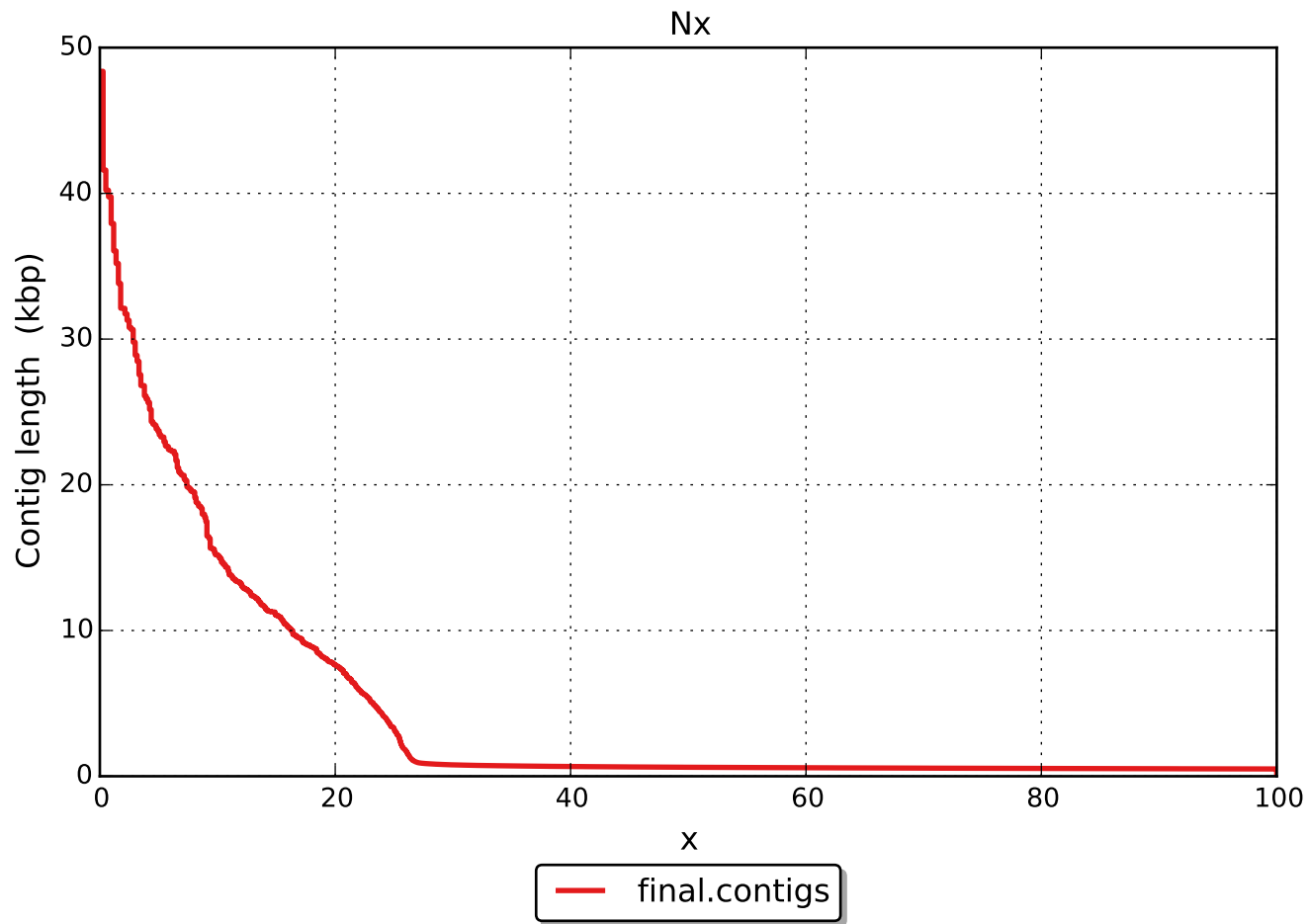
	final.contigs
# misassemblies	17
# relocations	13
# translocations	0
# inversions	4
# misassembled contigs	17
Misassembled contigs length	38518
# local misassemblies	12
# mismatches	12005
# indels	22
# short indels	22
# long indels	0
Indels length	24

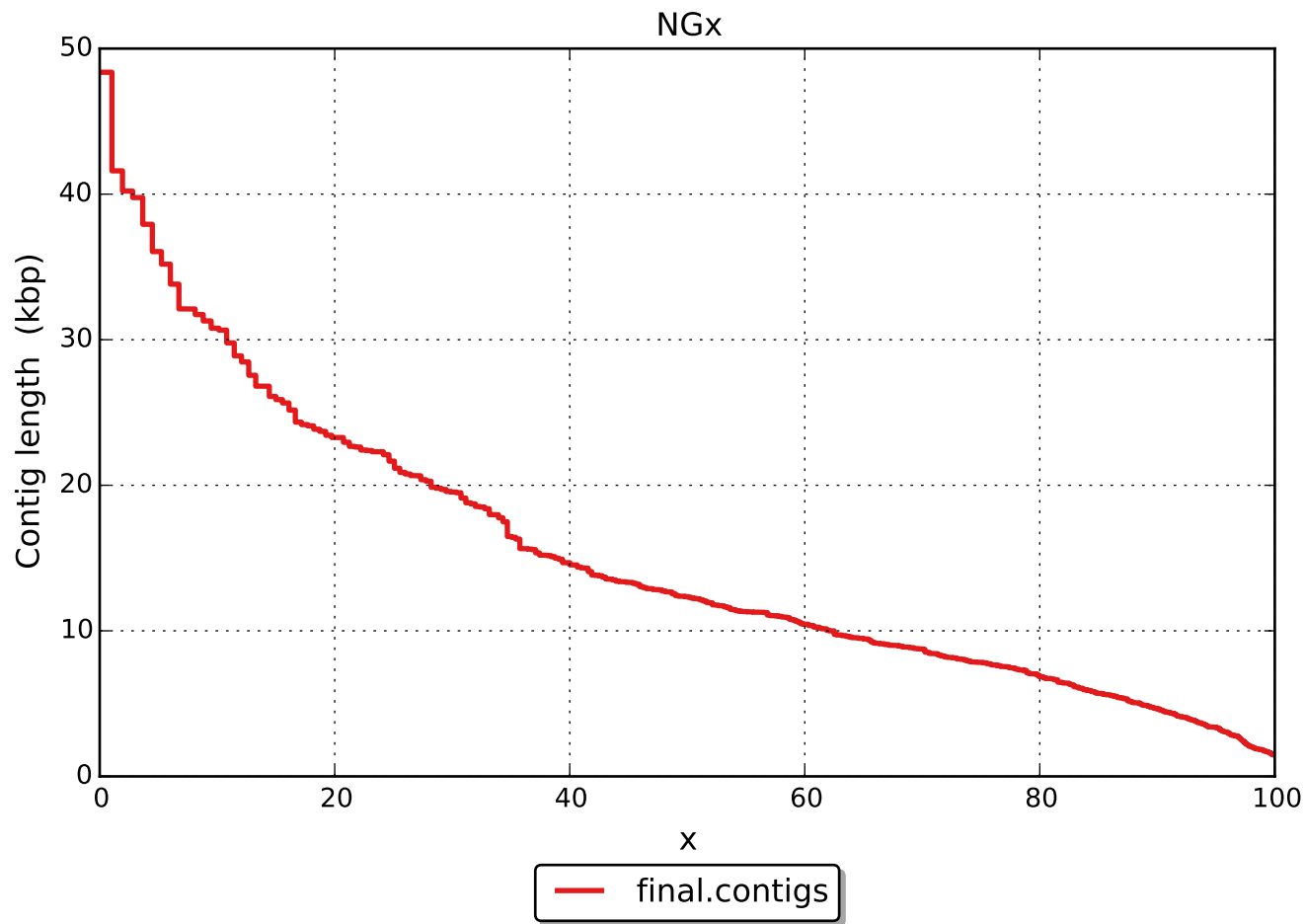
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

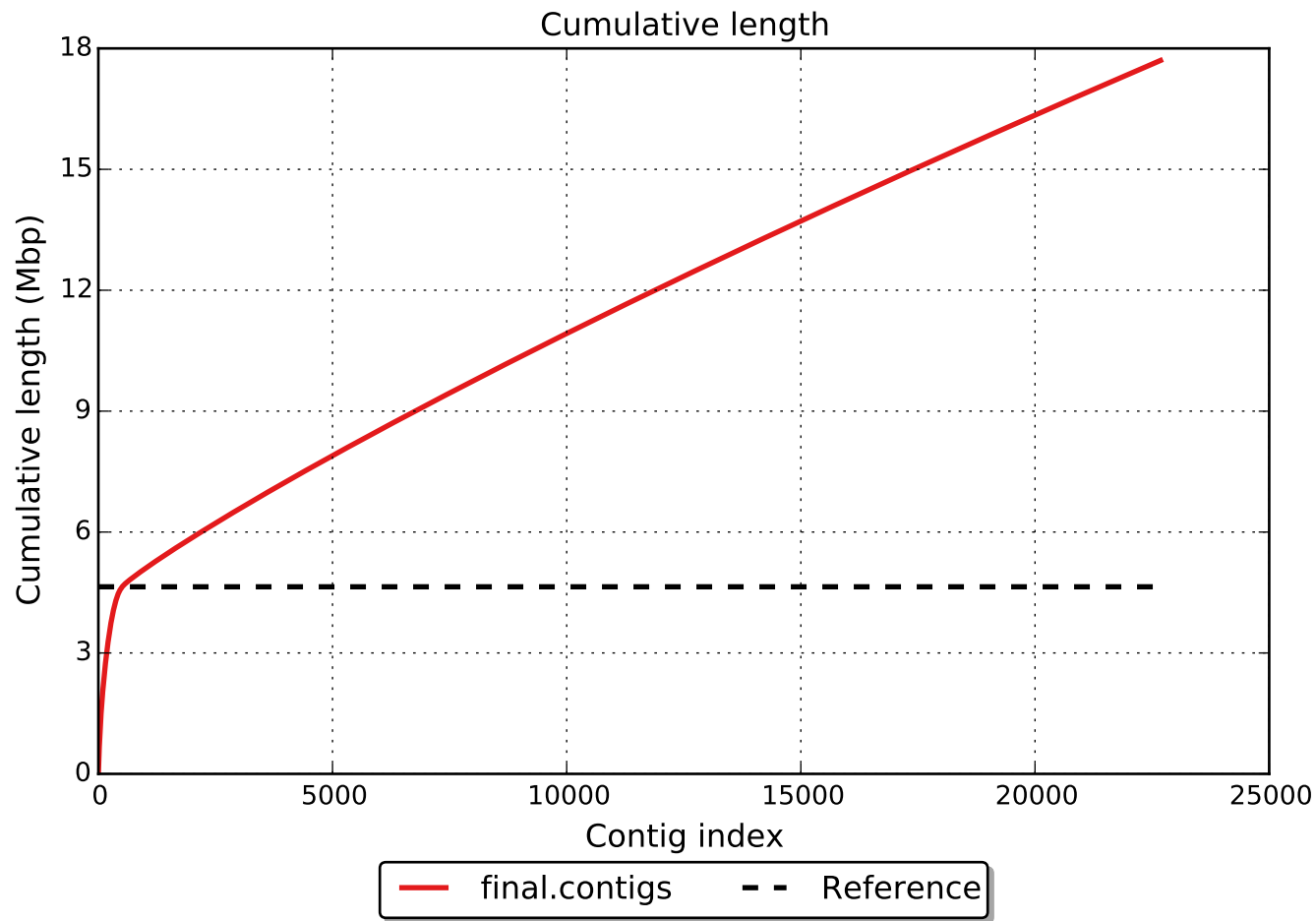
Unaligned report

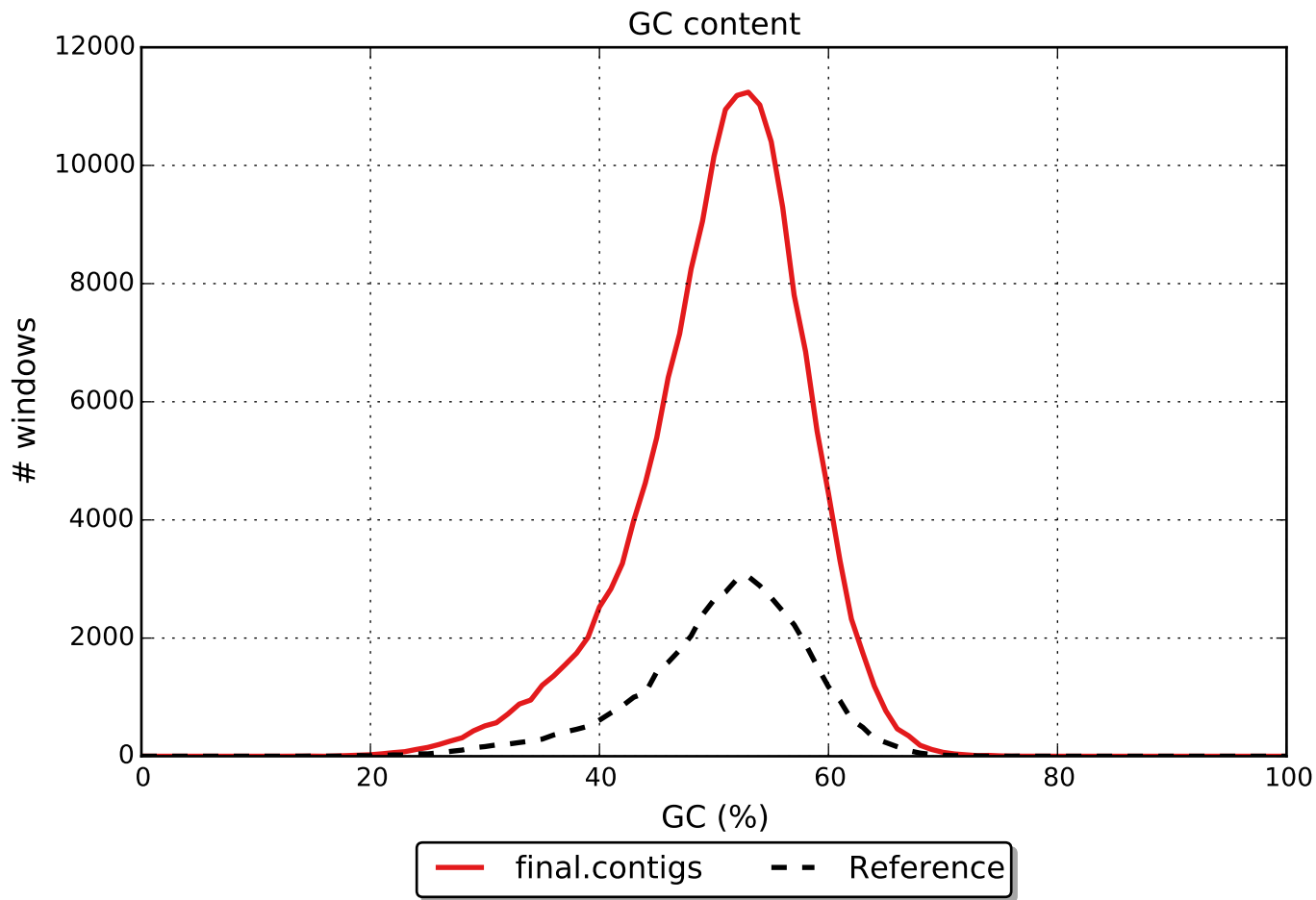
	final.contigs
# fully unaligned contigs	13217
Fully unaligned length	7642117
# partially unaligned contigs	259
# with misassembly	0
# both parts are significant	1
Partially unaligned length	49692
# N's	0

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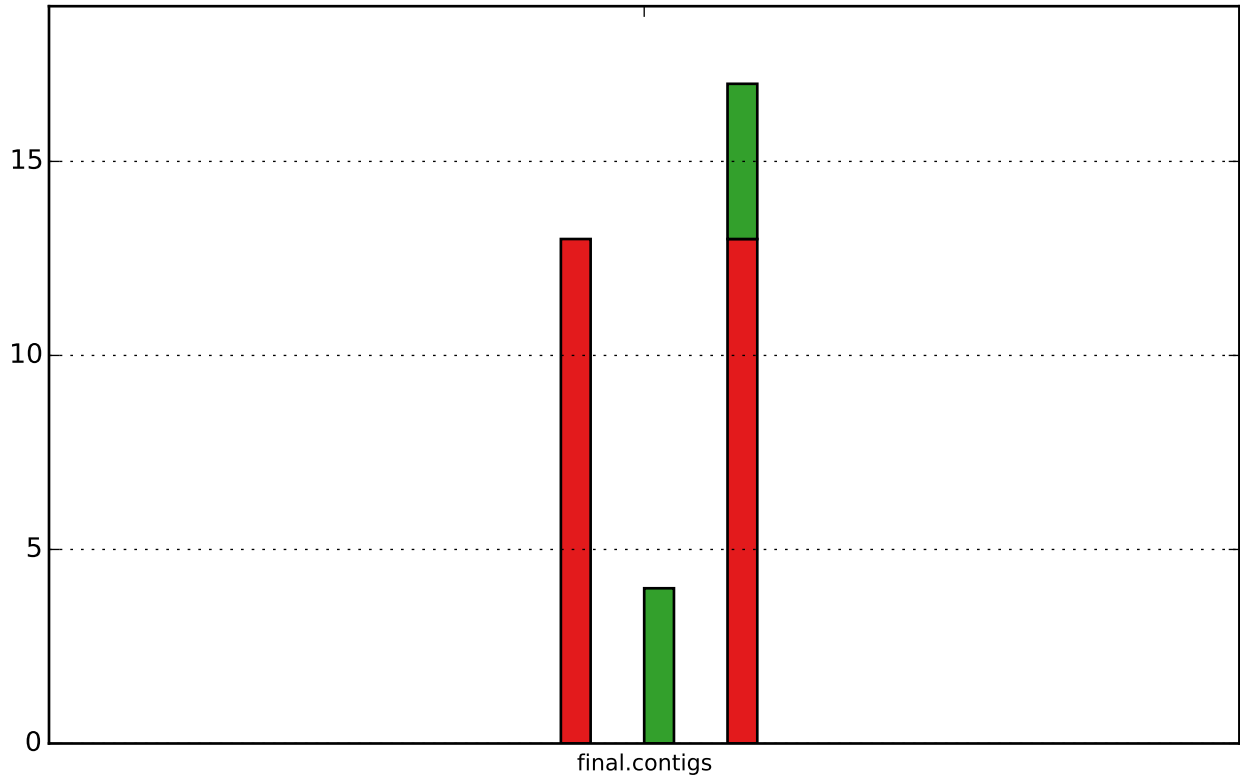


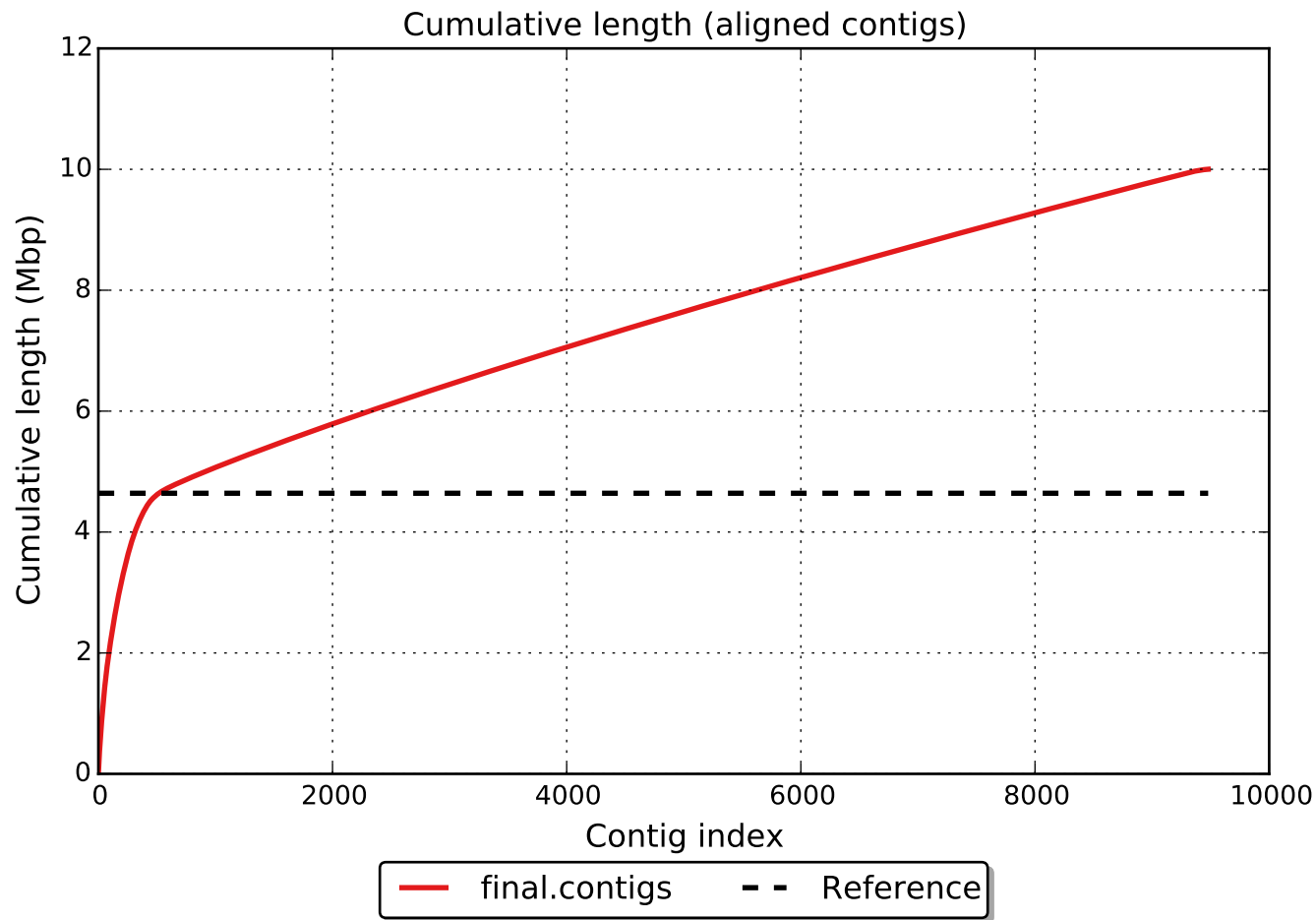


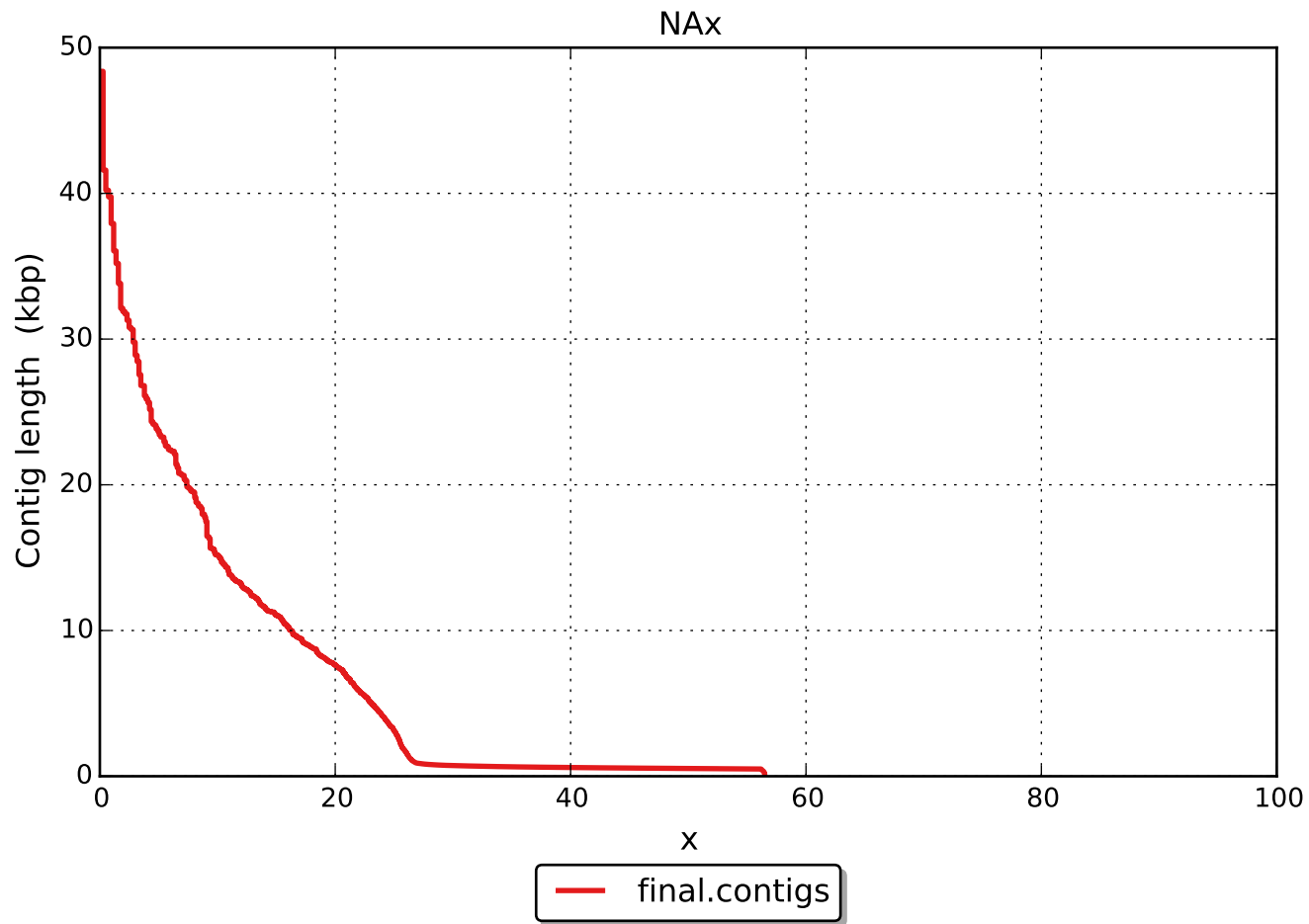




Misassemblies







NGAx

