

Report

	final.contigs
# contigs (≥ 0 bp)	11043
# contigs (≥ 1000 bp)	1822
Total length (≥ 0 bp)	8080274
Total length (≥ 1000 bp)	3618008
# contigs	5605
Largest contig	10039
Total length	6195528
Reference length	11094646
GC (%)	50.33
Reference GC (%)	50.48
N50	1217
NG50	588
N75	736
L50	1347
LG50	4408
L75	3035
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	25
Genome fraction (%)	53.730
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	323.98
# indels per 100 kbp	0.07
Largest alignment	10039
NA50	1217
NGA50	588
NA75	736
LA50	1347
LGA50	4408
LA75	3035

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

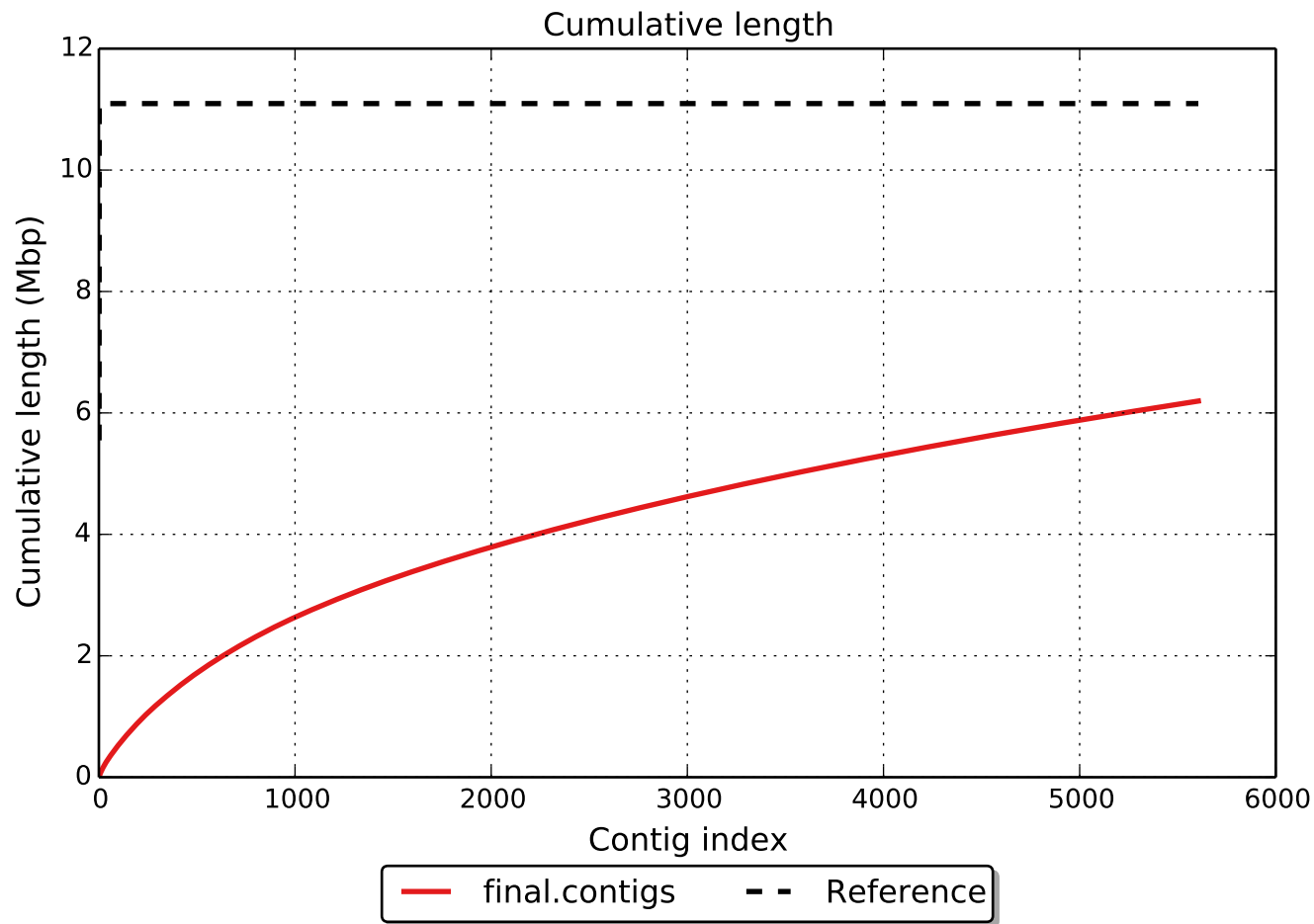
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	19313
# indels	4
# short indels	4
# long indels	0
Indels length	8

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).

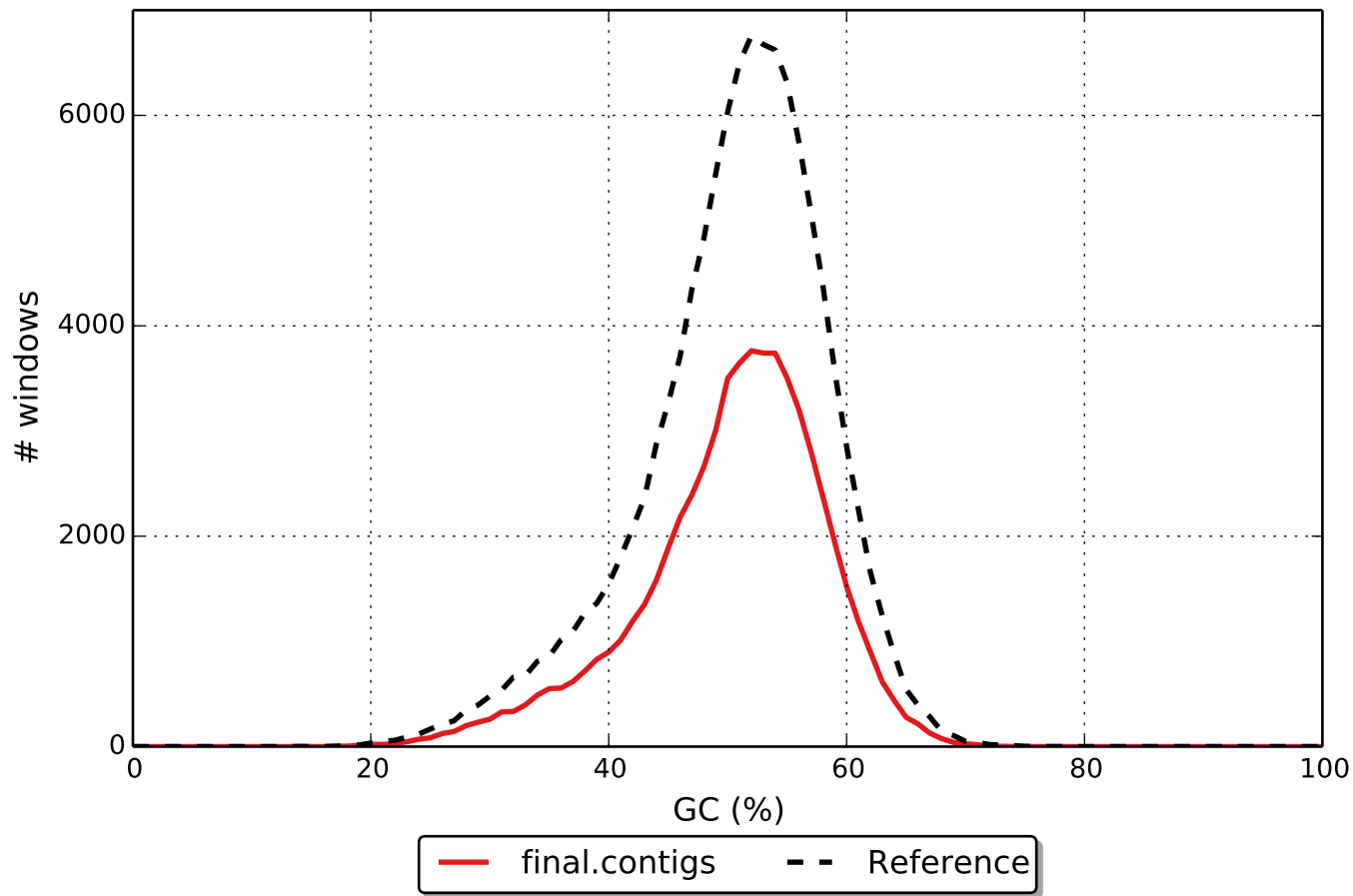
Unaligned report

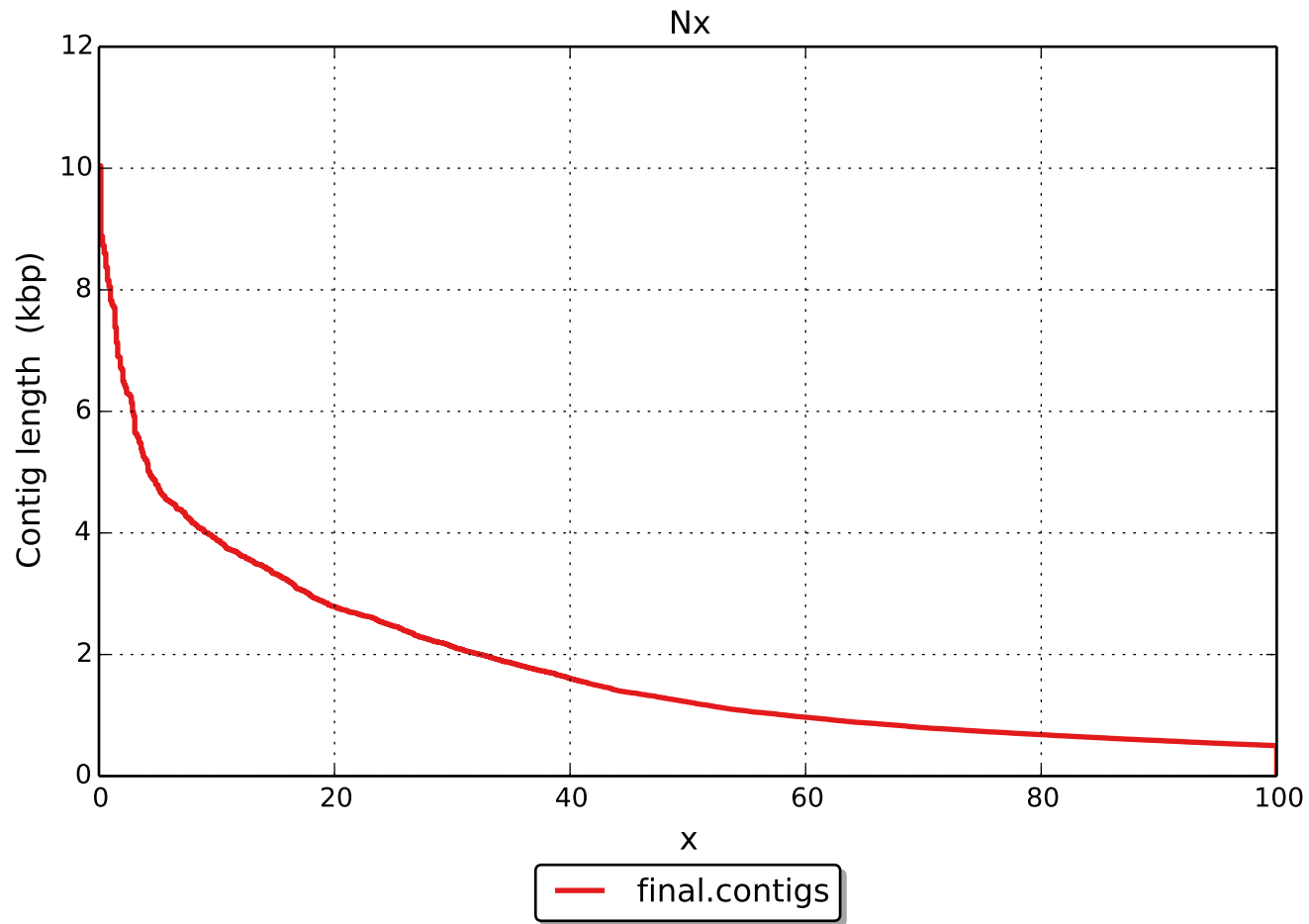
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	25
# N's	0

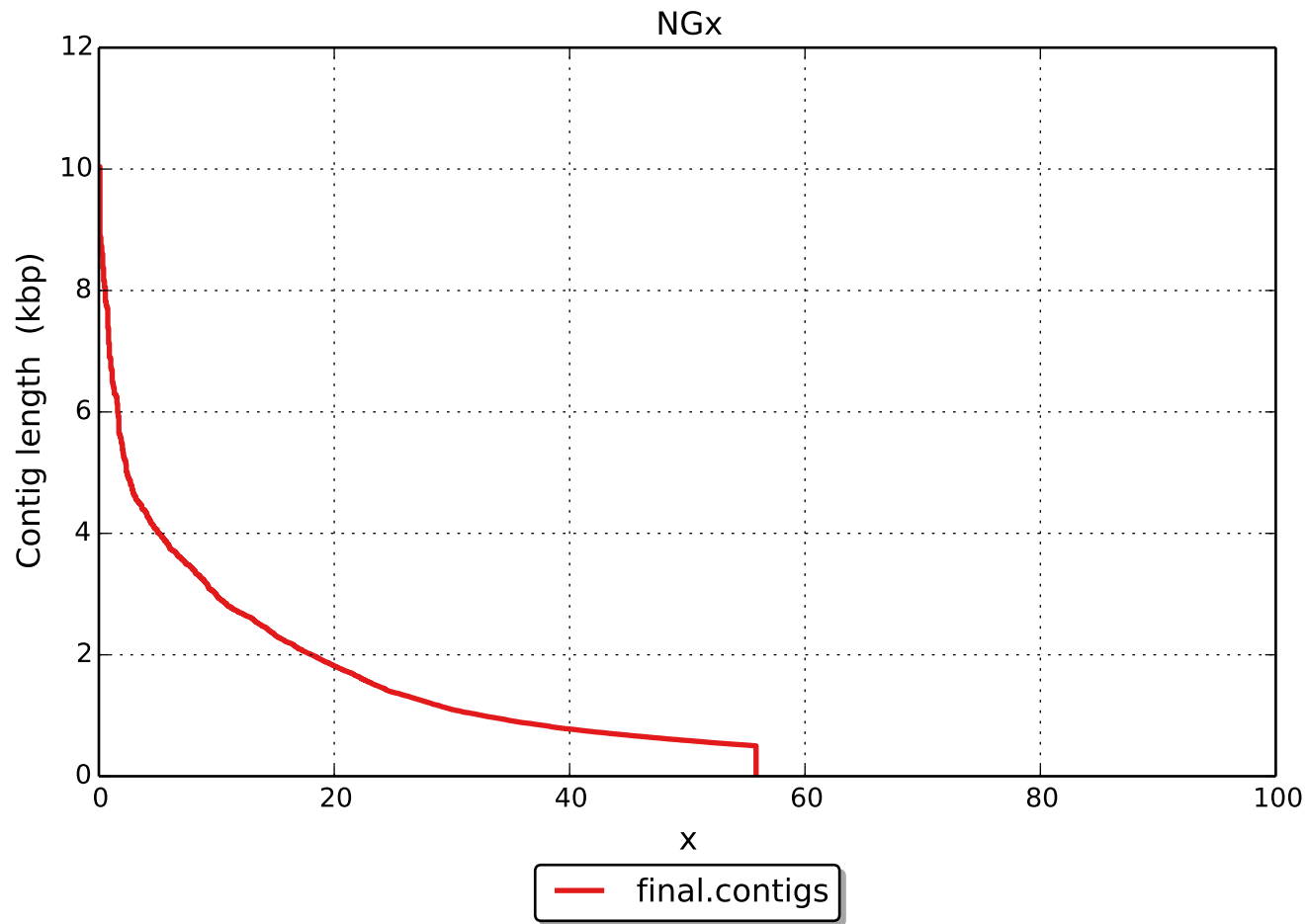
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

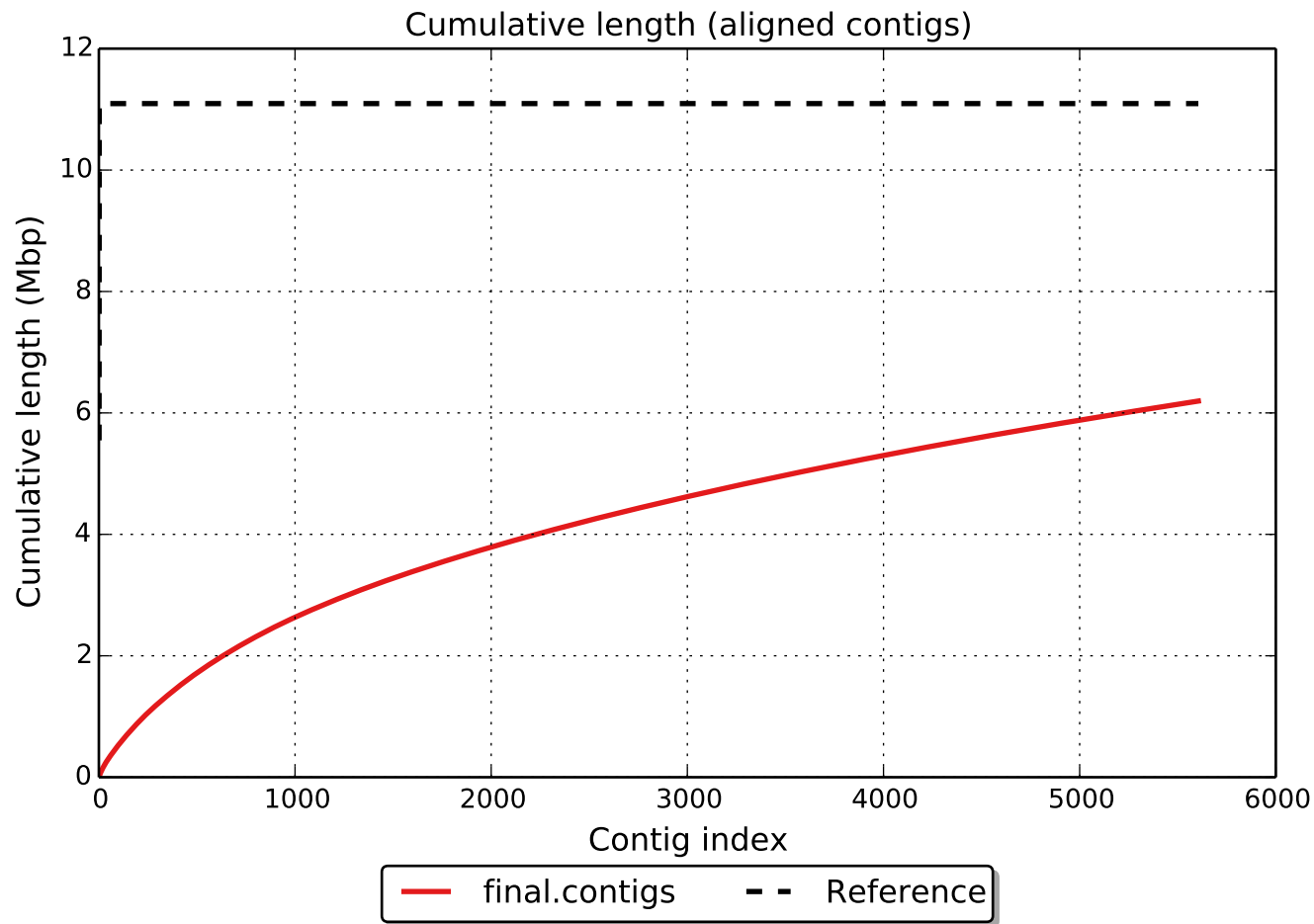


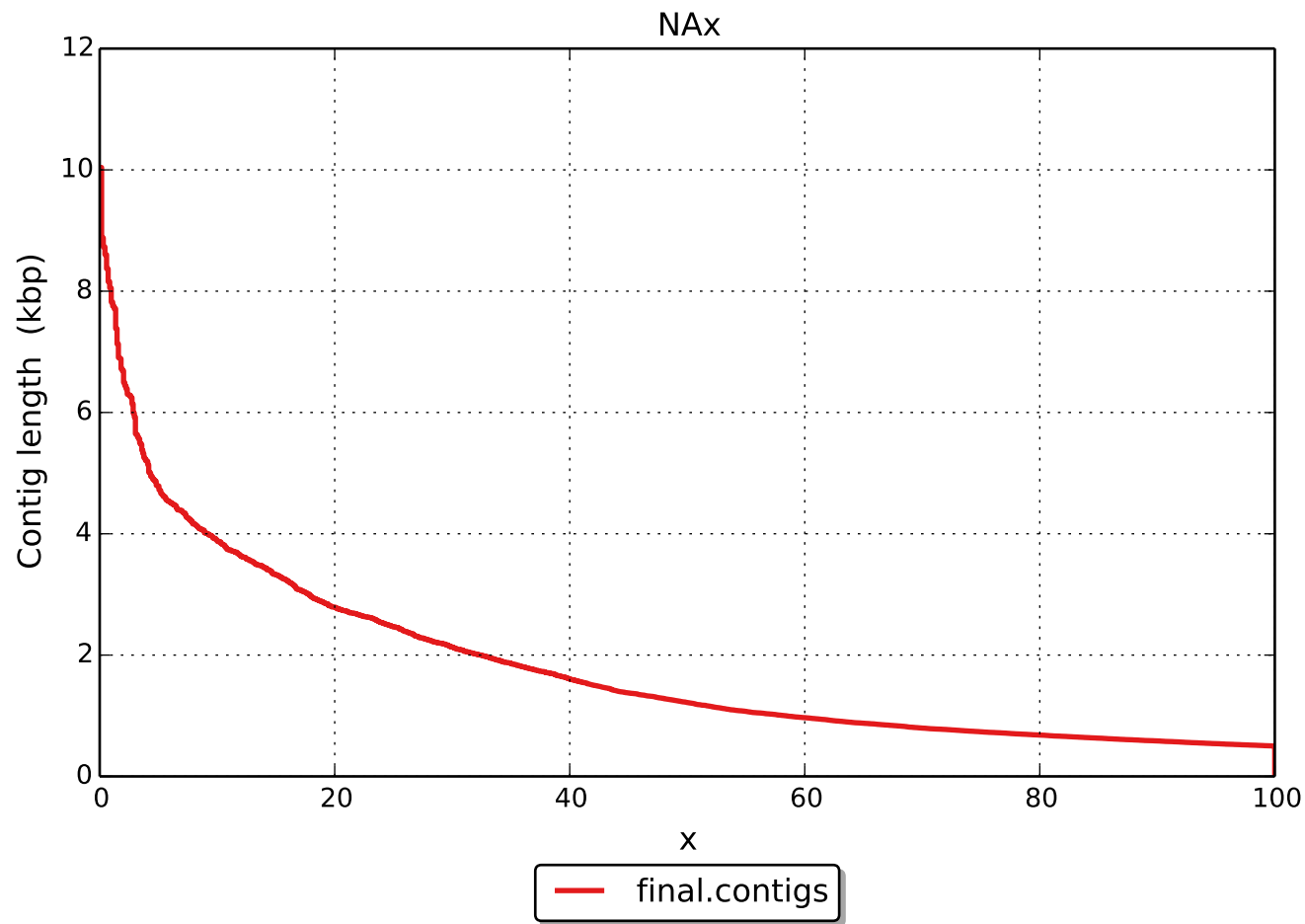




Misassemblies







NGAx

