

Report

	final.contigs
# contigs (≥ 0 bp)	3836
# contigs (≥ 1000 bp)	1550
Total length (≥ 0 bp)	4800121
Total length (≥ 1000 bp)	3230980
# contigs	3836
Largest contig	10039
Total length	4800121
Reference length	5547323
GC (%)	50.34
Reference GC (%)	50.49
N50	1554
NG50	1272
N75	838
NG75	655
L50	875
LG50	1142
L75	1955
LG75	2716
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	25
Genome fraction (%)	81.876
Duplication ratio	1.057
# N's per 100 kbp	0.00
# mismatches per 100 kbp	556.50
# indels per 100 kbp	0.13
Largest alignment	10039
NA50	1554
NGA50	1272
NA75	838
NGA75	655
LA50	875
LGA50	1142
LA75	1955
LGA75	2716

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

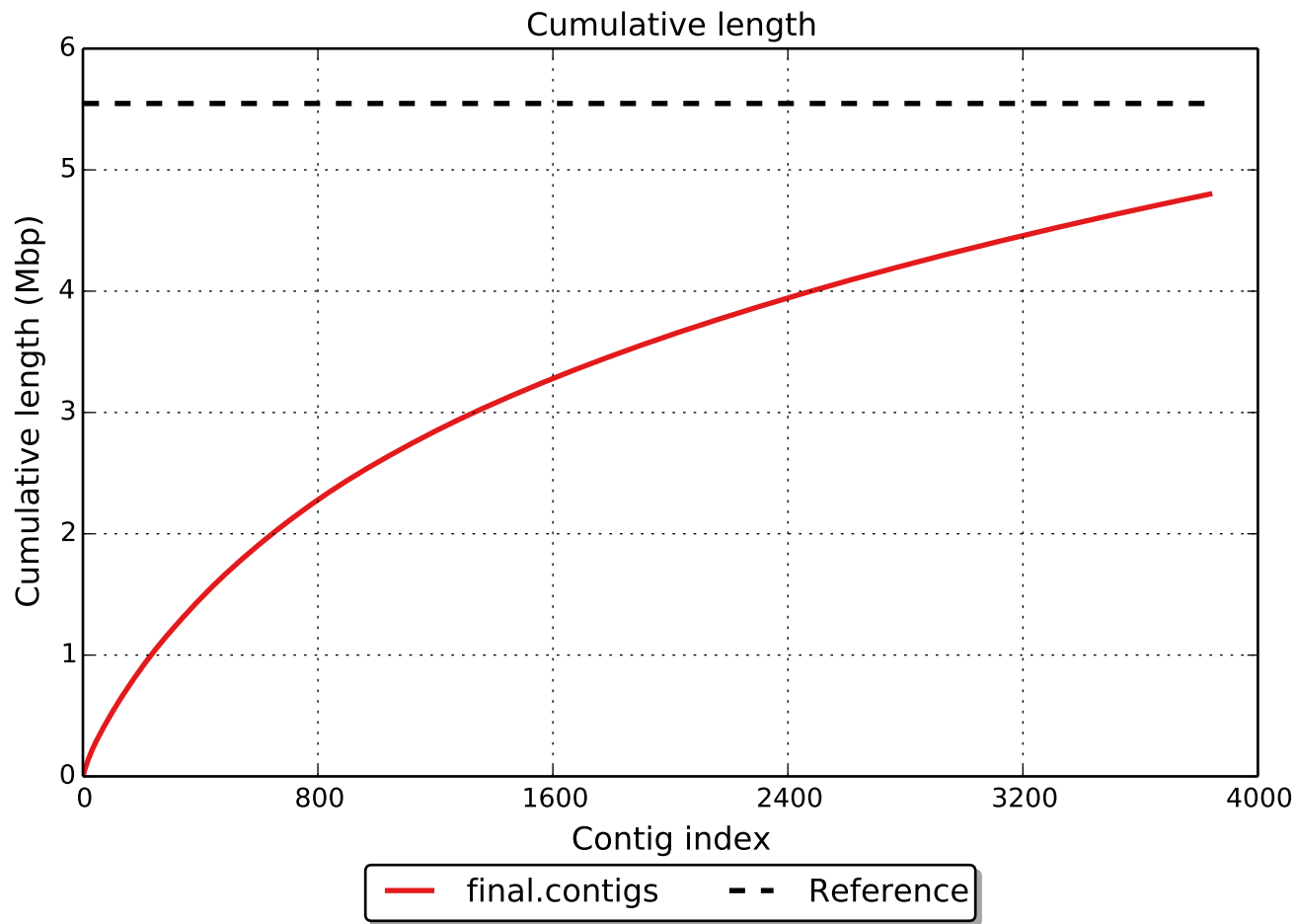
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	25276
# indels	6
# short indels	6
# long indels	0
Indels length	9

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).

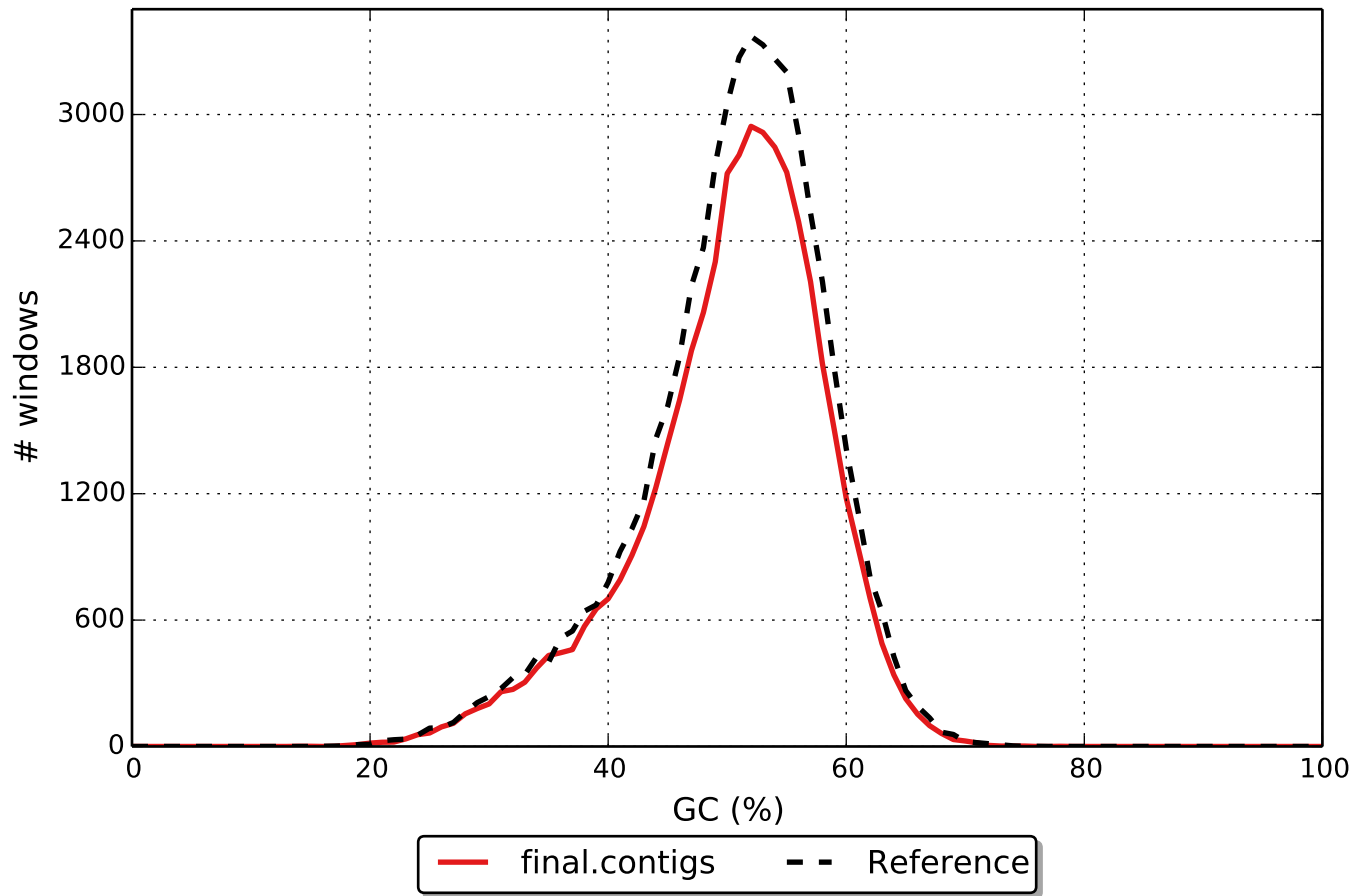
Unaligned report

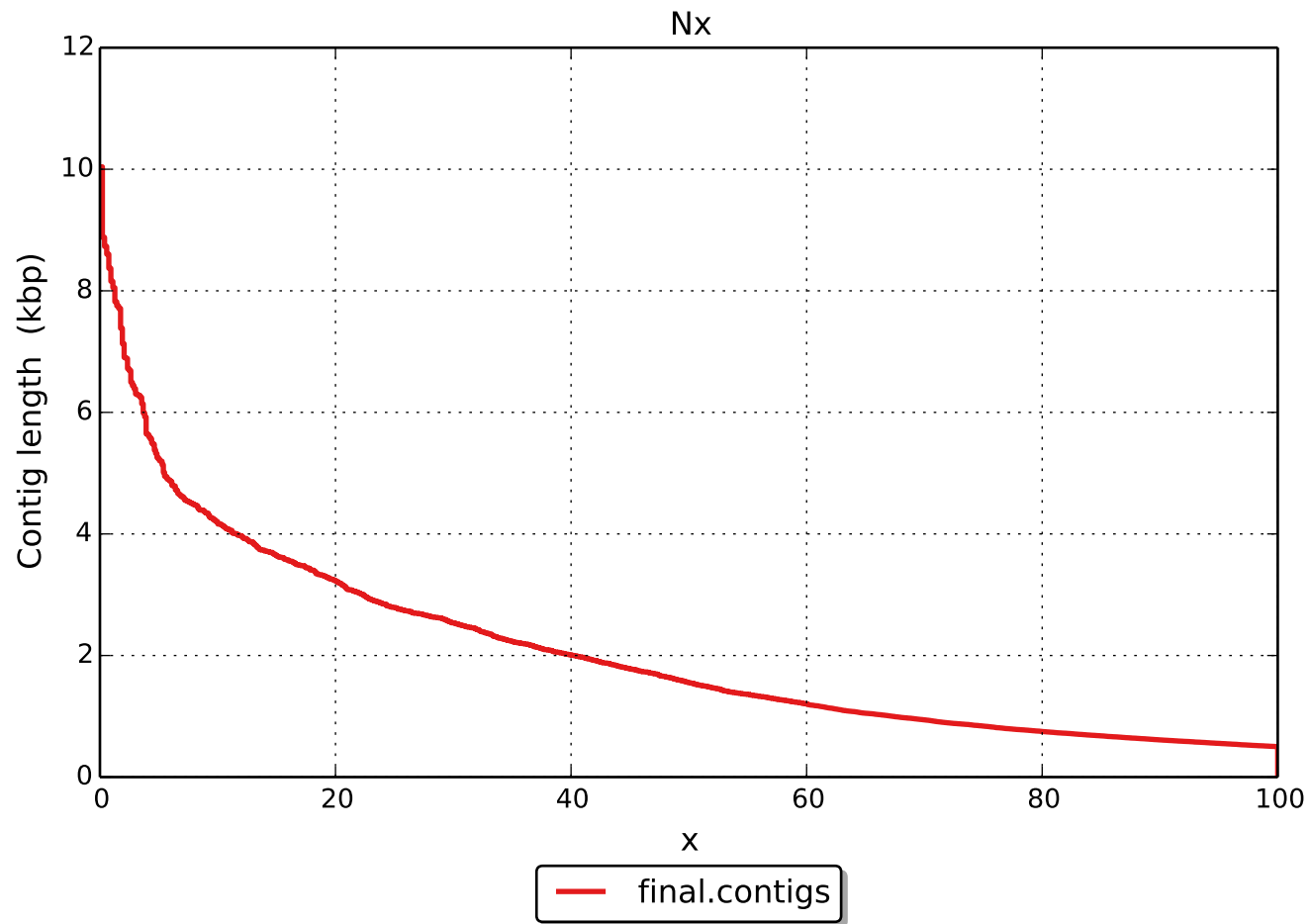
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	25
# N's	0

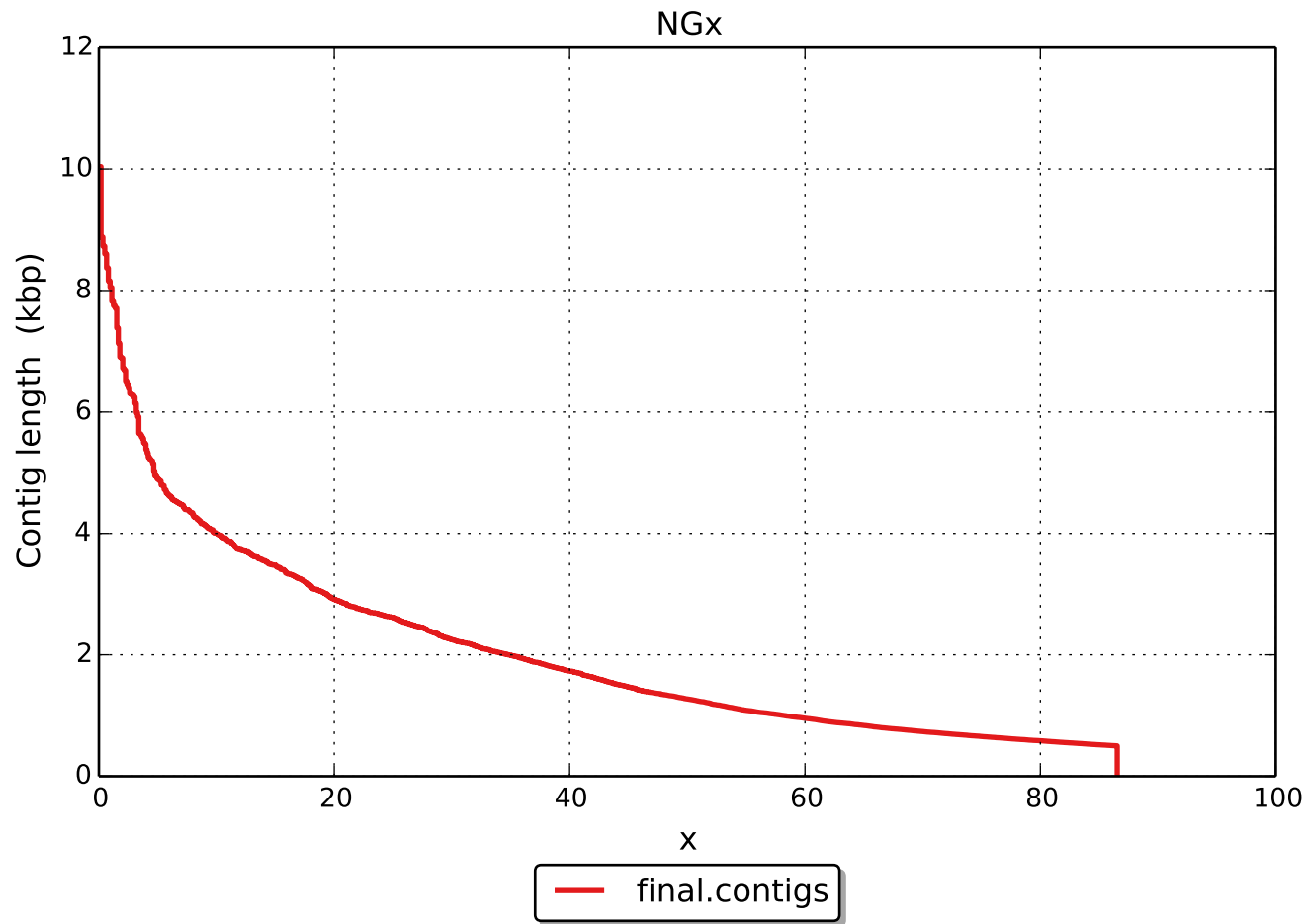
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

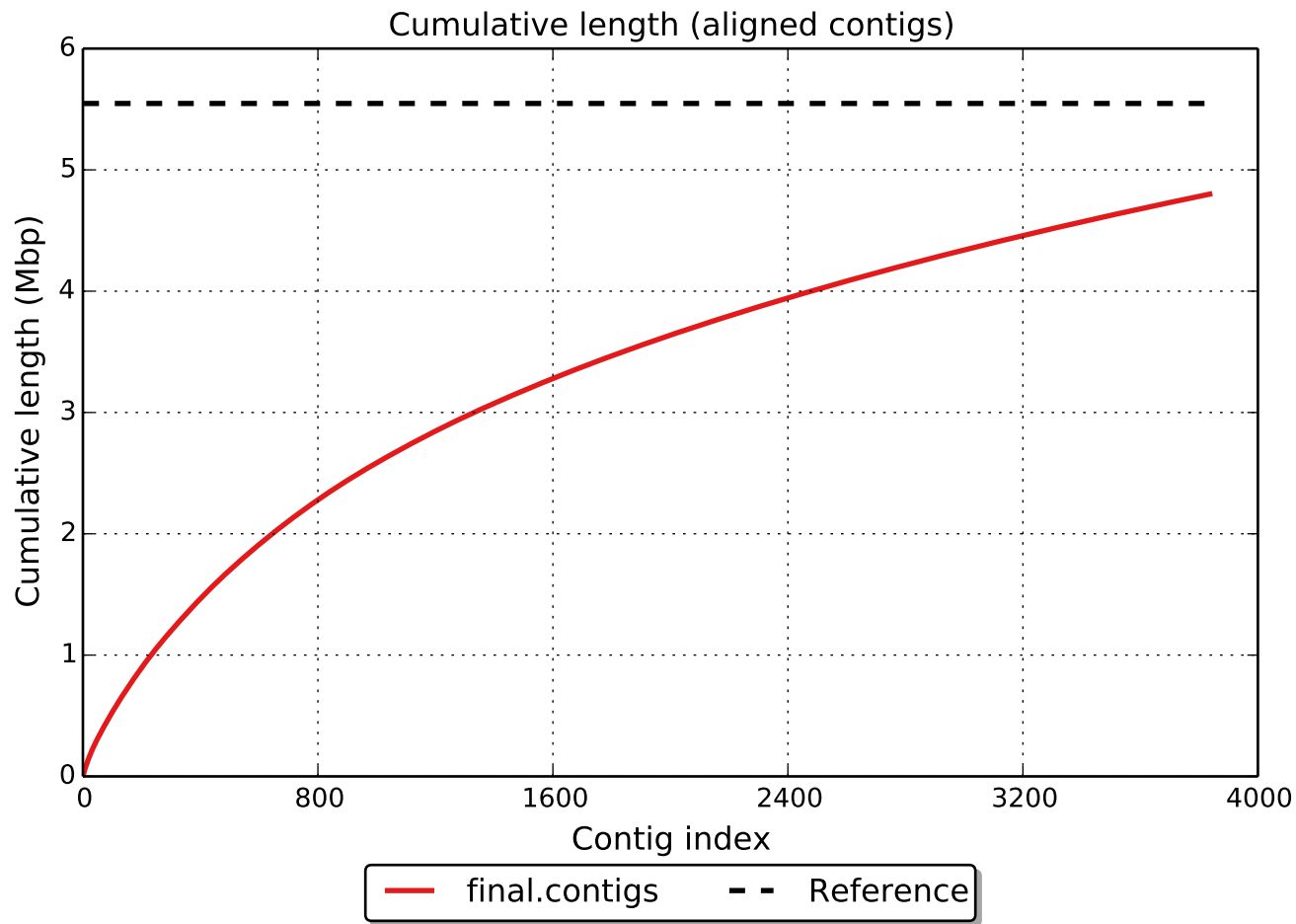


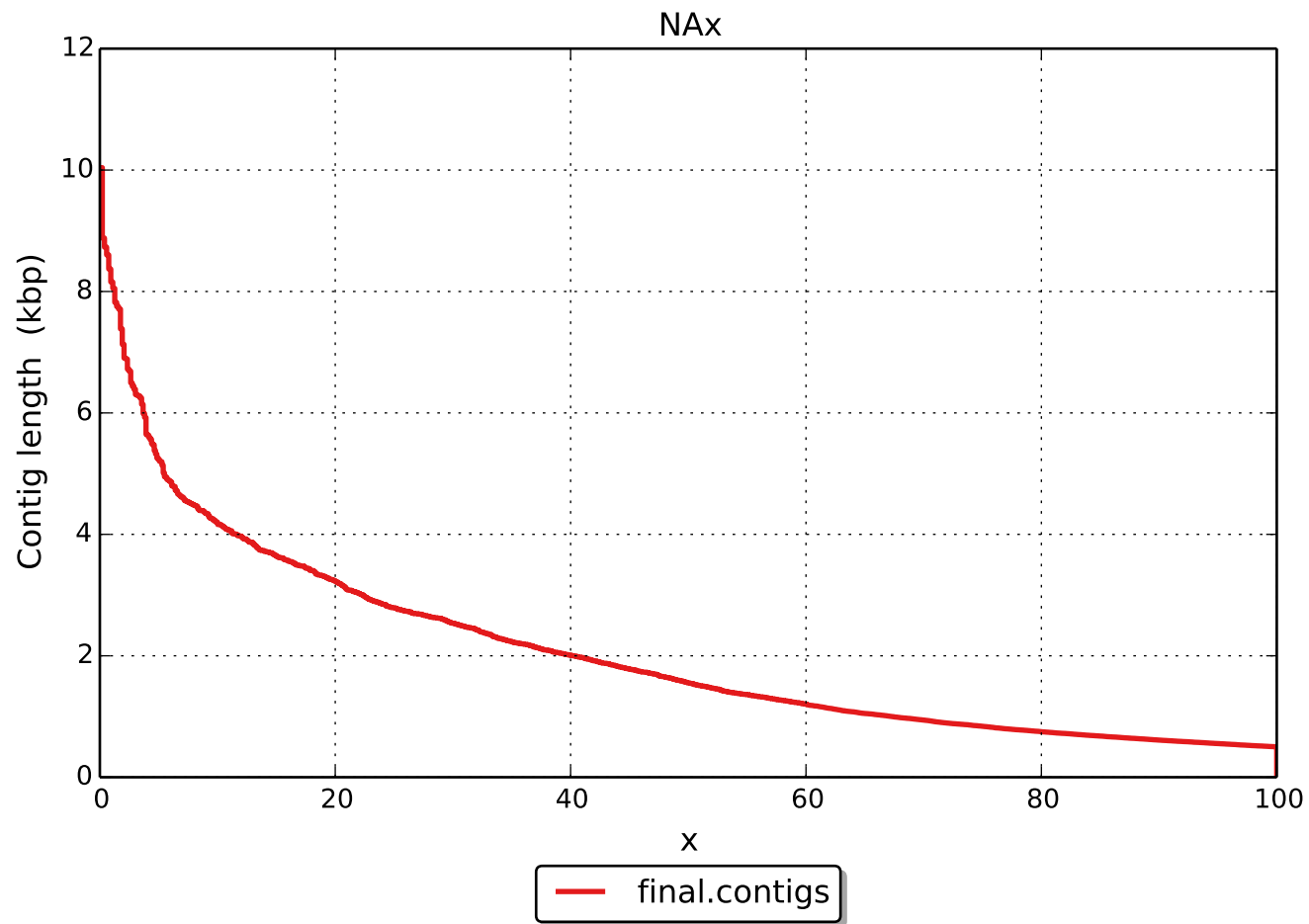




Misassemblies







NGAx

