

Report

	final.contigs
# contigs (≥ 0 bp)	2111
# contigs (≥ 1000 bp)	1669
Total length (≥ 0 bp)	5650166
Total length (≥ 1000 bp)	5316214
# contigs	2111
Largest contig	16890
Total length	5650166
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	3685
NG50	3768
N75	2207
NG75	2277
L50	478
LG50	464
L75	971
LG75	936
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	180
Genome fraction (%)	98.098
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	35.59
# indels per 100 kbp	0.04
Largest alignment	16890
NA50	3685
NGA50	3768
NA75	2207
NGA75	2277
LA50	478
LGA50	464
LA75	971
LGA75	936

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

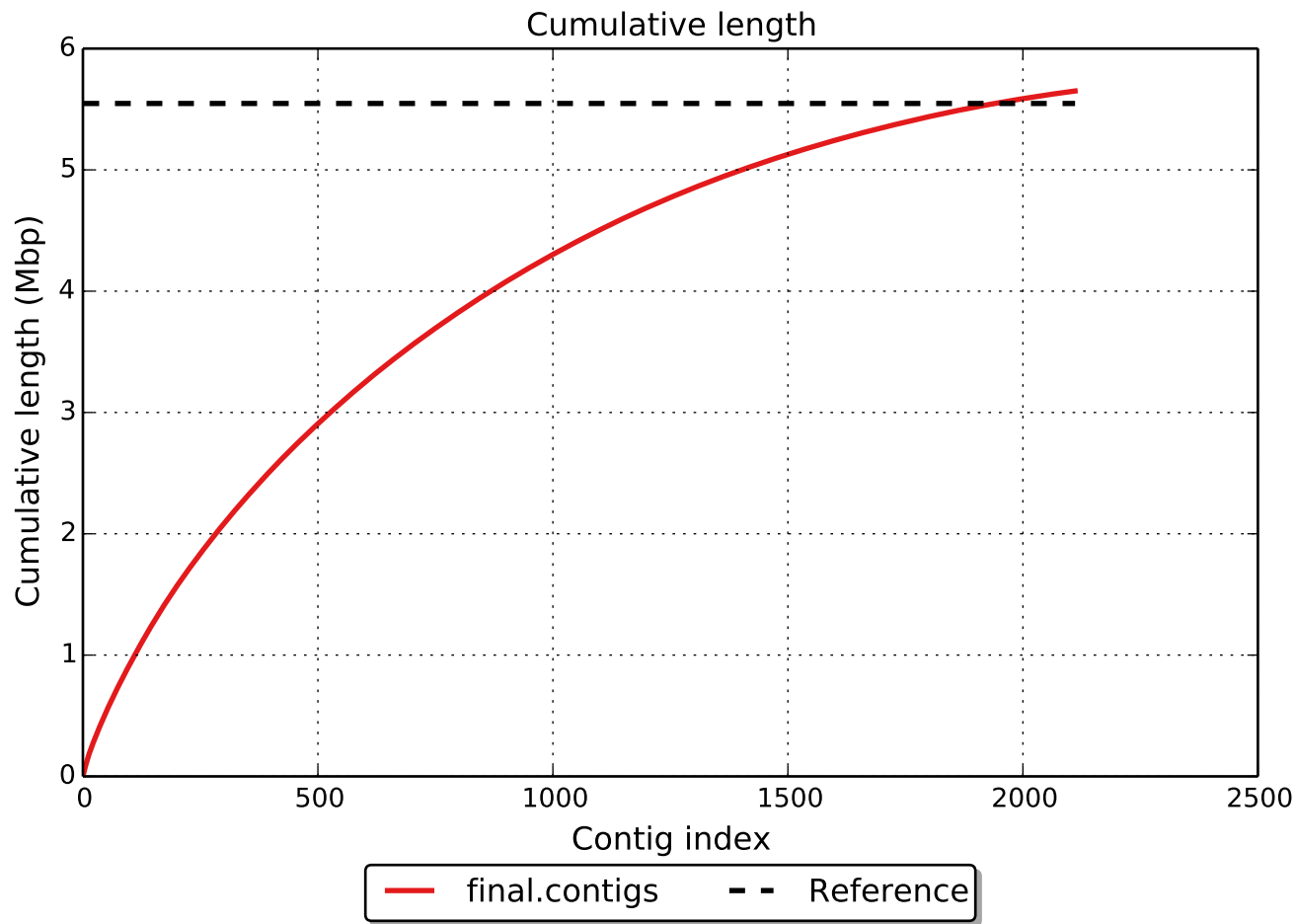
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1937
# indels	2
# short indels	1
# long indels	1
Indels length	24

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).

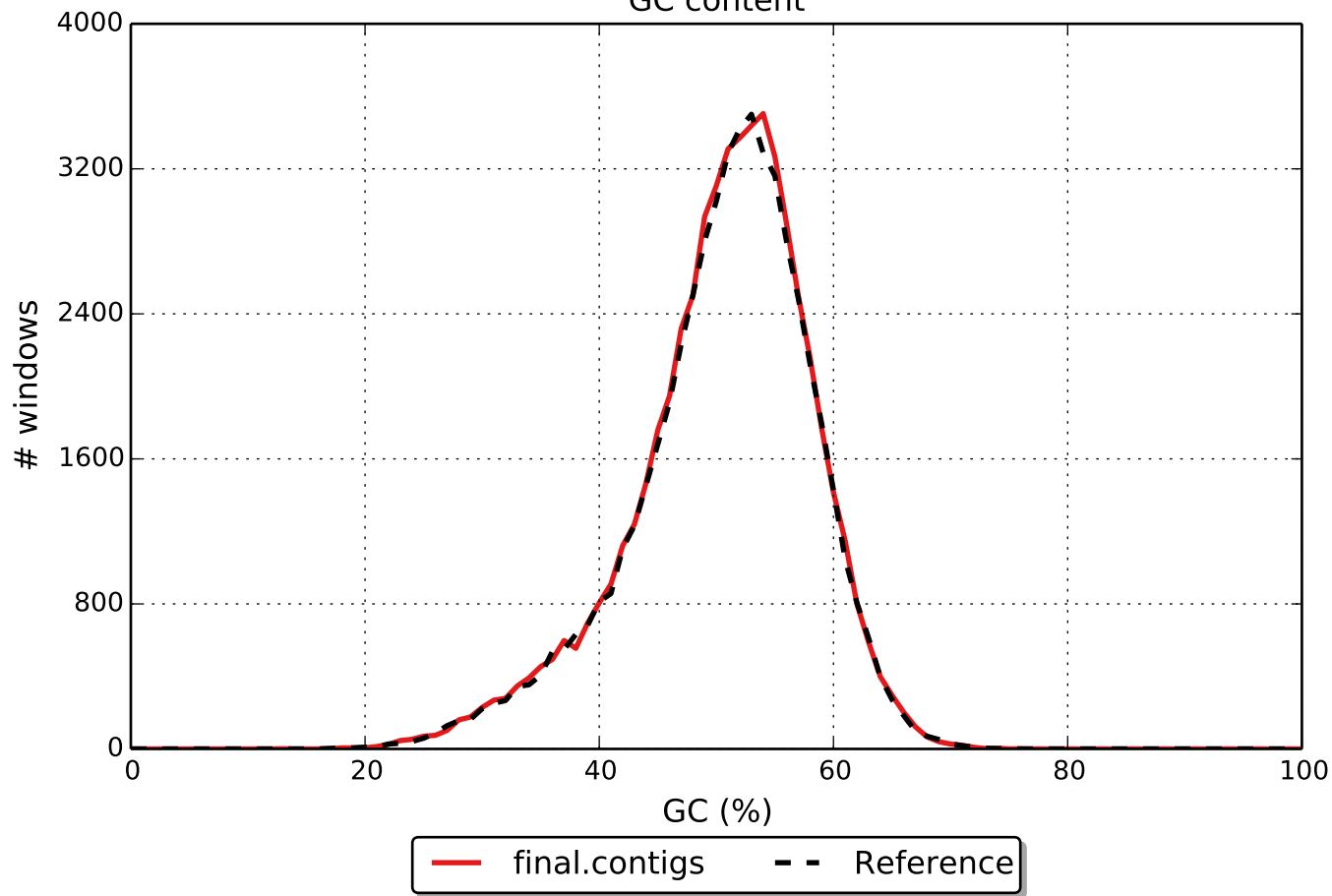
Unaligned report

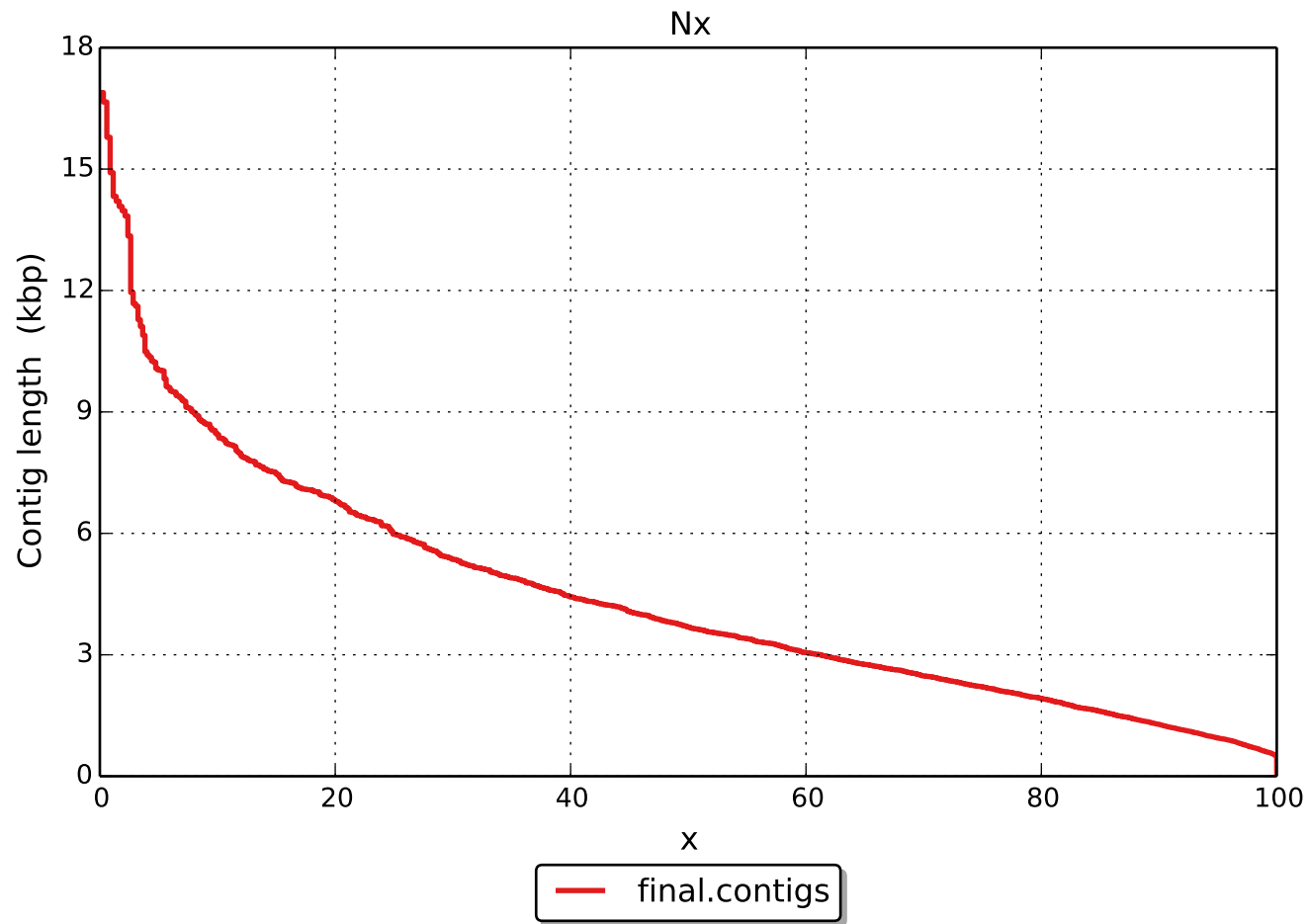
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	180
# N's	0

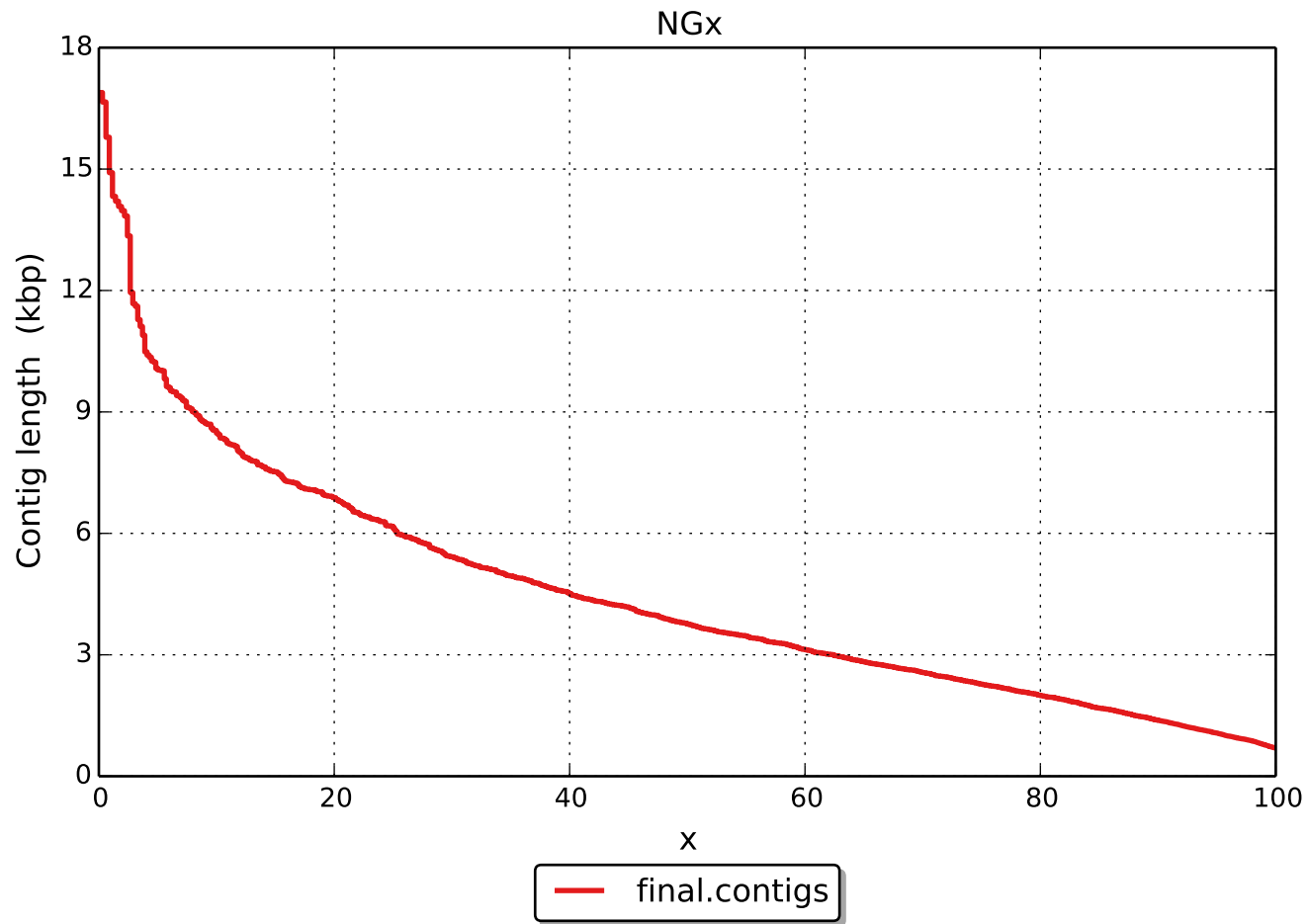
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

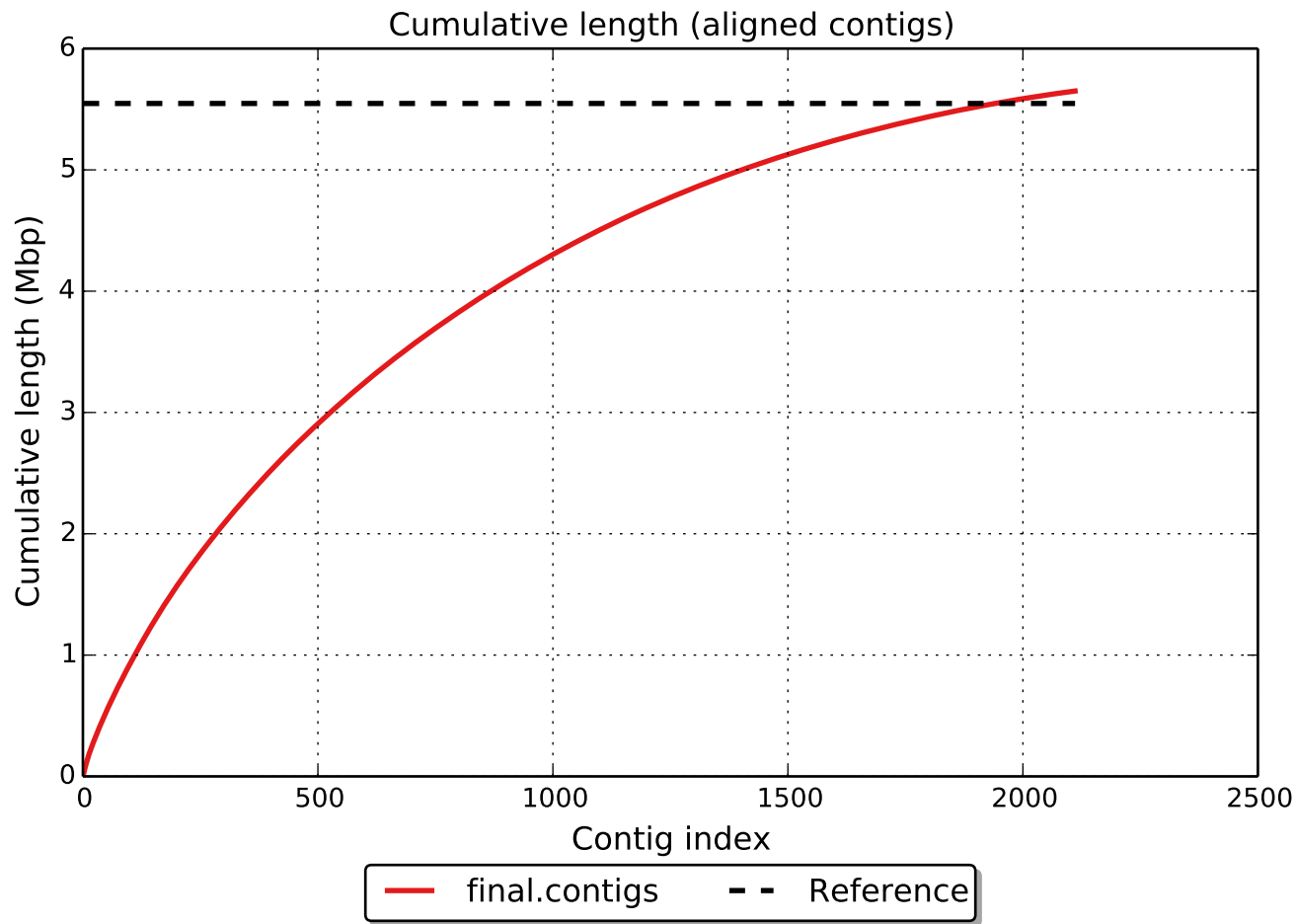


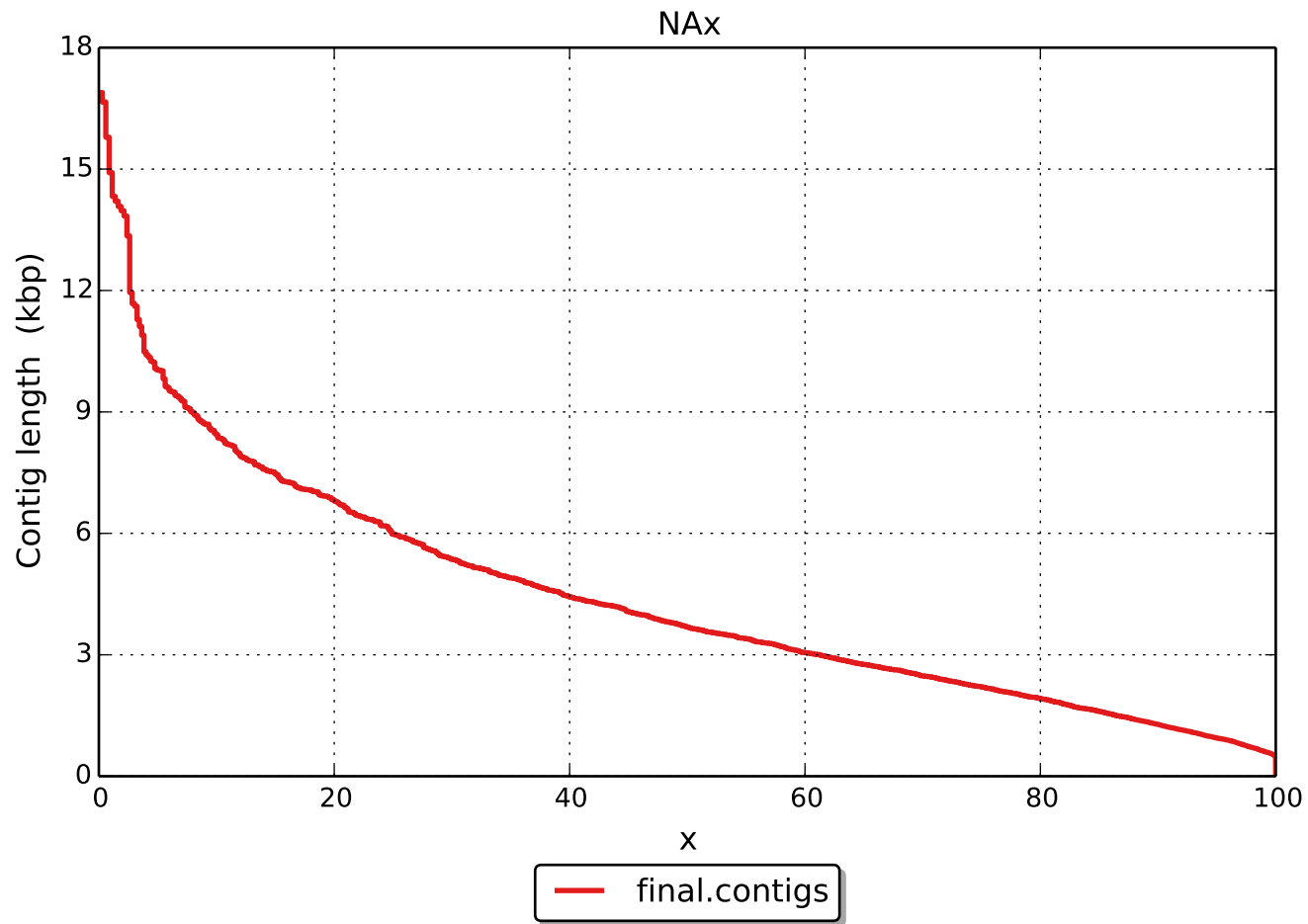




Misassemblies







NGAx

