

Report

	final.contigs
# contigs (≥ 0 bp)	3161
# contigs (≥ 1000 bp)	1302
Total length (≥ 0 bp)	3355636
Total length (≥ 1000 bp)	2023352
# contigs	3161
Largest contig	5155
Total length	3355636
Reference length	1892775
GC (%)	32.26
Reference GC (%)	32.26
N50	1165
NG50	1576
N75	812
NG75	1292
L50	984
LG50	441
L75	1848
LG75	774
# misassemblies	57
# misassembled contigs	55
Misassembled contigs length	85490
# local misassemblies	0
# unaligned contigs	1 + 3 part
Unaligned length	1890
Genome fraction (%)	90.601
Duplication ratio	1.956
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1419.52
# indels per 100 kbp	0.47
Largest alignment	5155
NA50	1134
NGA50	1523
NA75	770
NGA75	1259
LA50	1012
LGA50	453
LA75	1908
LGA75	796

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

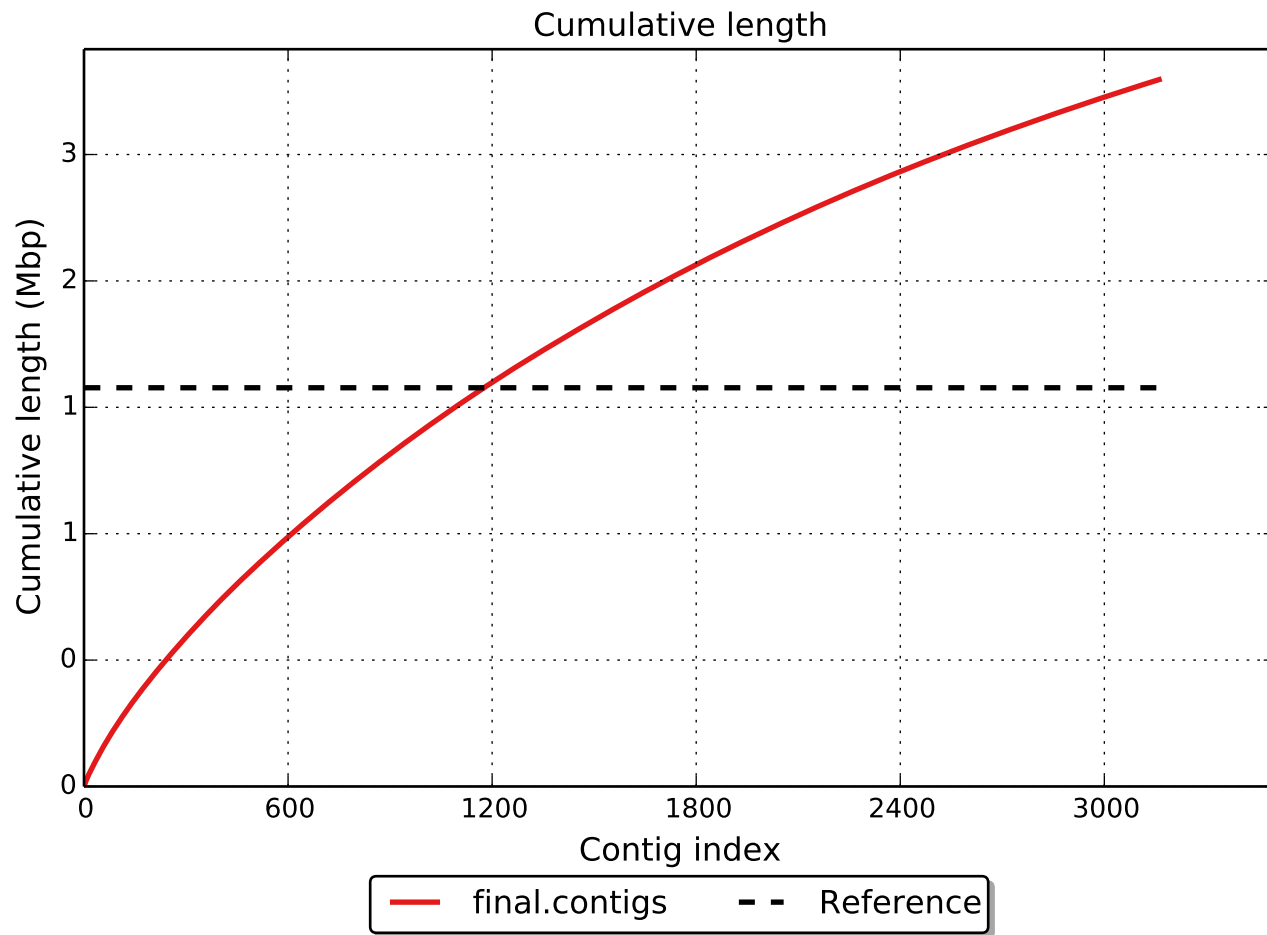
	final.contigs
# misassemblies	57
# relocations	57
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	55
Misassembled contigs length	85490
# local misassemblies	0
# mismatches	24343
# indels	8
# short indels	8
# long indels	0
Indels length	8

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).

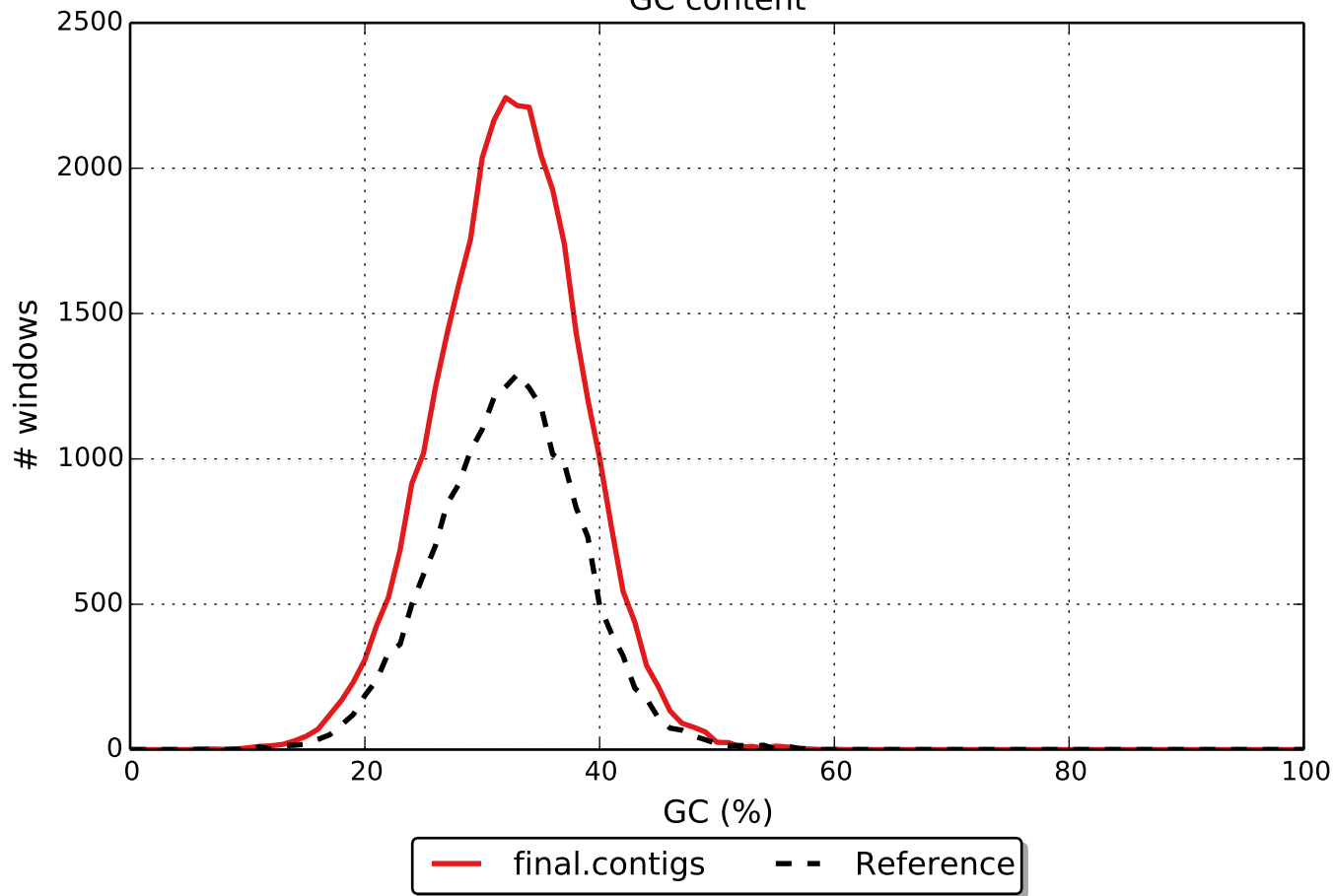
Unaligned report

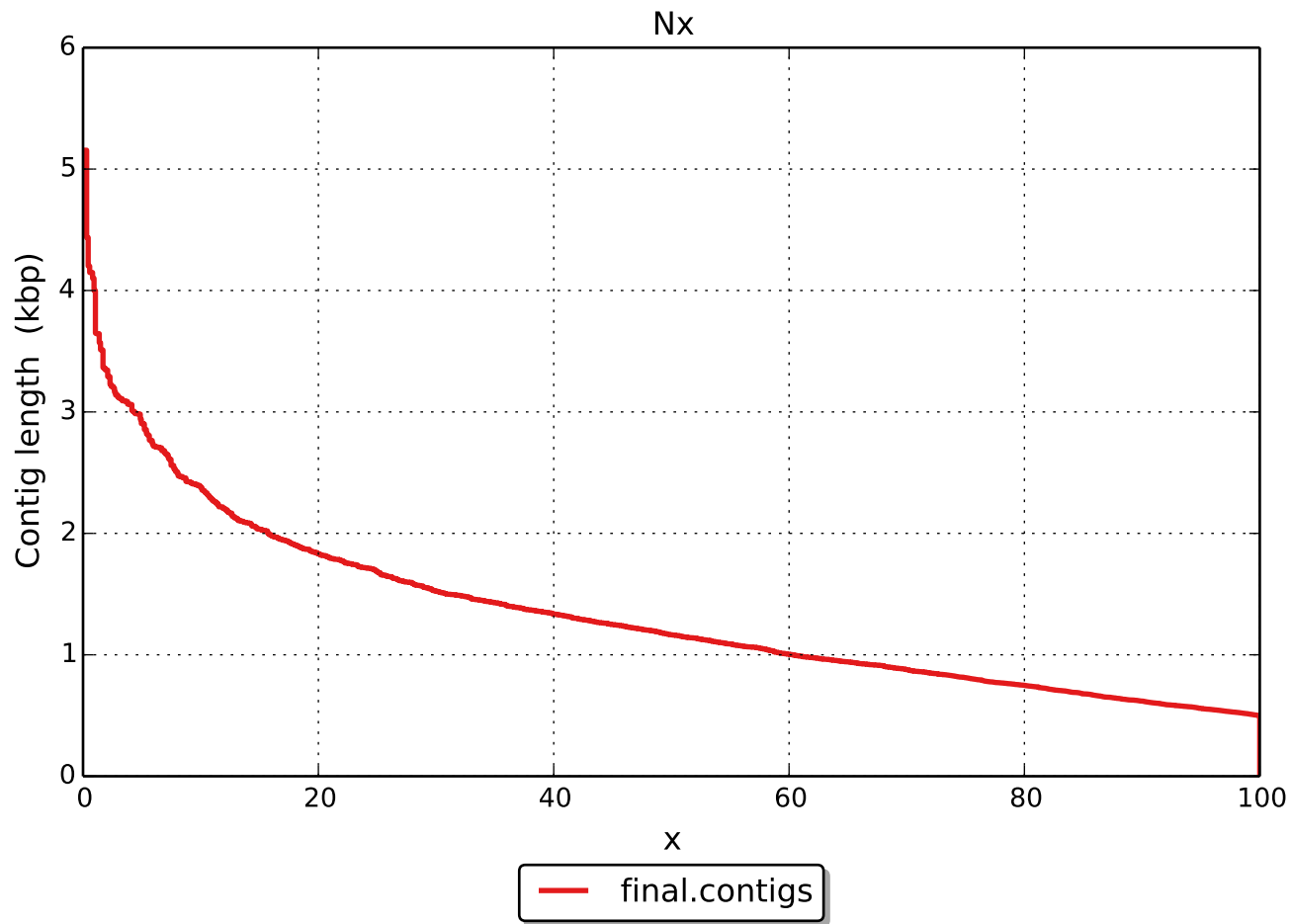
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	924
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	966
# N's	0

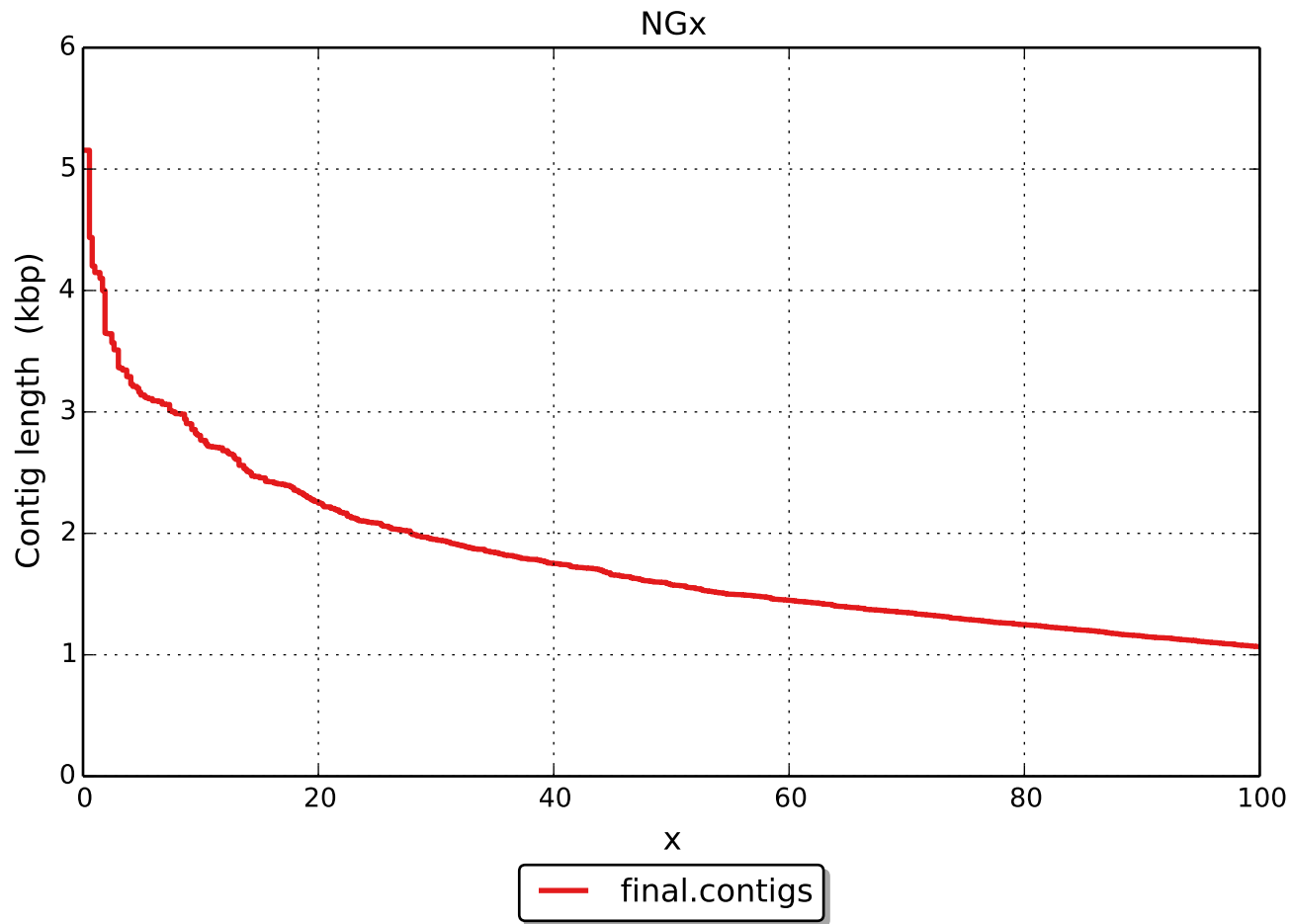
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



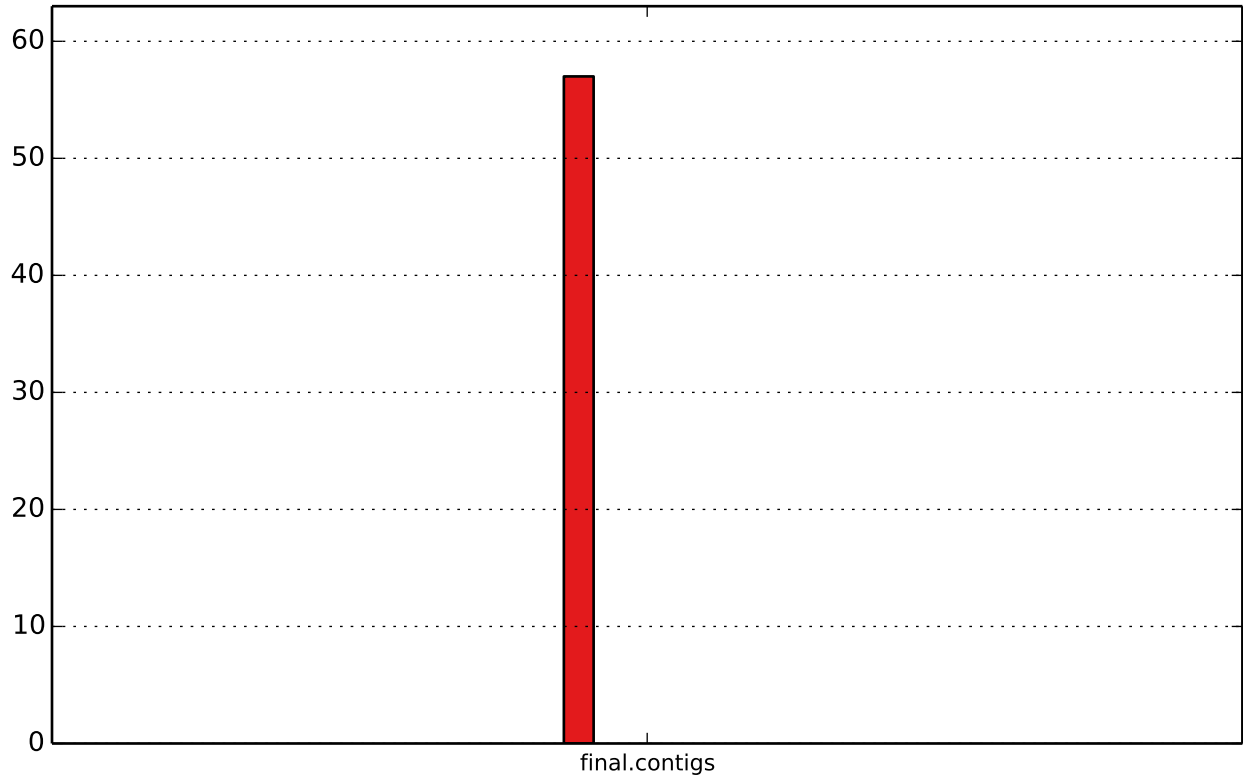
GC content



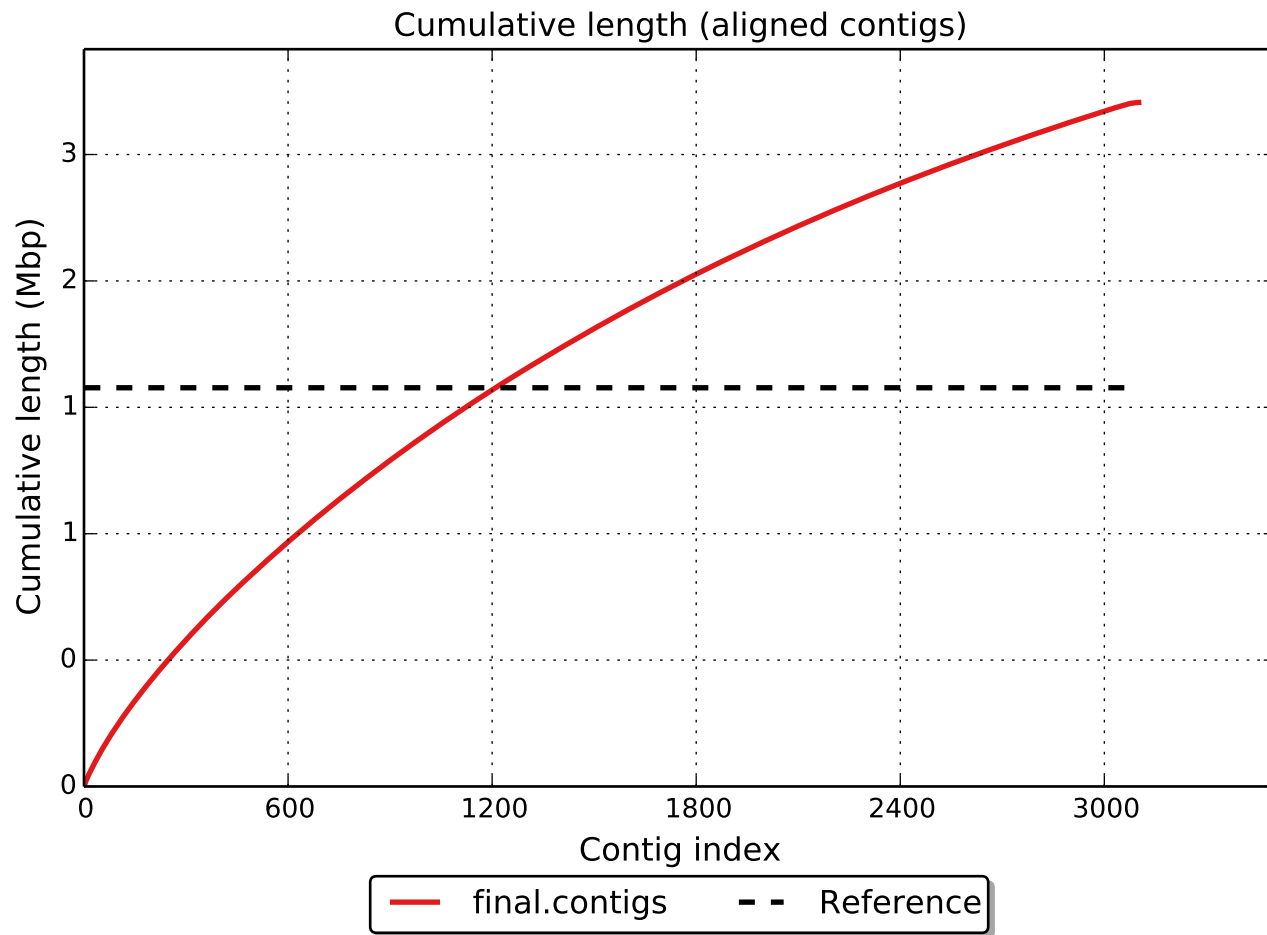


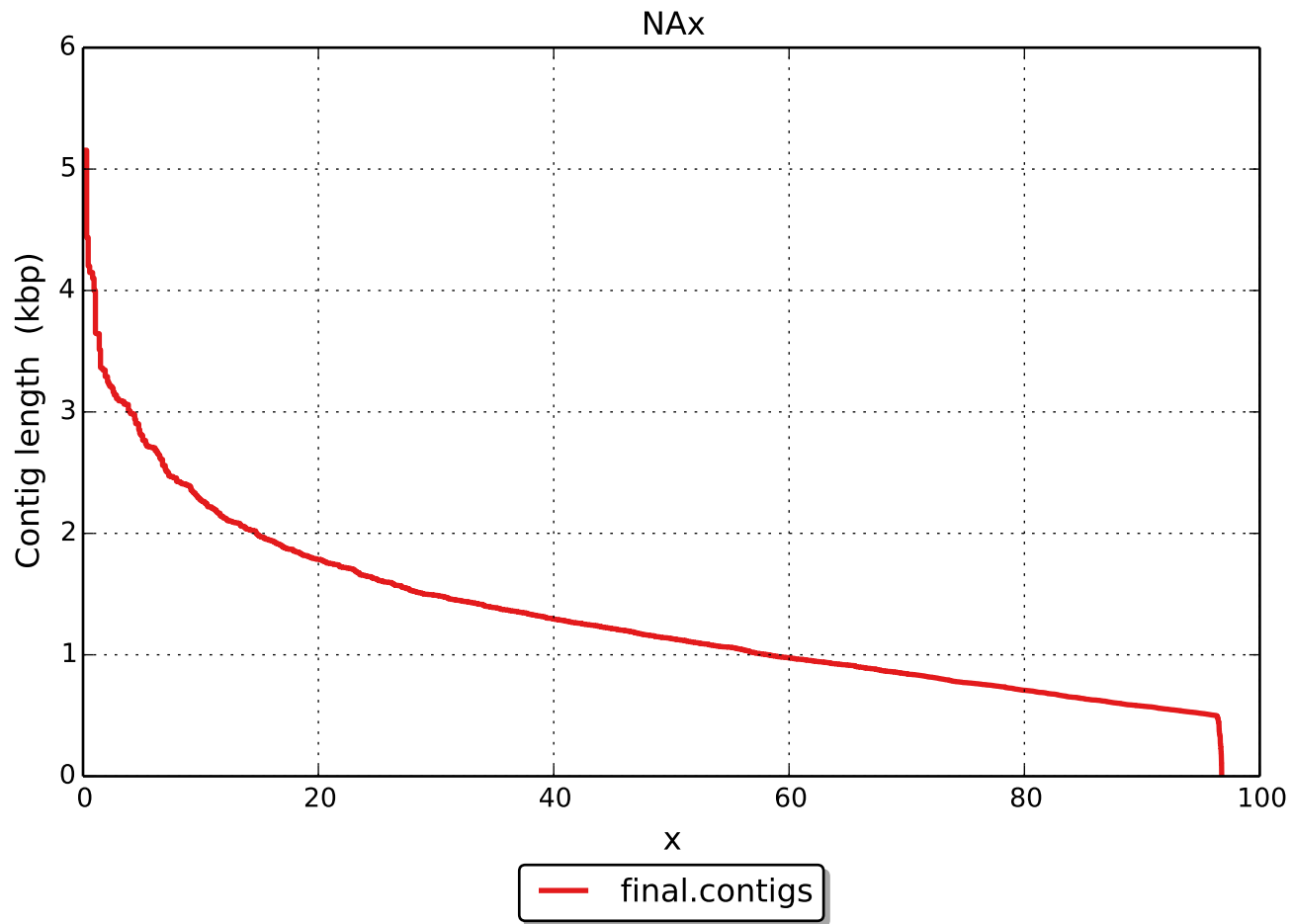


Misassemblies



 # relocations





NGAx

