

Report

	final.contigs
# contigs (≥ 0 bp)	3351
# contigs (≥ 1000 bp)	1113
Total length (≥ 0 bp)	3215840
Total length (≥ 1000 bp)	1629271
# contigs	3351
Largest contig	4208
Total length	3215840
Reference length	1892775
GC (%)	32.28
Reference GC (%)	32.26
N50	1009
NG50	1350
N75	732
NG75	1101
L50	1092
LG50	522
L75	2027
LG75	913
# misassemblies	53
# misassembled contigs	52
Misassembled contigs length	61830
# local misassemblies	0
# unaligned contigs	2 + 1 part
Unaligned length	3088
Genome fraction (%)	88.152
Duplication ratio	1.926
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1339.39
# indels per 100 kbp	0.48
Largest alignment	4208
NA50	952
NGA50	1291
NA75	678
NGA75	1032
LA50	1138
LGA50	539
LA75	2138
LGA75	948

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

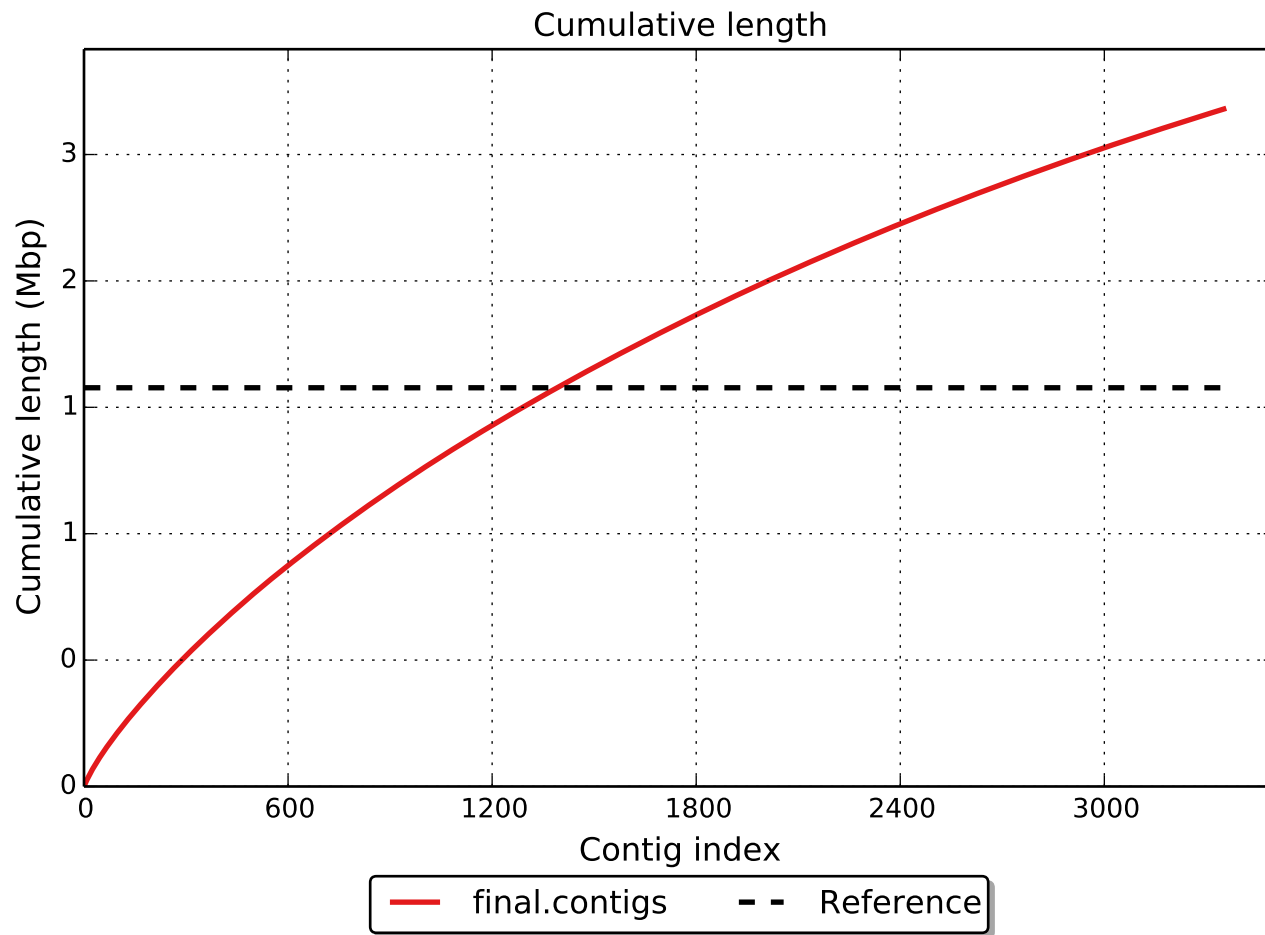
	final.contigs
# misassemblies	53
# relocations	53
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	52
Misassembled contigs length	61830
# local misassemblies	0
# mismatches	22348
# indels	8
# short indels	8
# long indels	0
Indels length	8

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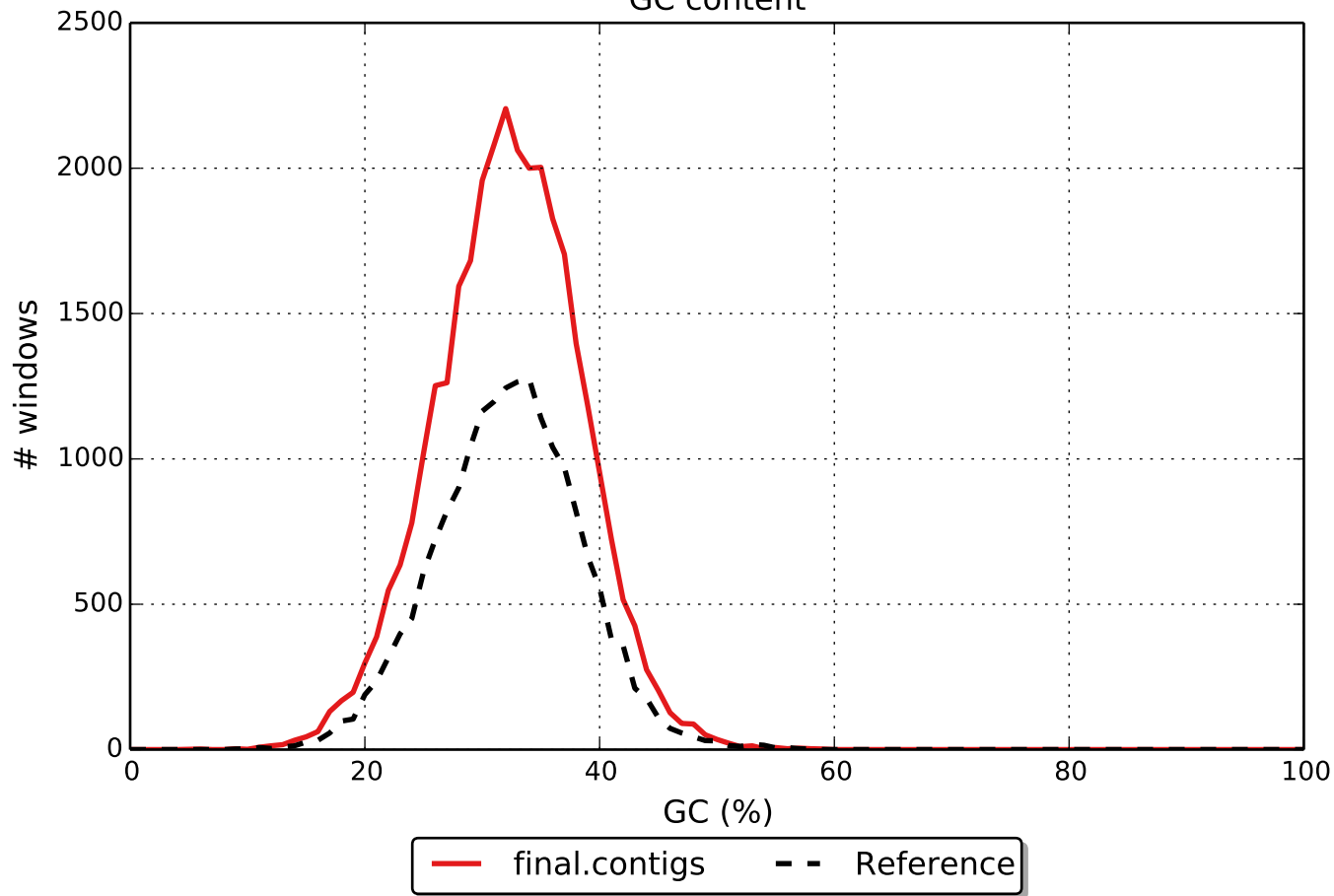
Unaligned report

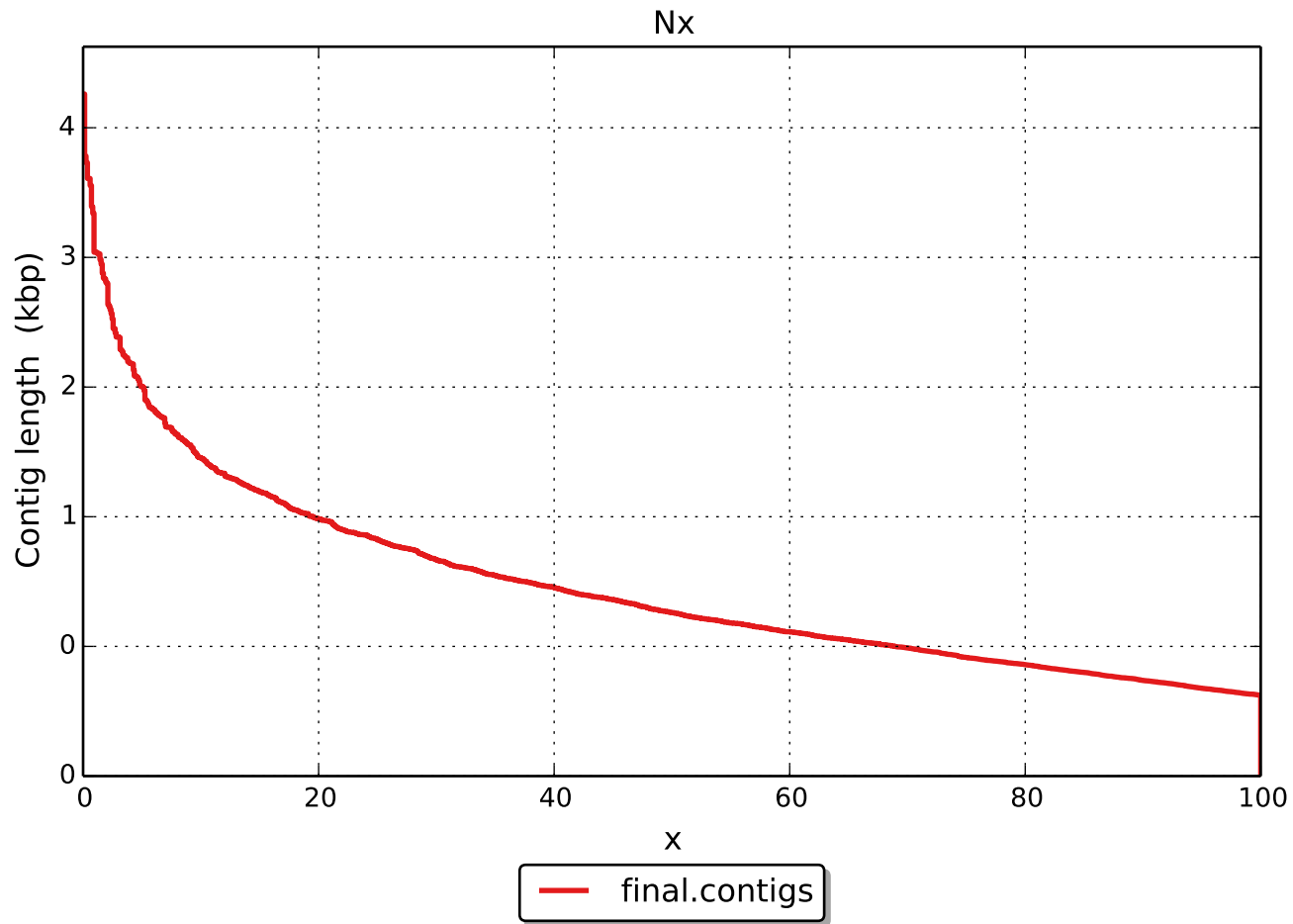
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1784
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1304
# N's	0

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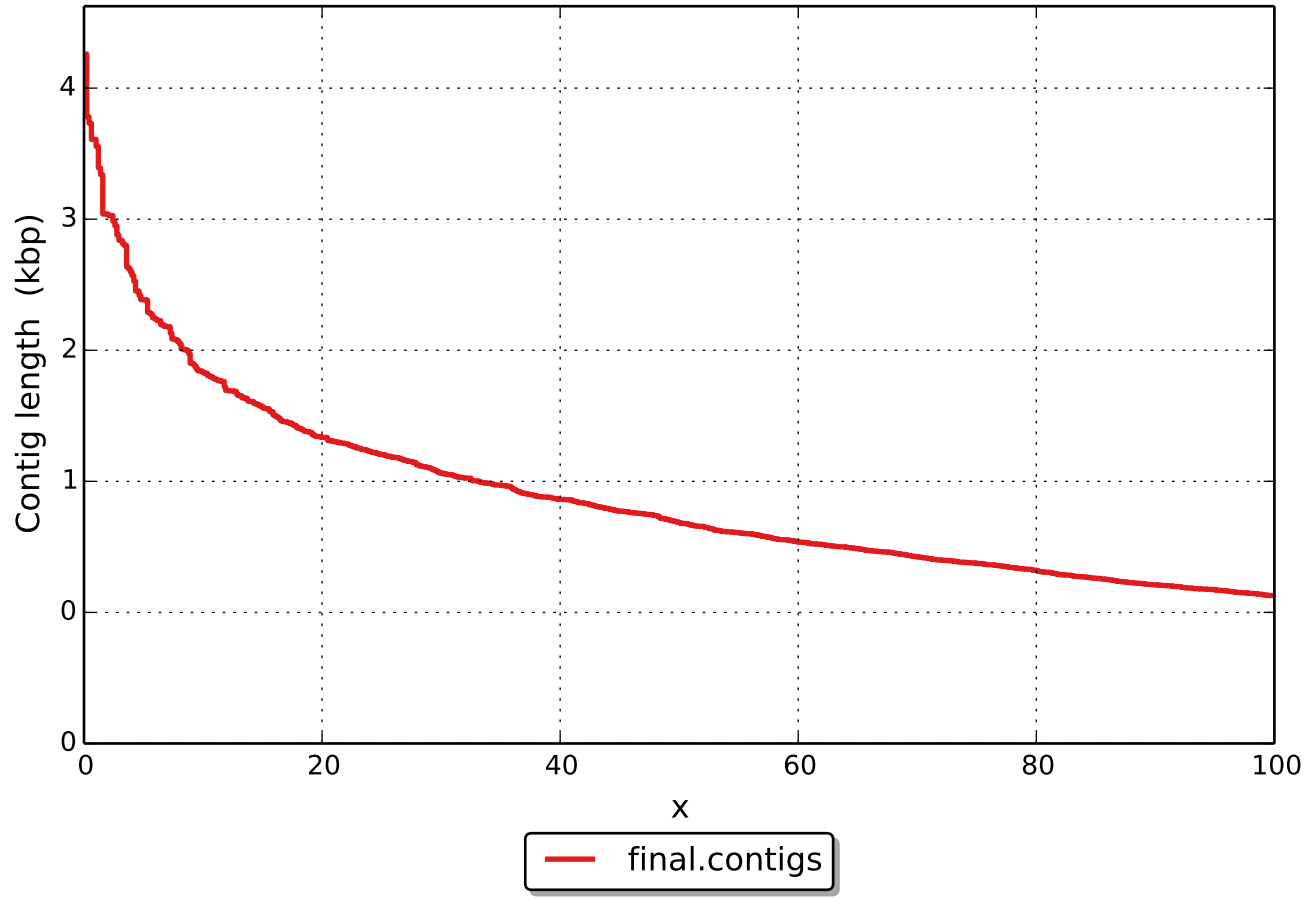


GC content

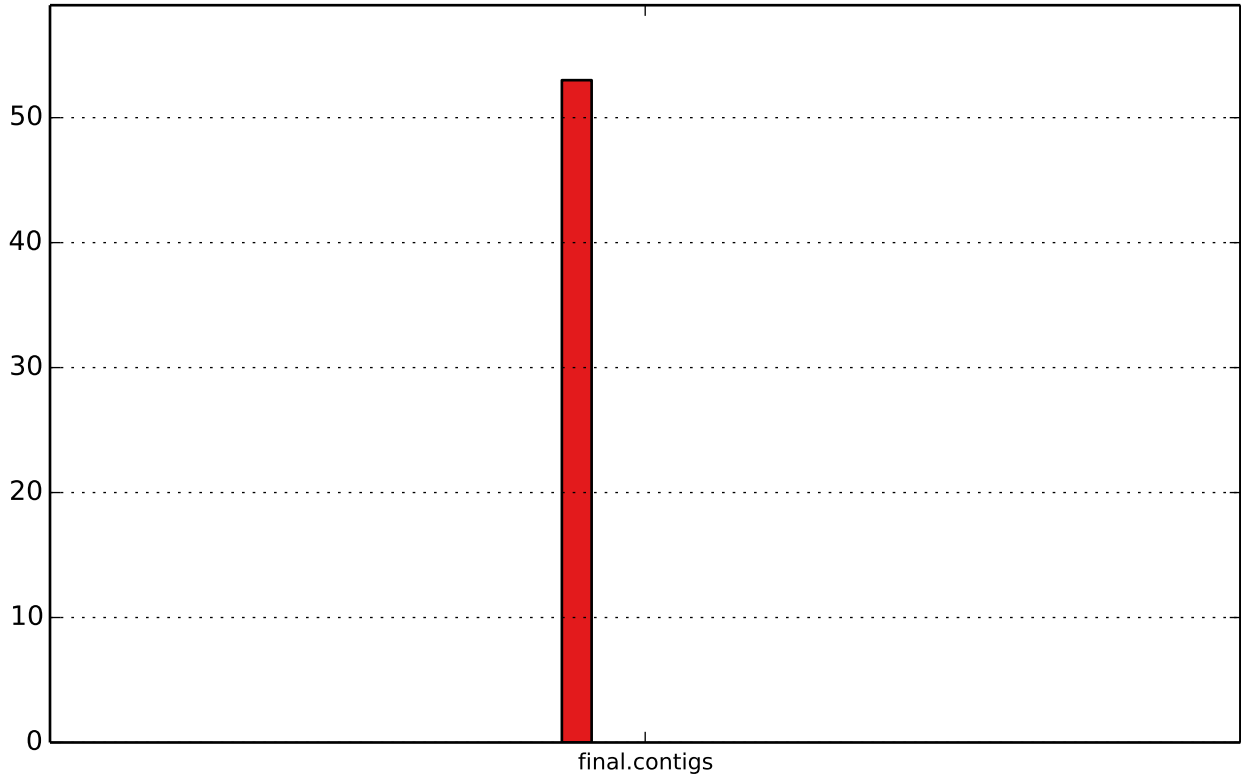




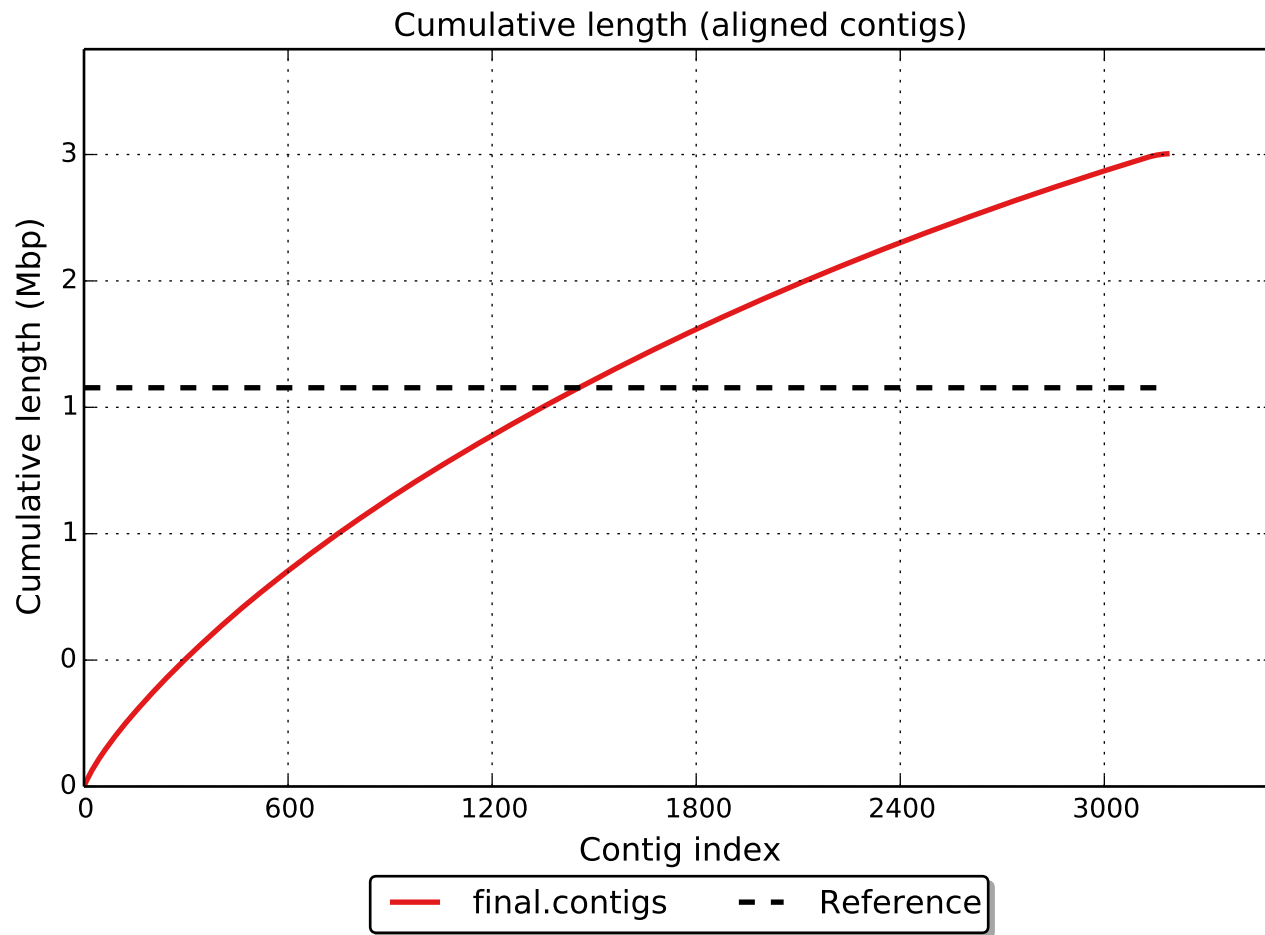
NGx



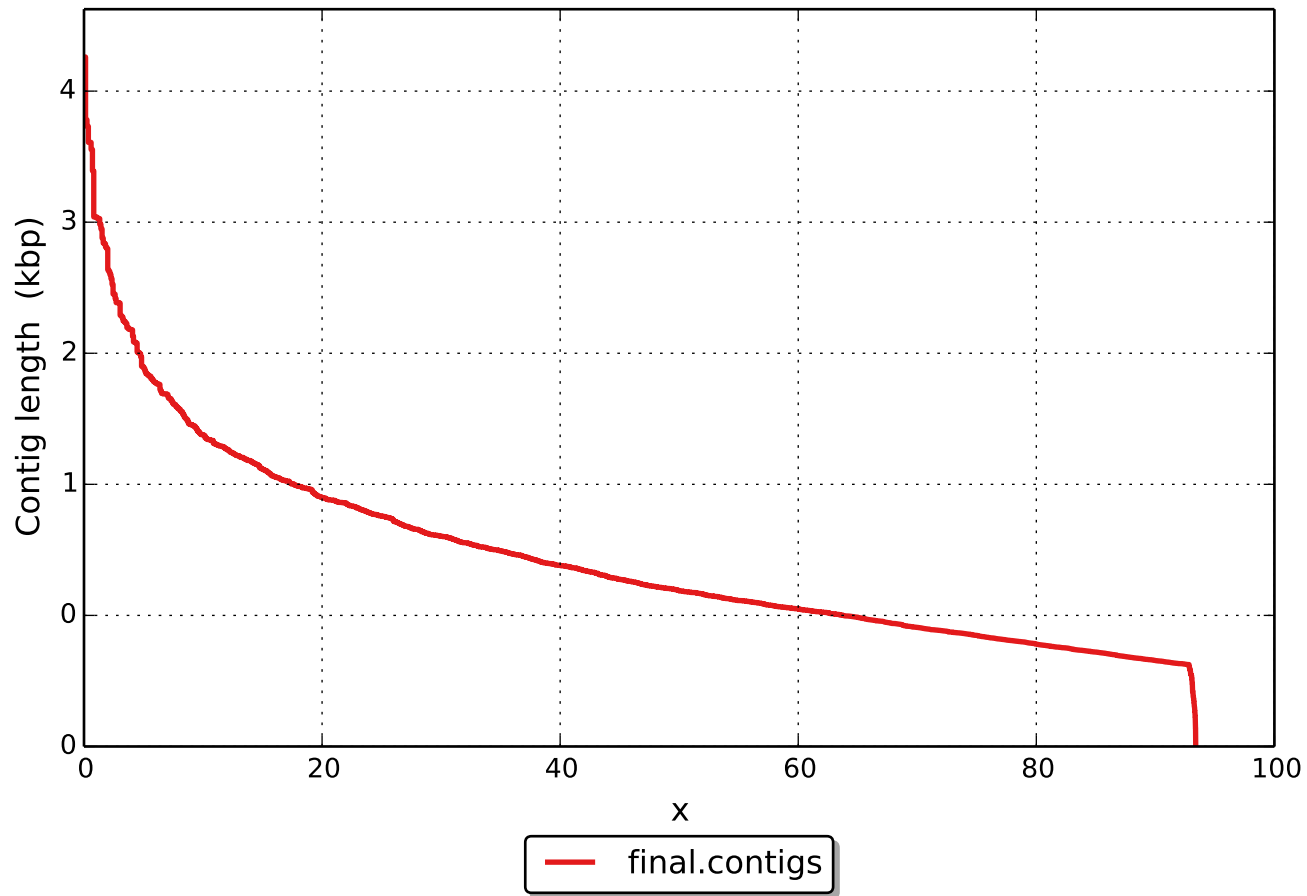
Misassemblies



 # relocations



NAx



NGAx

