

Report

	final.contigs
# contigs (≥ 0 bp)	513
# contigs (≥ 1000 bp)	484
Total length (≥ 0 bp)	5615184
Total length (≥ 1000 bp)	5593937
# contigs	513
Largest contig	61625
Total length	5615184
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	17478
NG50	17650
N75	9713
NG75	9885
L50	104
LG50	102
L75	214
LG75	208
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 4 part
Unaligned length	25765
Genome fraction (%)	99.838
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.77
# indels per 100 kbp	0.00
Largest alignment	61625
NA50	17215
NGA50	17478
NA75	9611
NGA75	9757
LA50	104
LGA50	103
LA75	215
LGA75	210

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

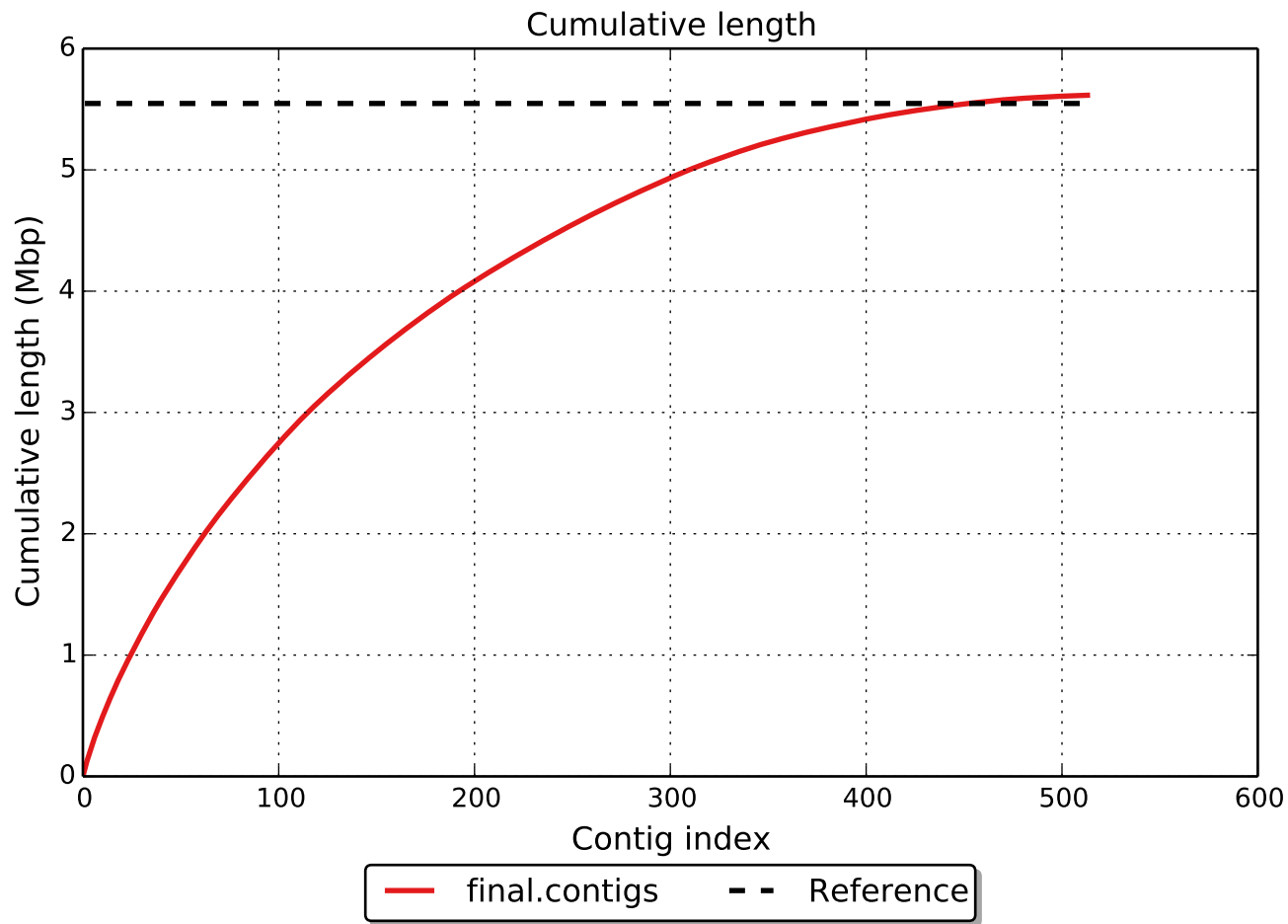
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	264
# indels	0
# short indels	0
# long indels	0
Indels length	0

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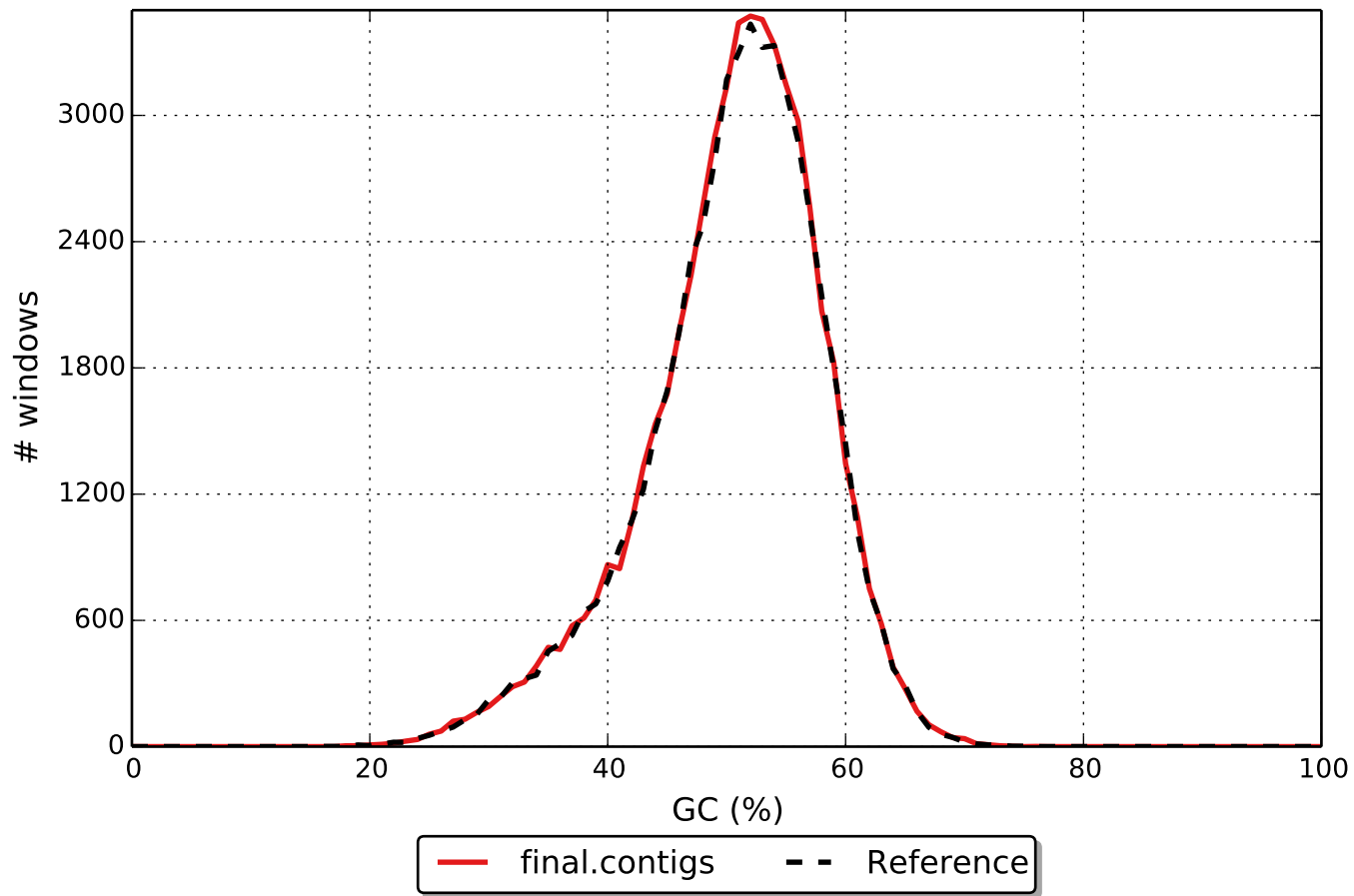
Unaligned report

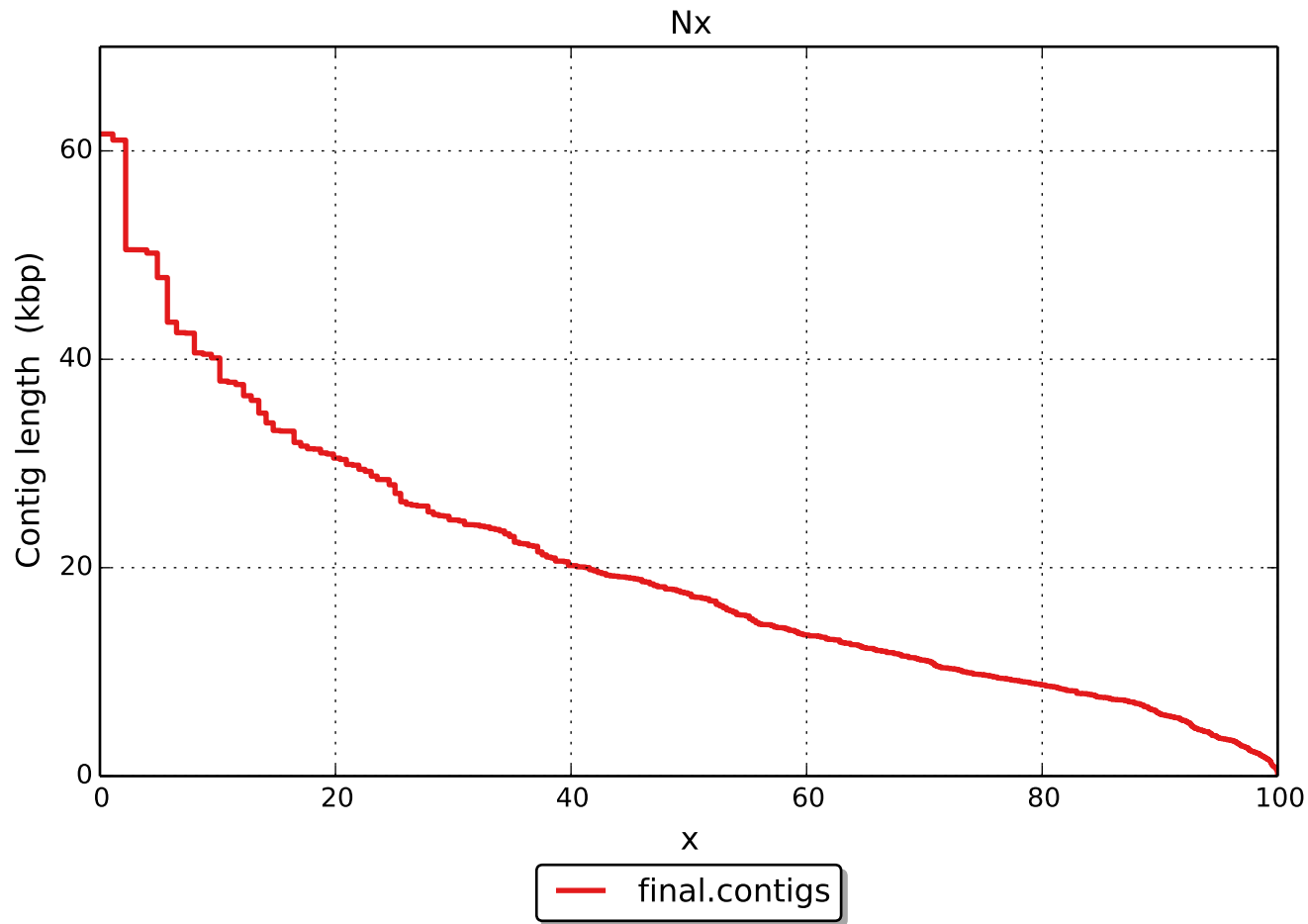
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	4
Partially unaligned length	25765
# N's	0

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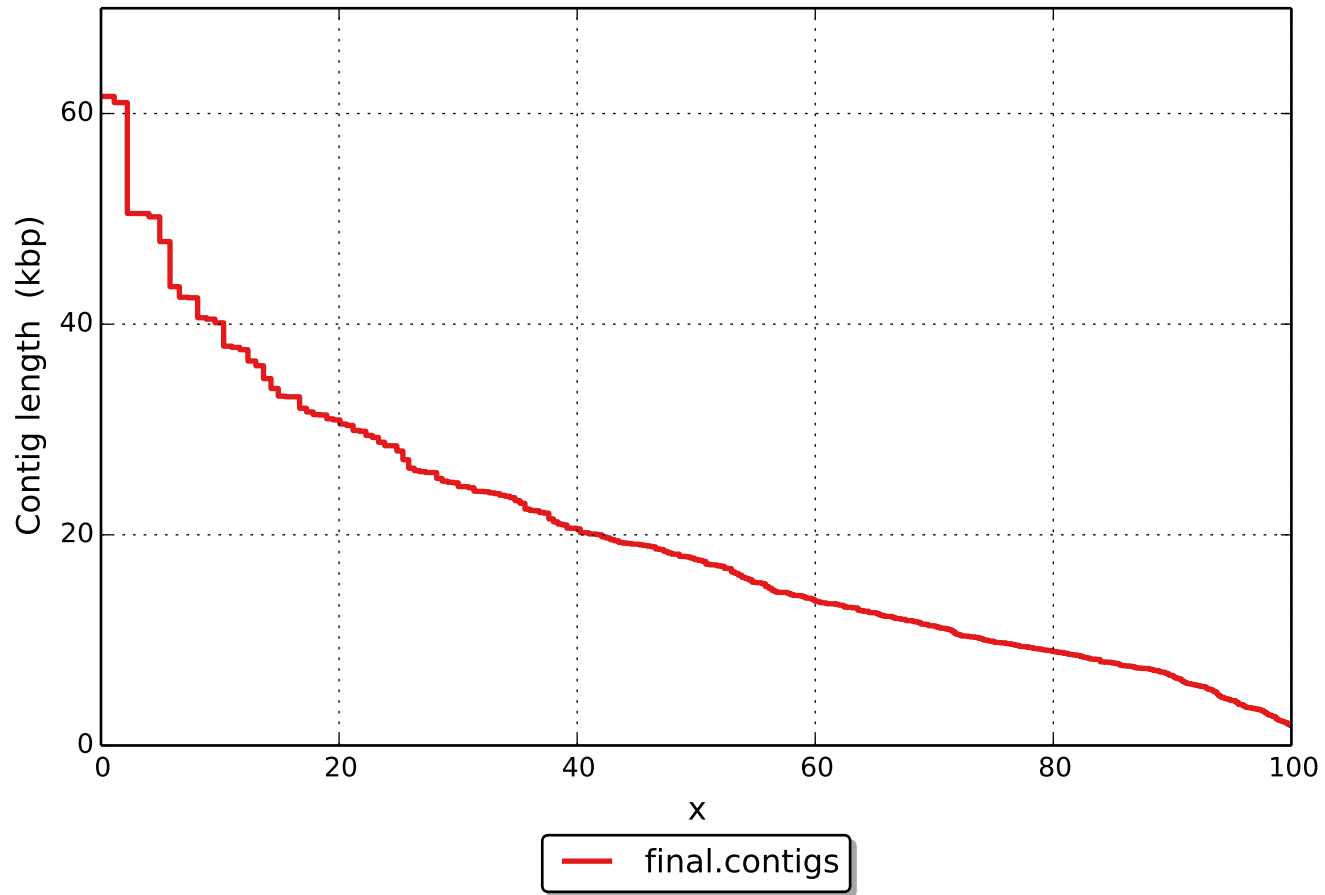


GC content



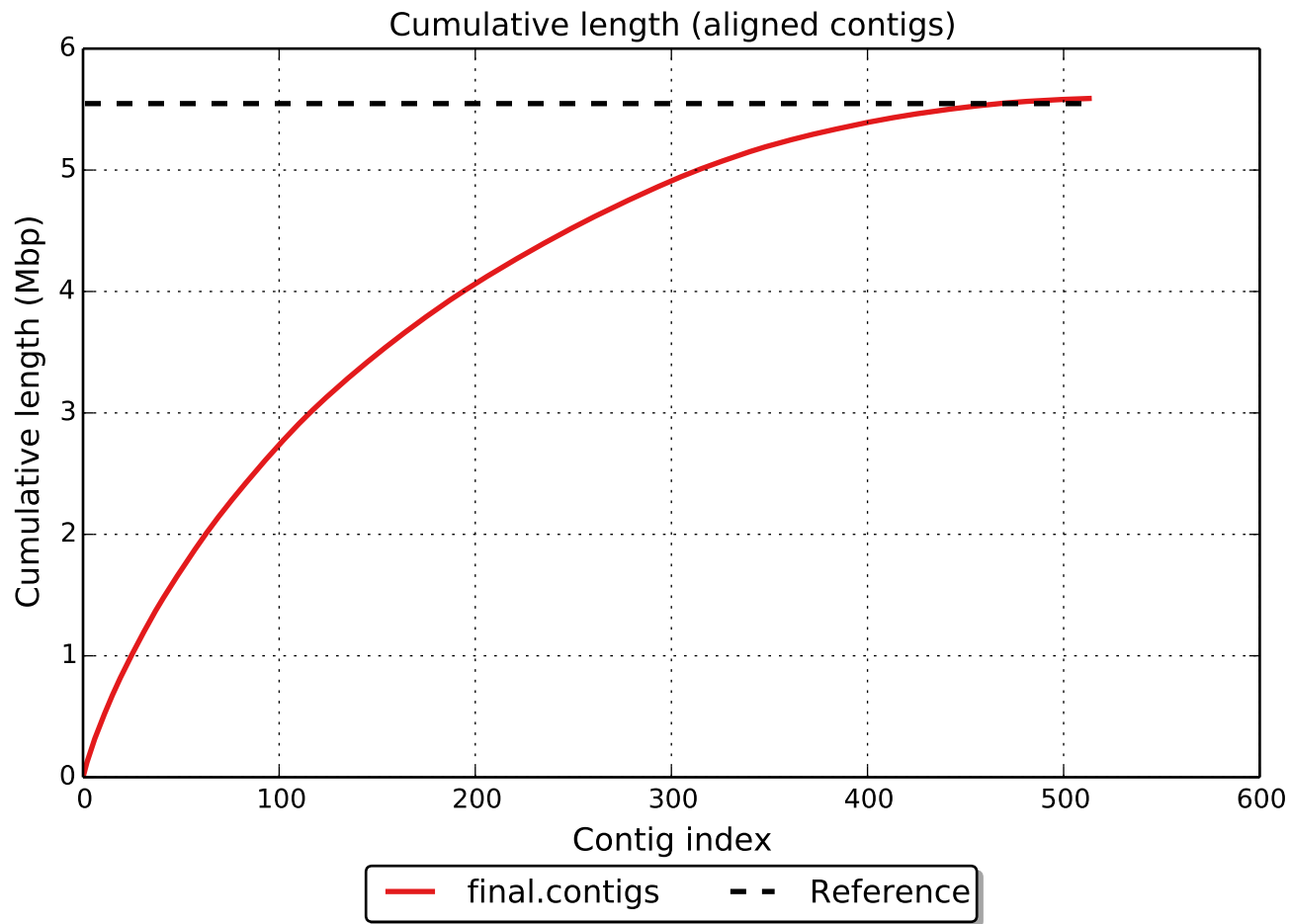


NGx

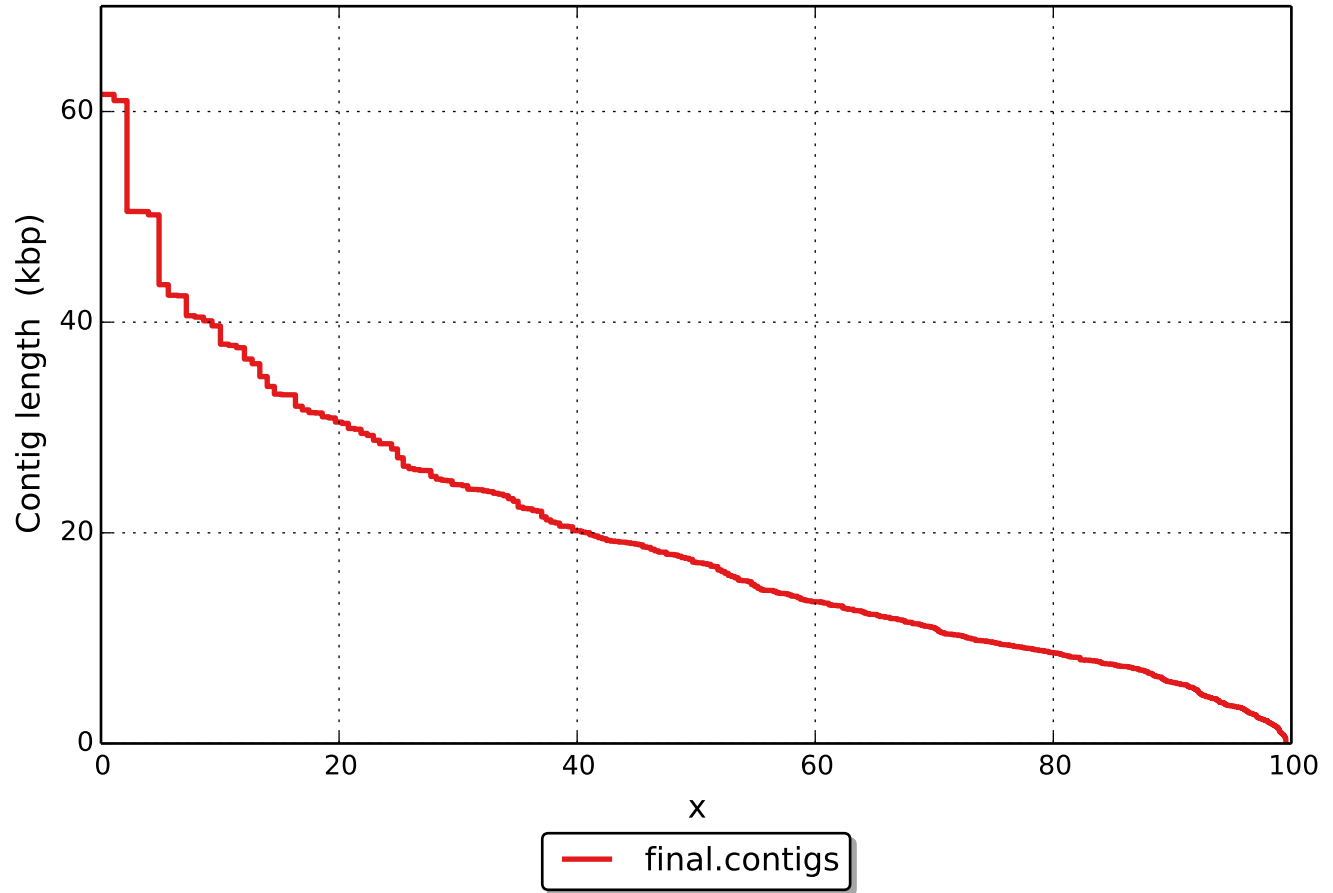


Misassemblies





NAx



NGAx

