

Report

	final.contigs
# contigs (≥ 0 bp)	602
# contigs (≥ 1000 bp)	477
Total length (≥ 0 bp)	3749312
Total length (≥ 1000 bp)	3697296
# contigs	506
Largest contig	40013
Total length	3720020
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.26
N50	11989
NG50	11968
N75	6586
NG75	6357
L50	103
LG50	105
L75	206
LG75	214
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	24084
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.856
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	42.87
# indels per 100 kbp	0.38
Largest alignment	40013
NA50	11989
NGA50	11899
NA75	6557
NGA75	6330
LA50	103
LGA50	106
LA75	207
LGA75	215

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

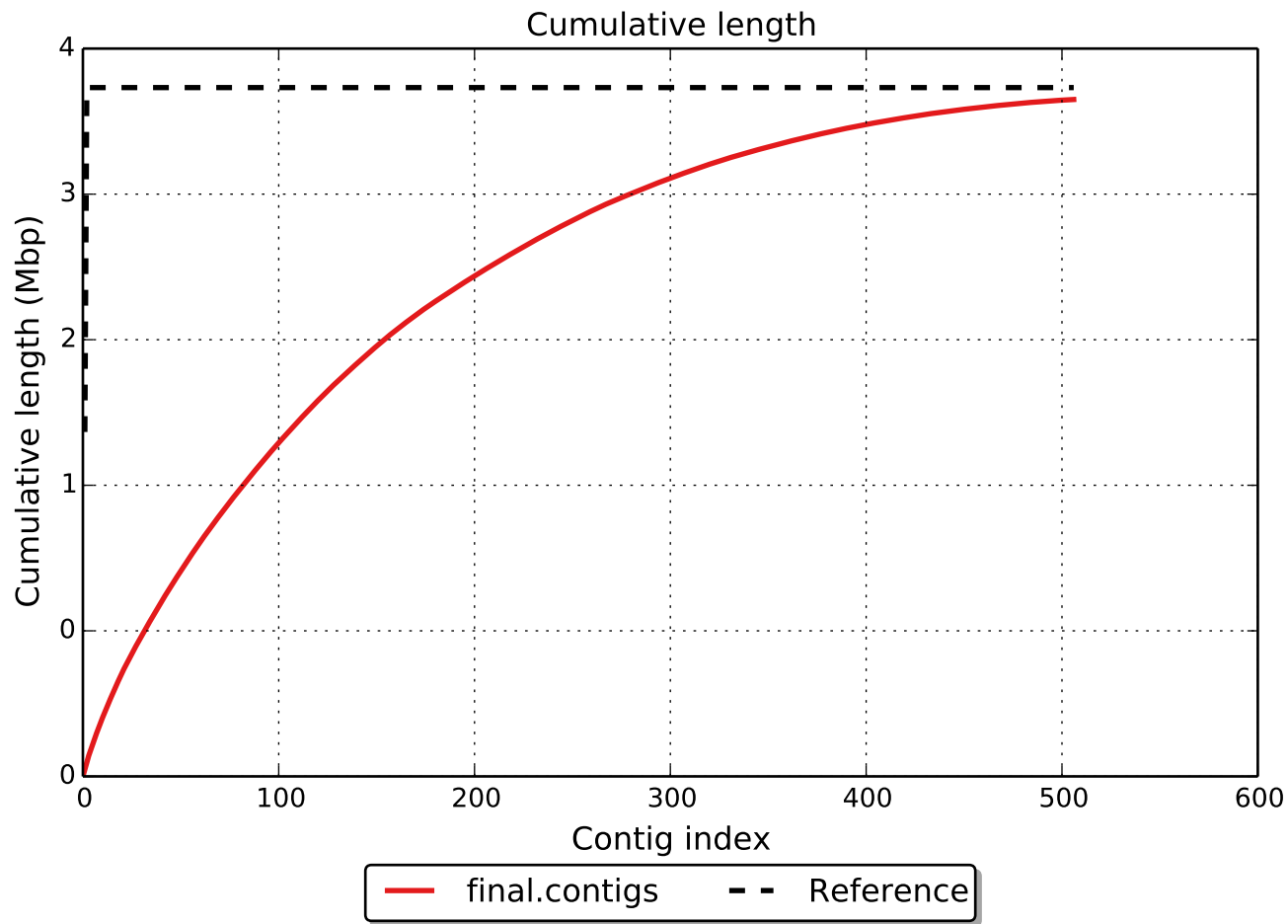
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	24084
# local misassemblies	0
# mismatches	1572
# indels	14
# short indels	8
# long indels	6
Indels length	76

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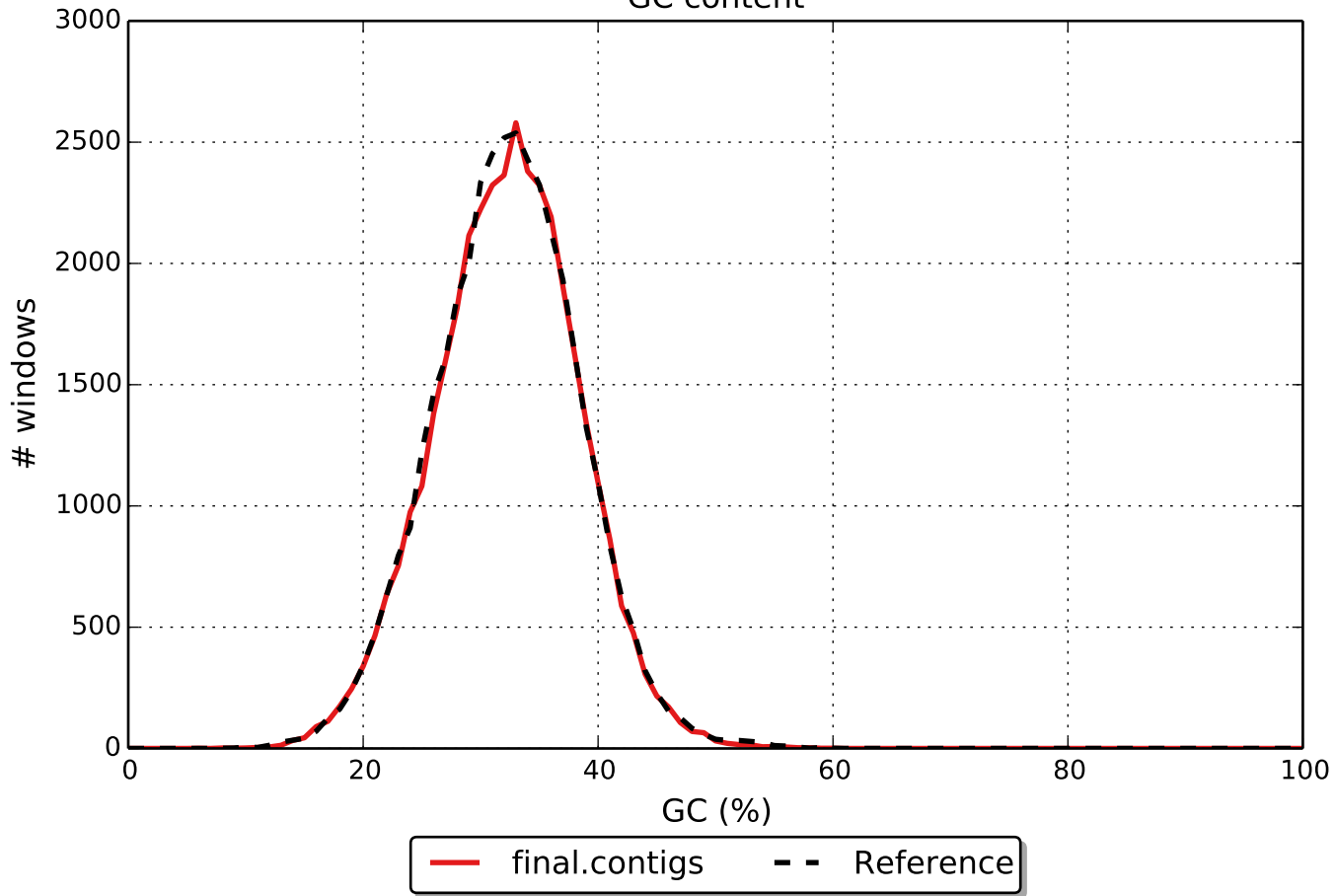
Unaligned report

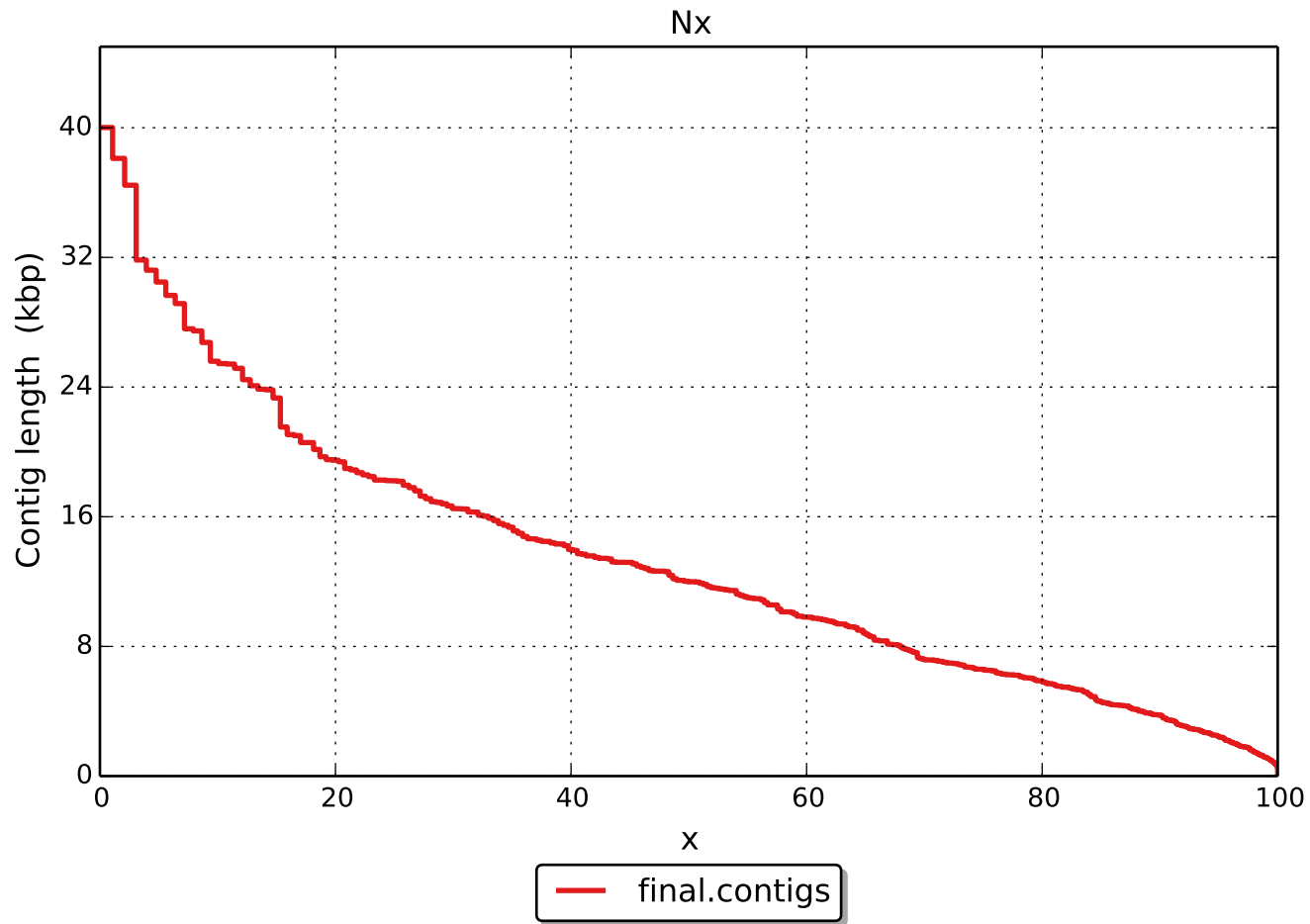
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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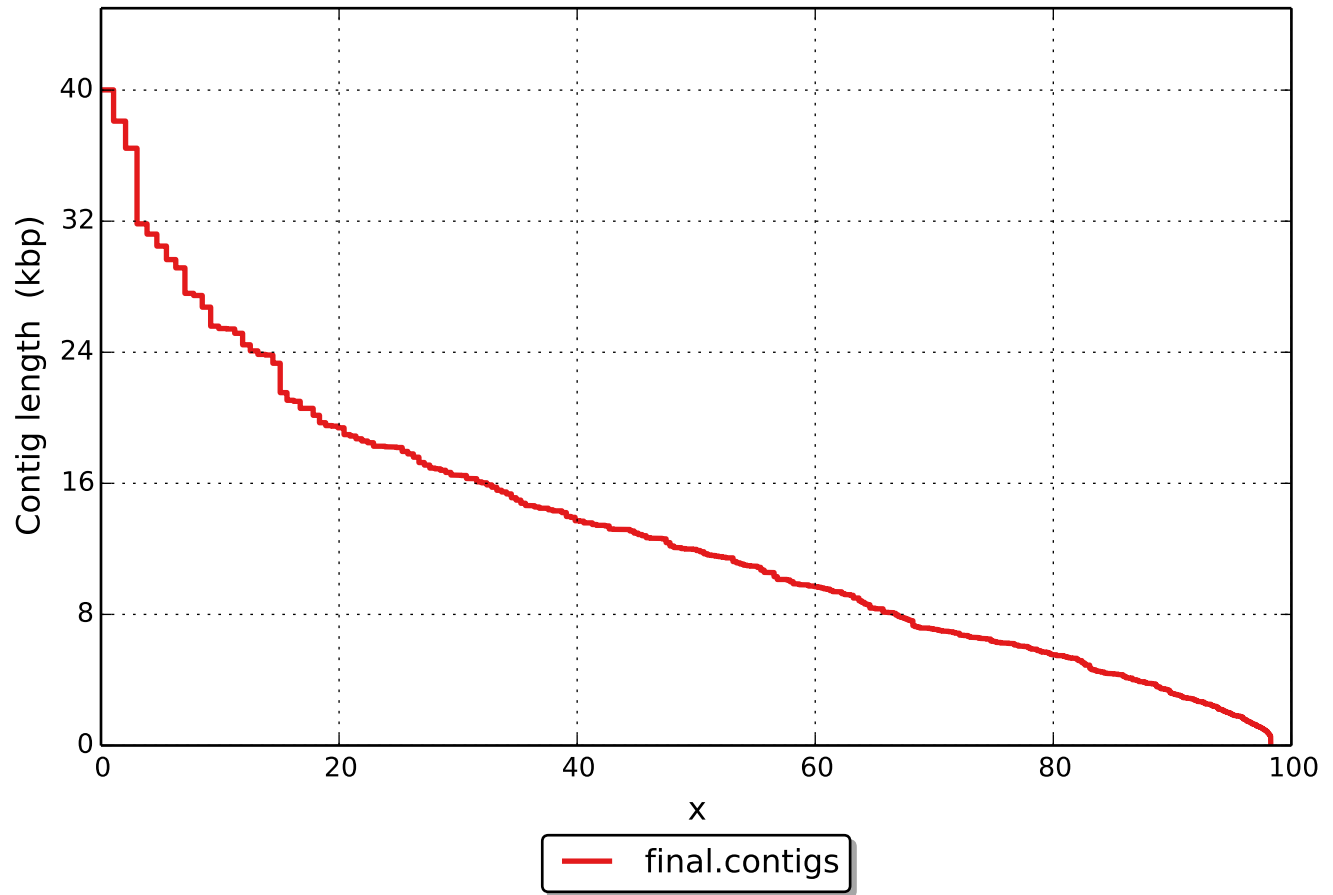


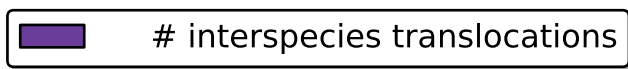
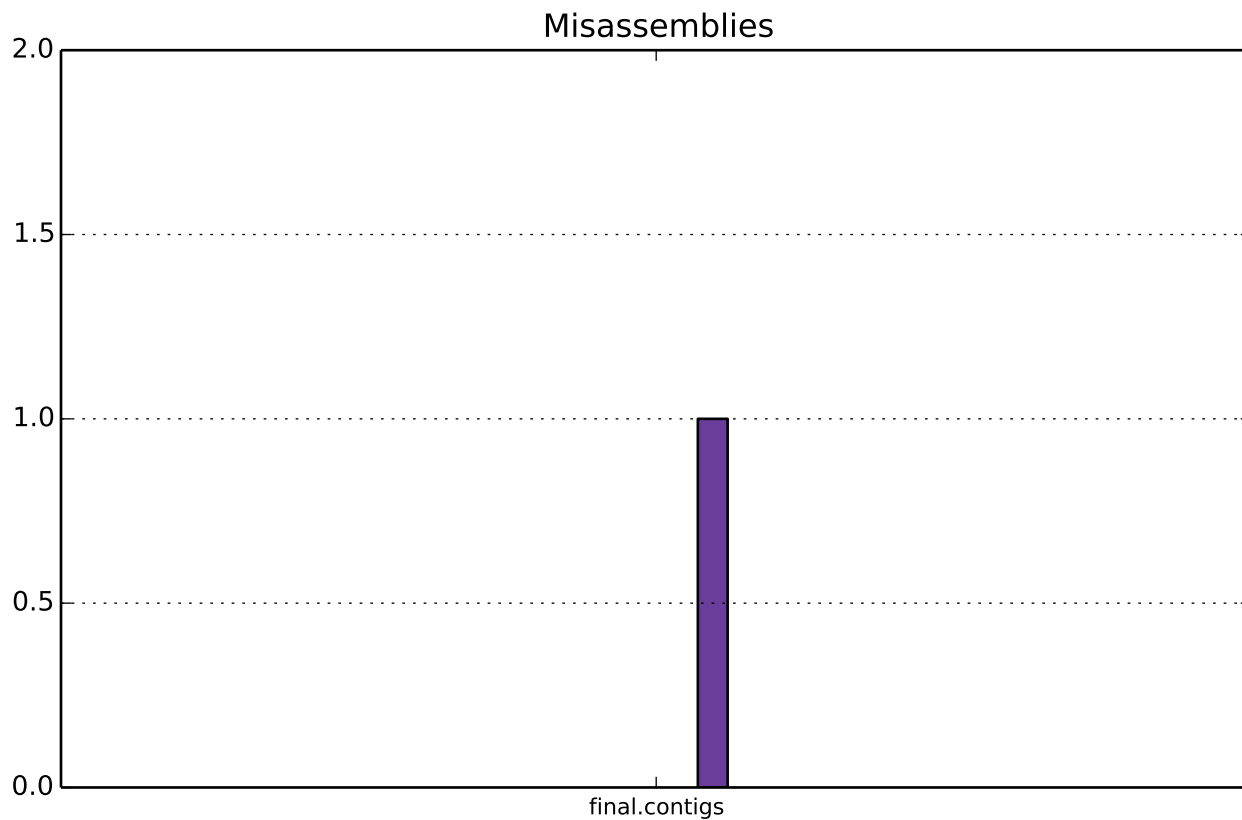
GC content

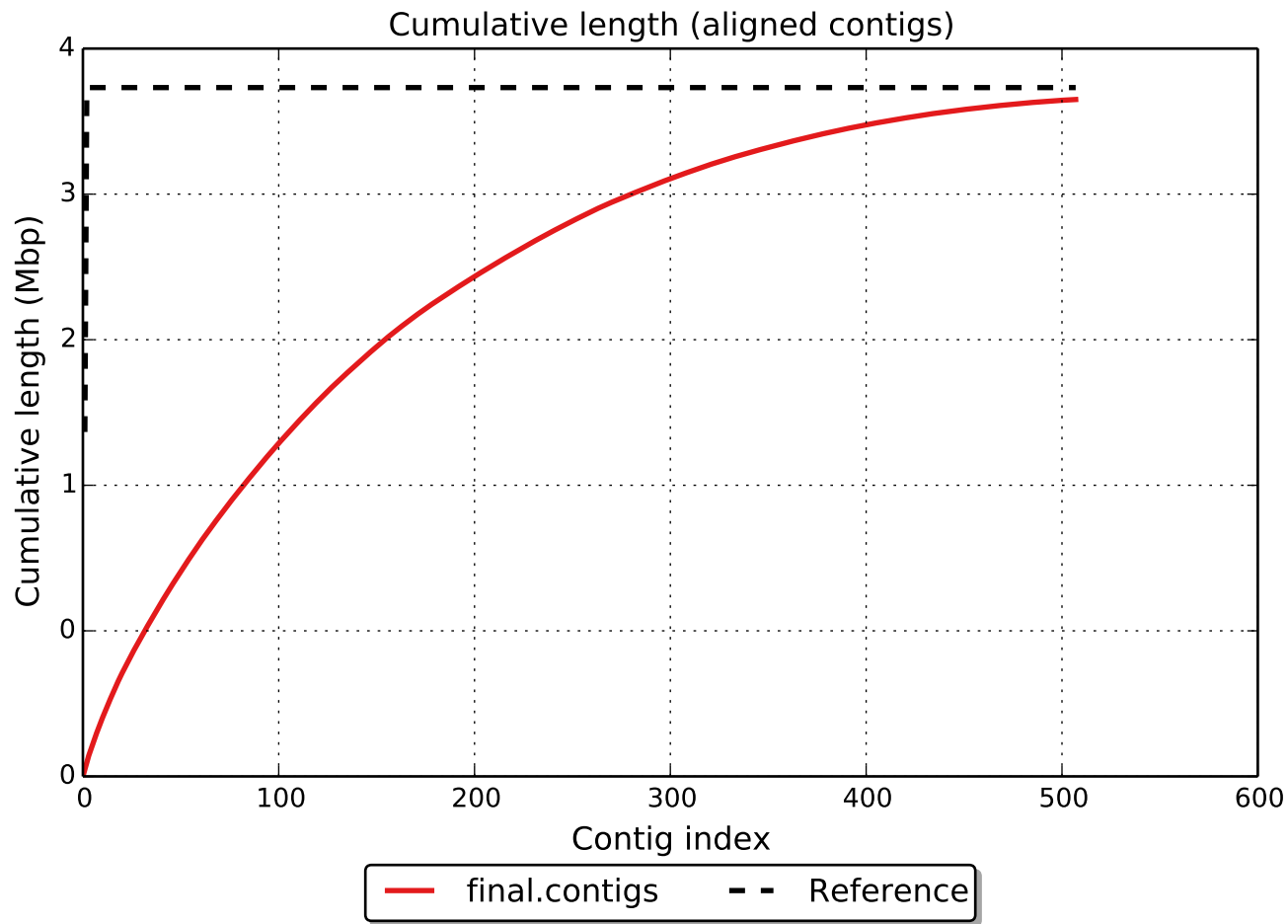




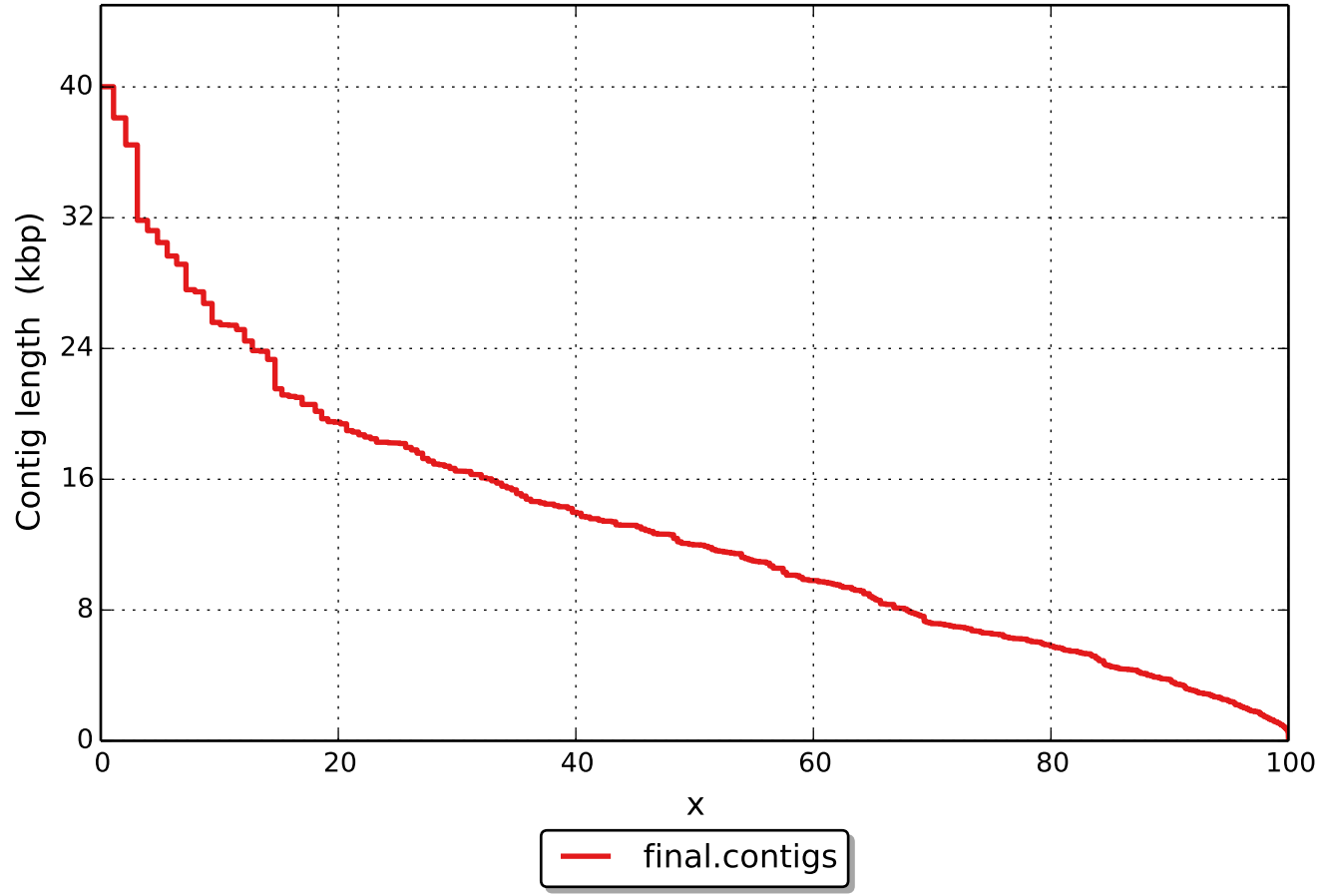
NGx







NAx



NGAx

