

Report

	final.contigs
# contigs (≥ 0 bp)	1703
# contigs (≥ 1000 bp)	1050
Total length (≥ 0 bp)	10948347
Total length (≥ 1000 bp)	10687616
# contigs	1208
Largest contig	61625
Total length	10797999
Reference length	11094646
GC (%)	50.39
Reference GC (%)	50.49
N50	15437
NG50	14590
N75	9016
NG75	8551
L50	216
LG50	226
L75	448
LG75	473
# misassemblies	4
# misassembled contigs	4
Misassembled contigs length	85153
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.498
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.55
# indels per 100 kbp	0.05
Largest alignment	61625
NA50	15397
NGA50	14577
NA75	8988
NGA75	8458
LA50	217
LGA50	227
LA75	449
LGA75	475

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

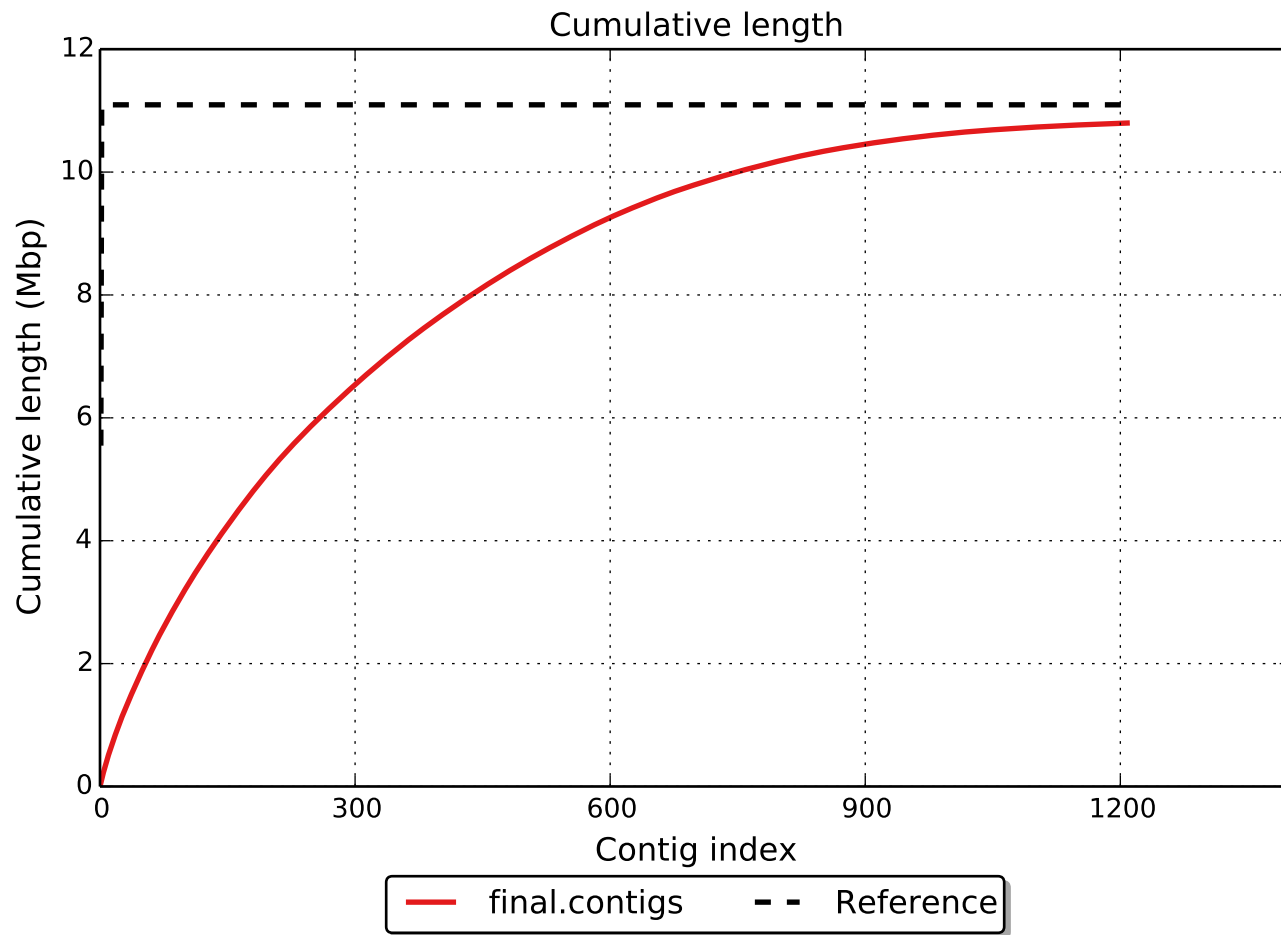
	final.contigs
# misassemblies	4
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	4
# possibly misassembled contigs	0
# misassembled contigs	4
Misassembled contigs length	85153
# local misassemblies	2
# mismatches	915
# indels	5
# short indels	4
# long indels	1
Indels length	10

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).

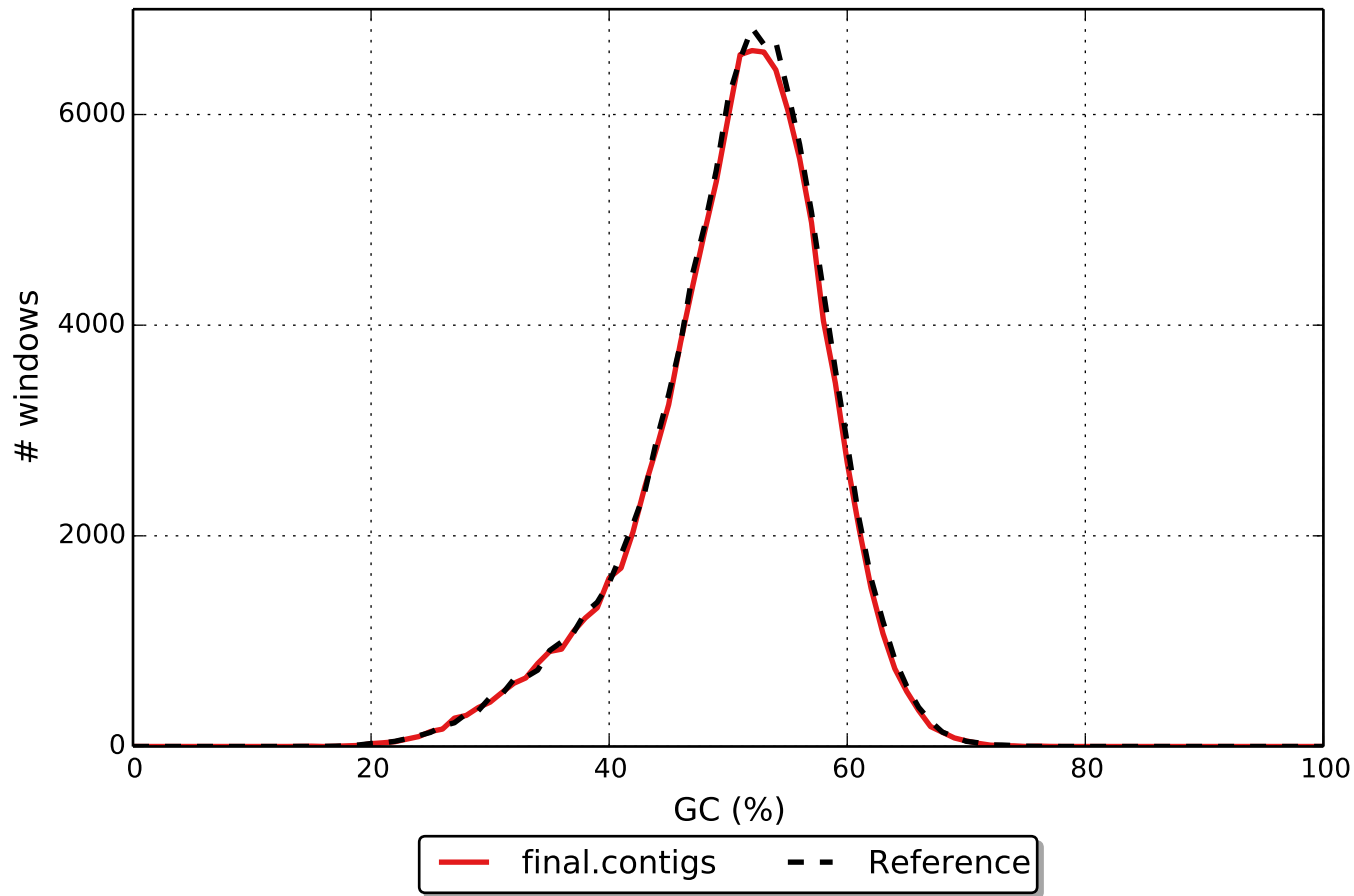
Unaligned report

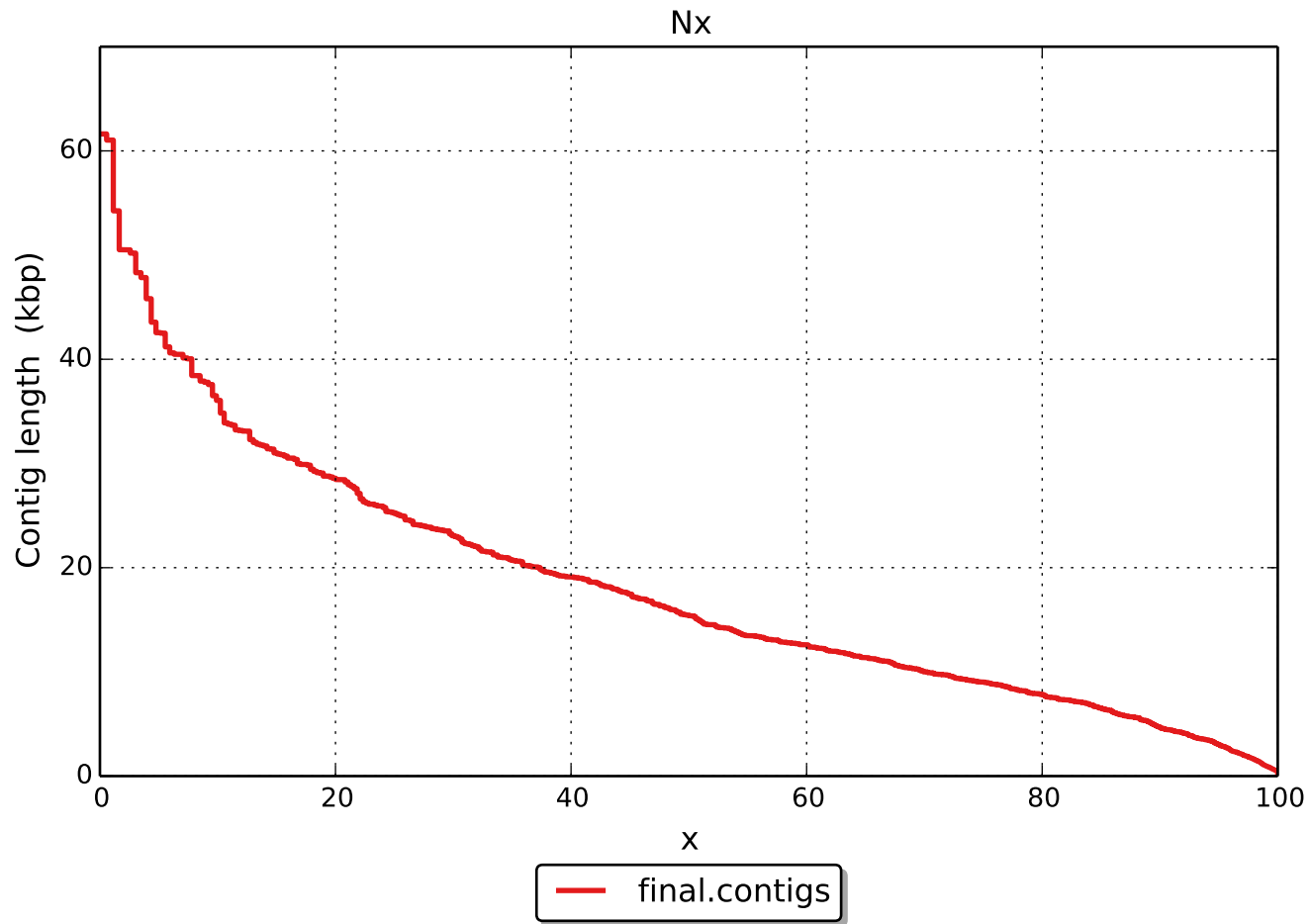
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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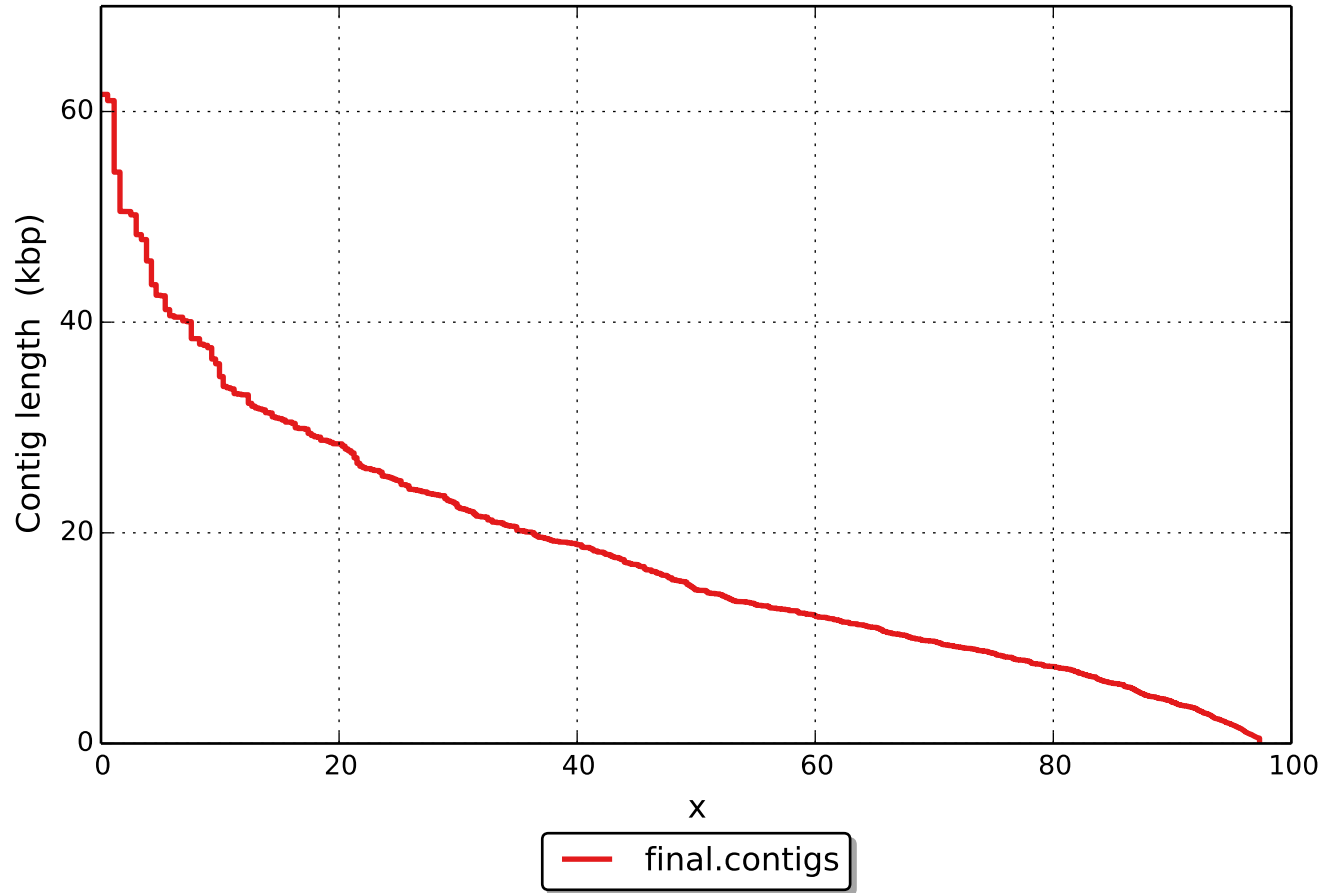


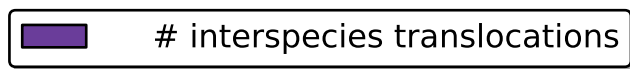
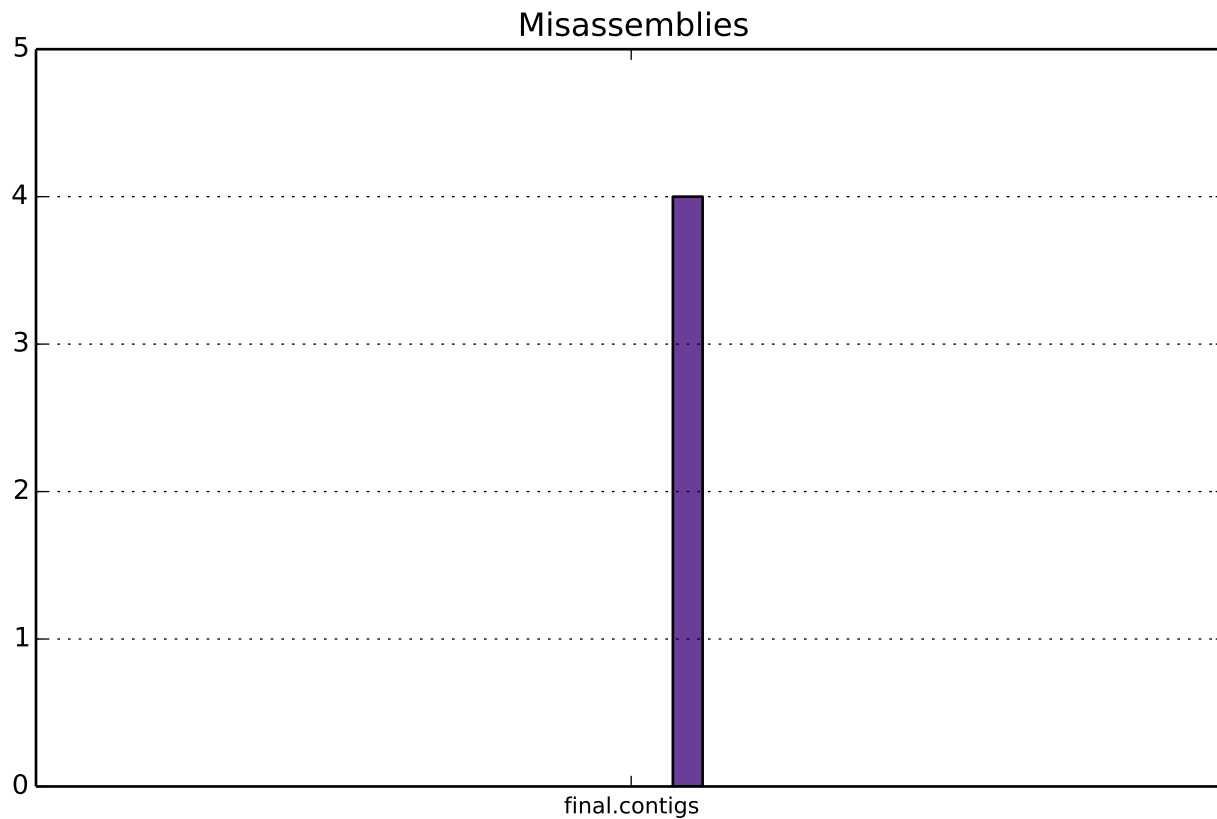
GC content

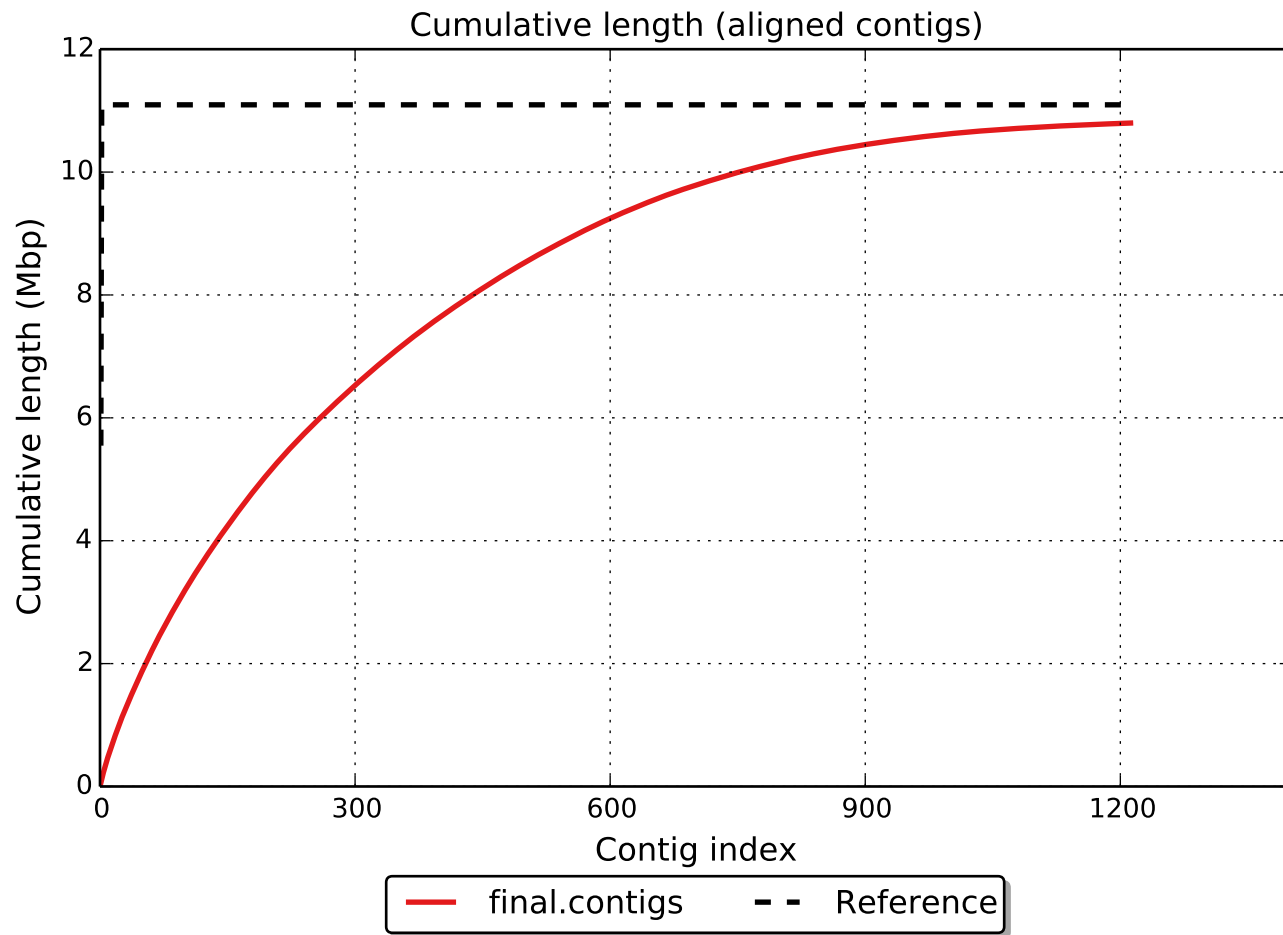




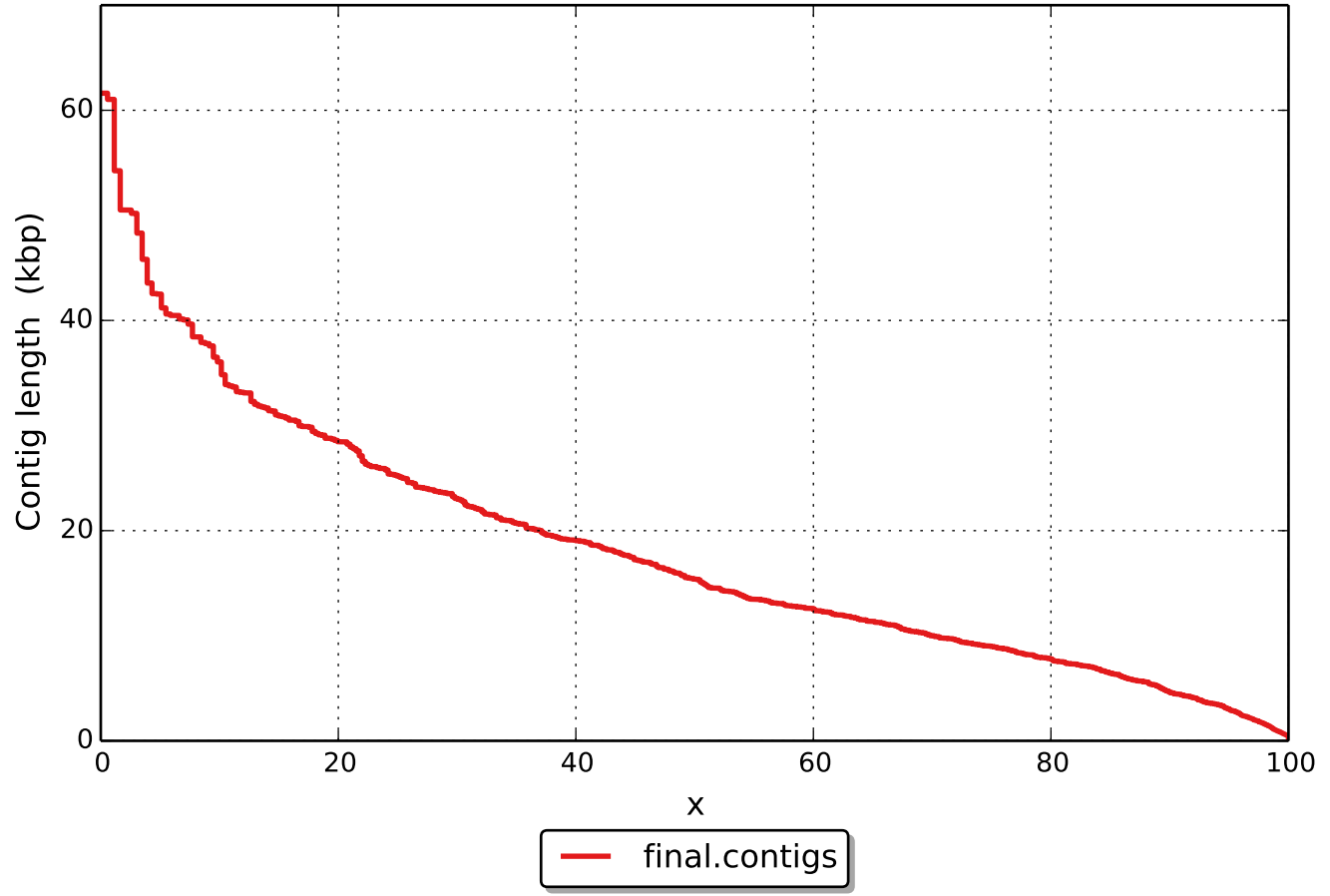
NGx







NAx



NGAx

