

Report

	final.contigs
# contigs (≥ 0 bp)	5200
# contigs (≥ 1000 bp)	1454
Total length (≥ 0 bp)	4690391
Total length (≥ 1000 bp)	2056543
# contigs	5200
Largest contig	4239
Total length	4690391
Reference length	5547323
GC (%)	50.46
Reference GC (%)	50.48
N50	933
NG50	836
N75	692
NG75	589
L50	1753
LG50	2239
L75	3219
LG75	4225
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	36
Genome fraction (%)	79.376
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	233.49
# indels per 100 kbp	0.14
Largest alignment	4239
NA50	933
NGA50	836
NA75	692
NGA75	589
LA50	1753
LGA50	2239
LA75	3219
LGA75	4226

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

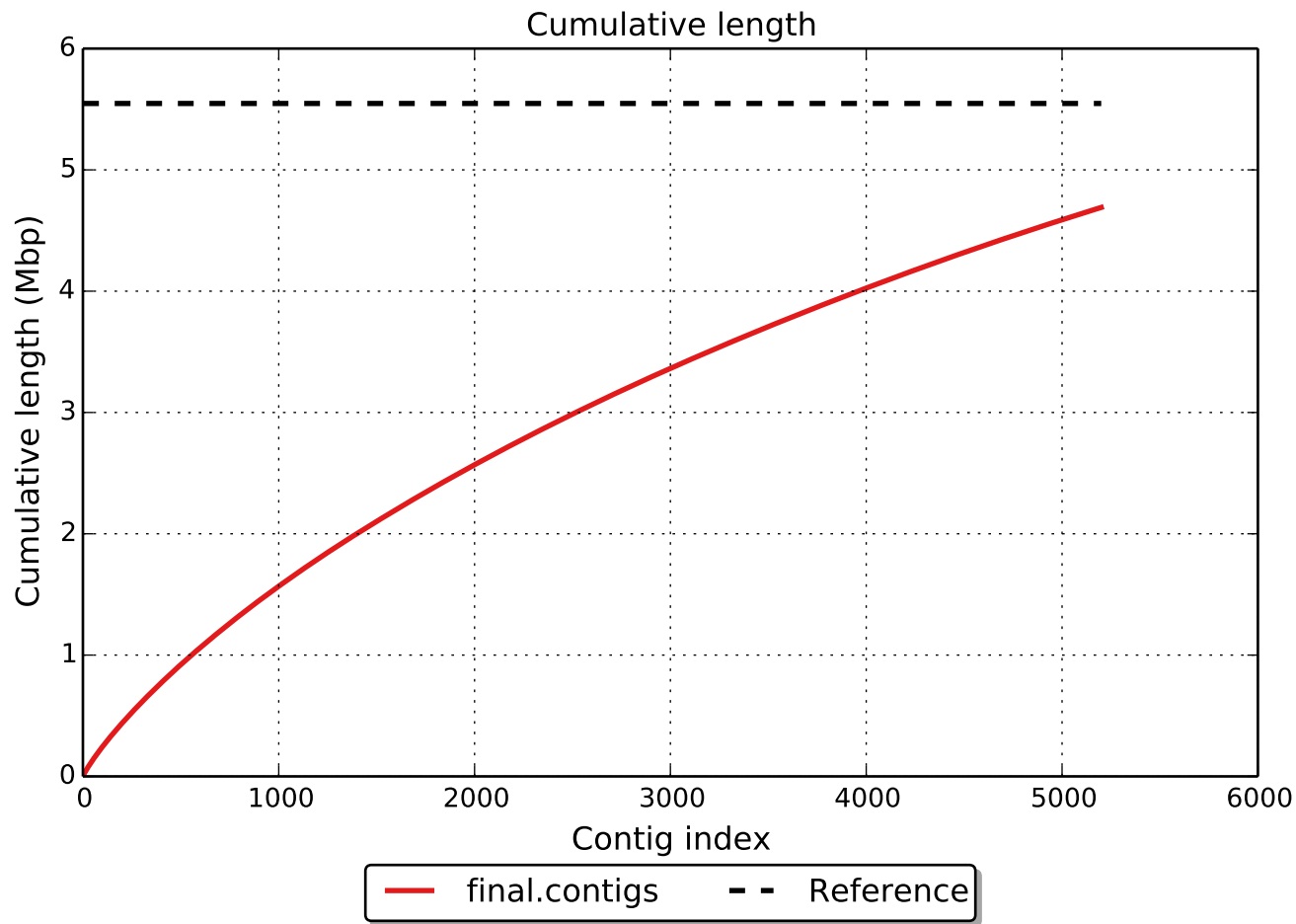
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	788
# local misassemblies	0
# mismatches	10281
# indels	6
# short indels	6
# long indels	0
Indels length	6

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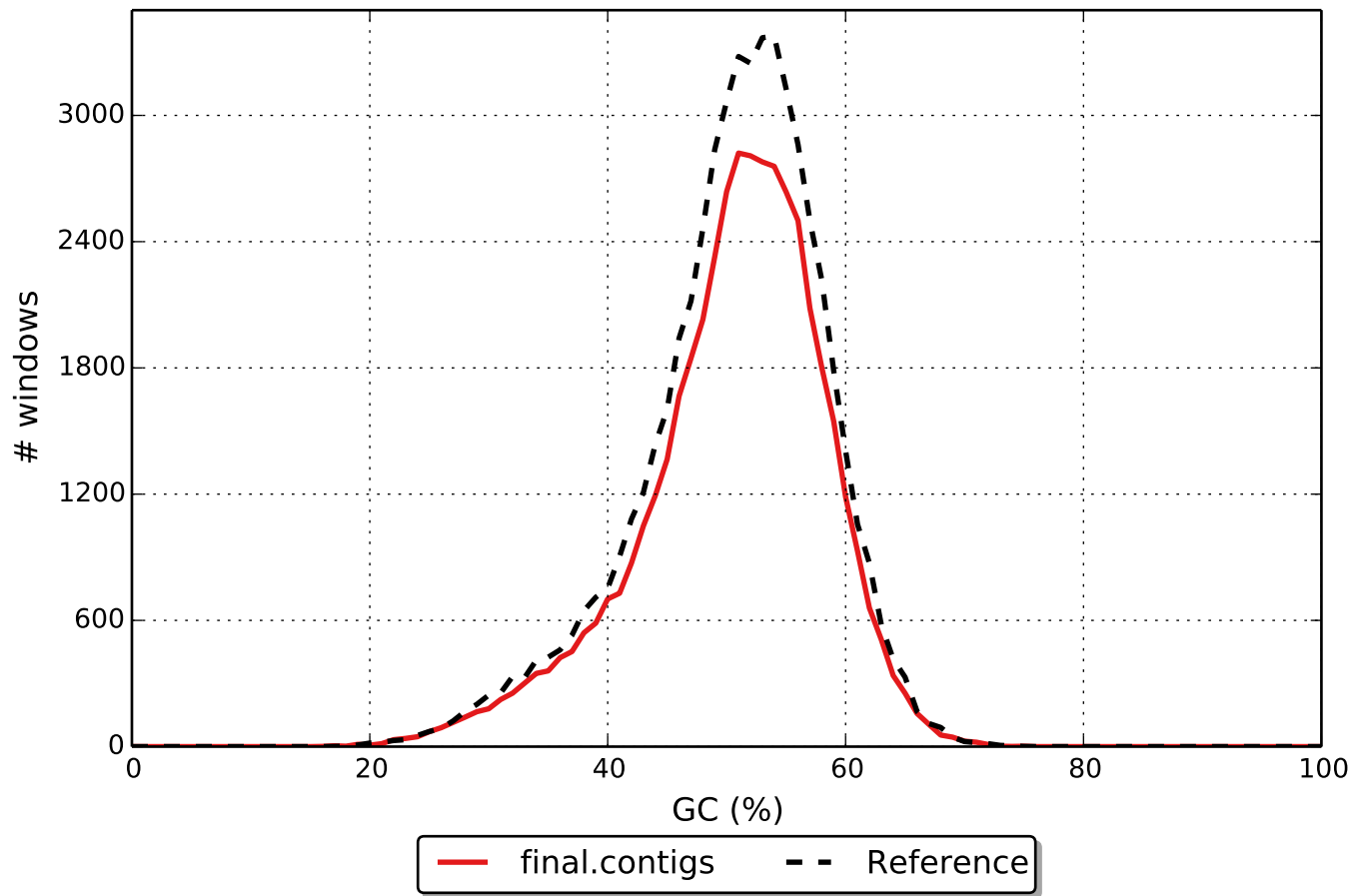
Unaligned report

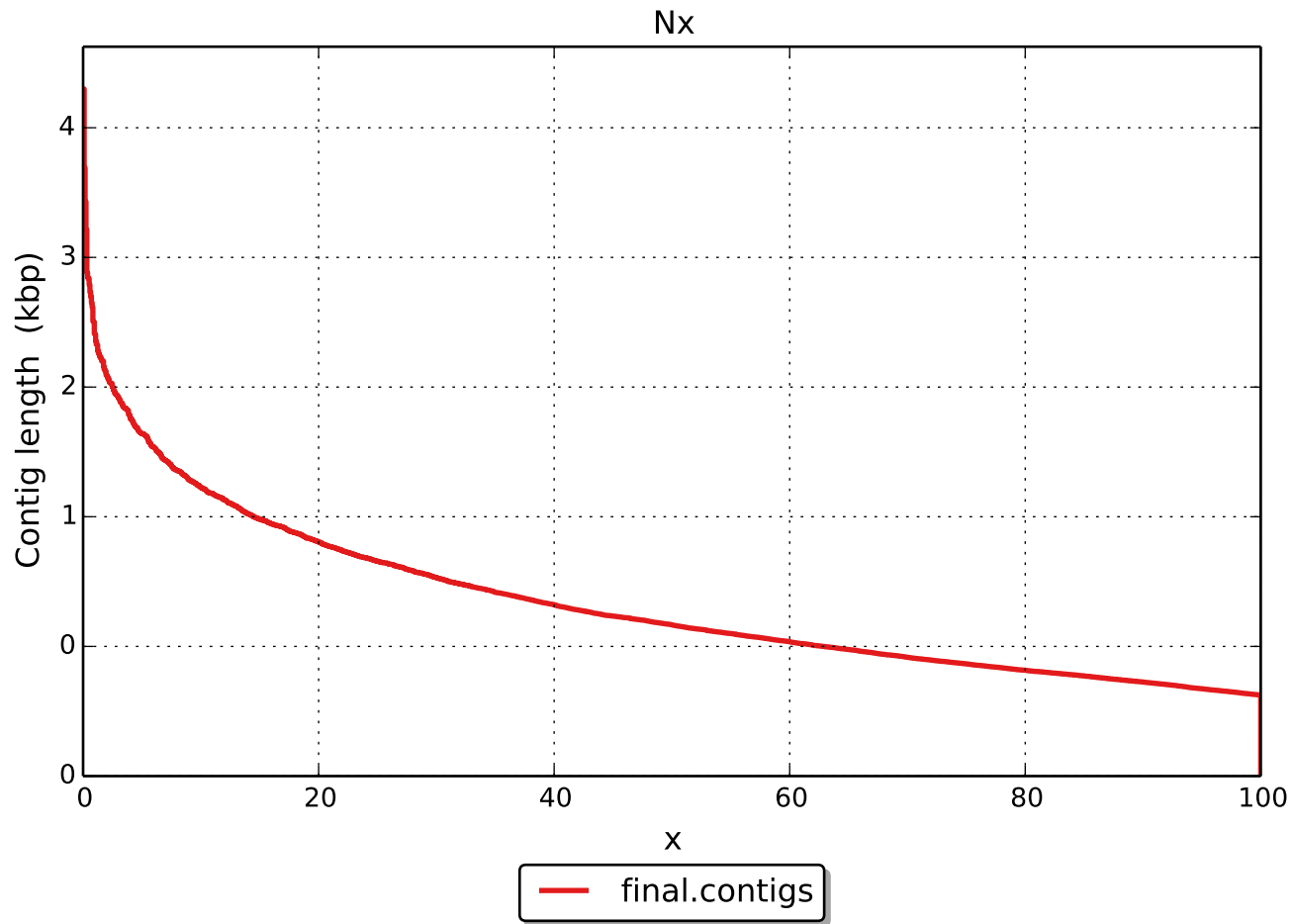
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	36
# N's	0

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).

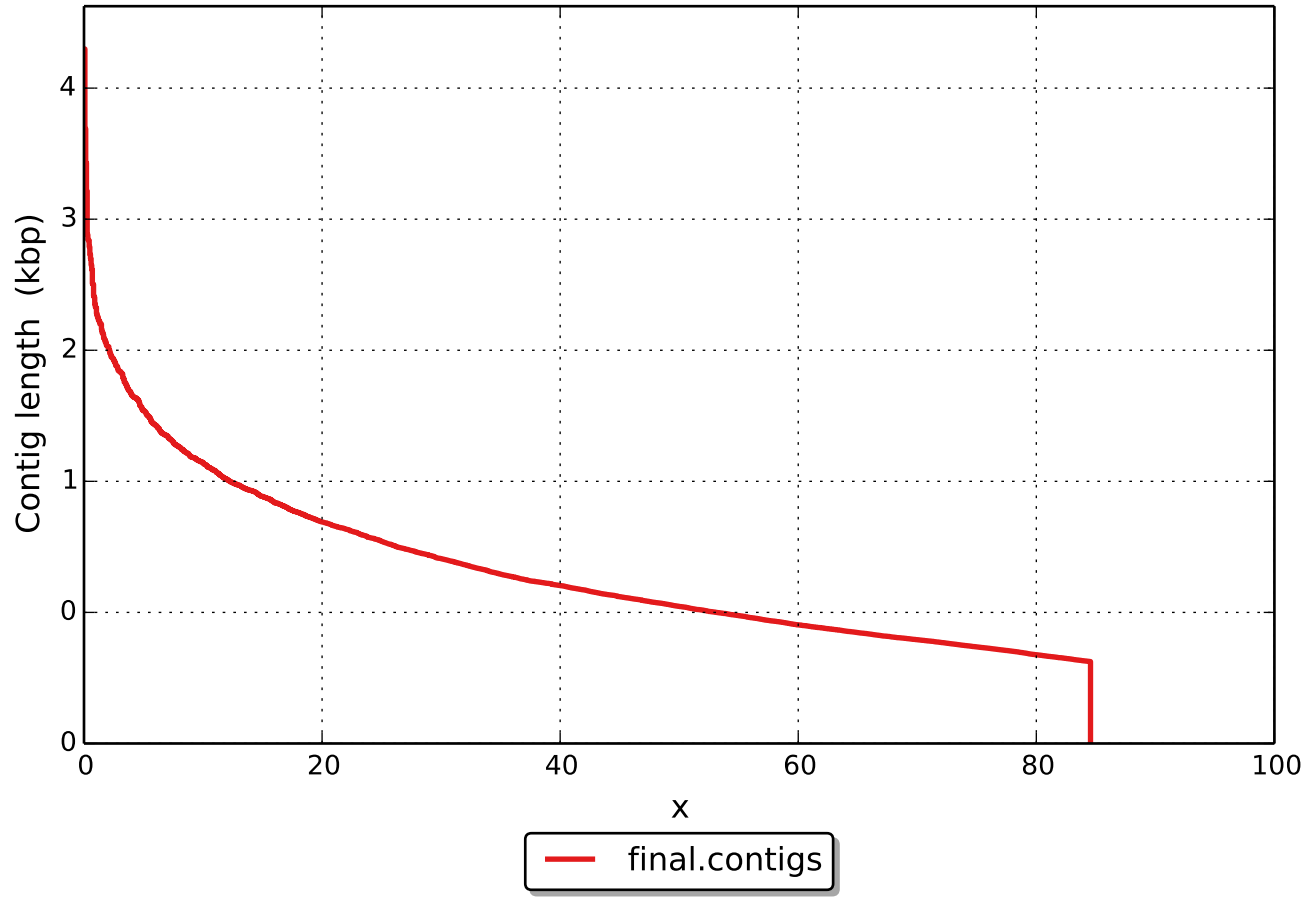


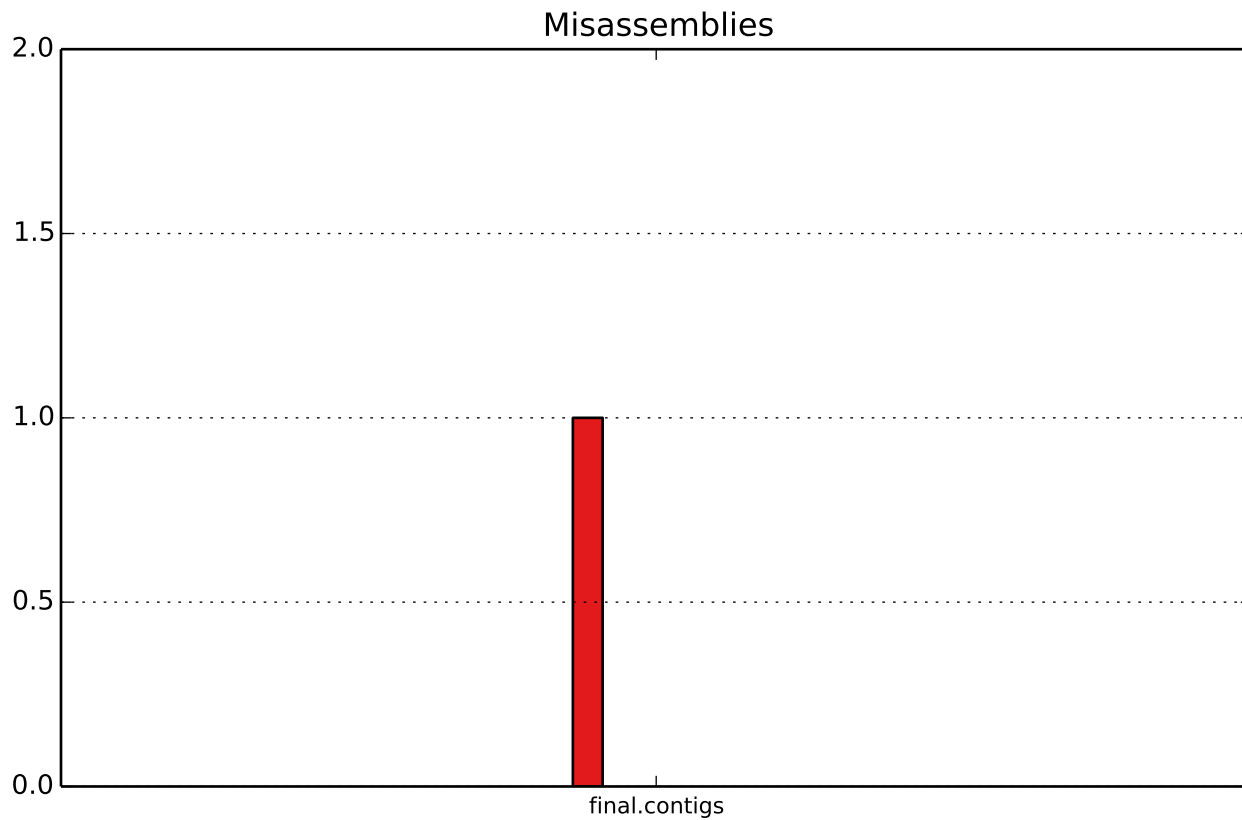
GC content

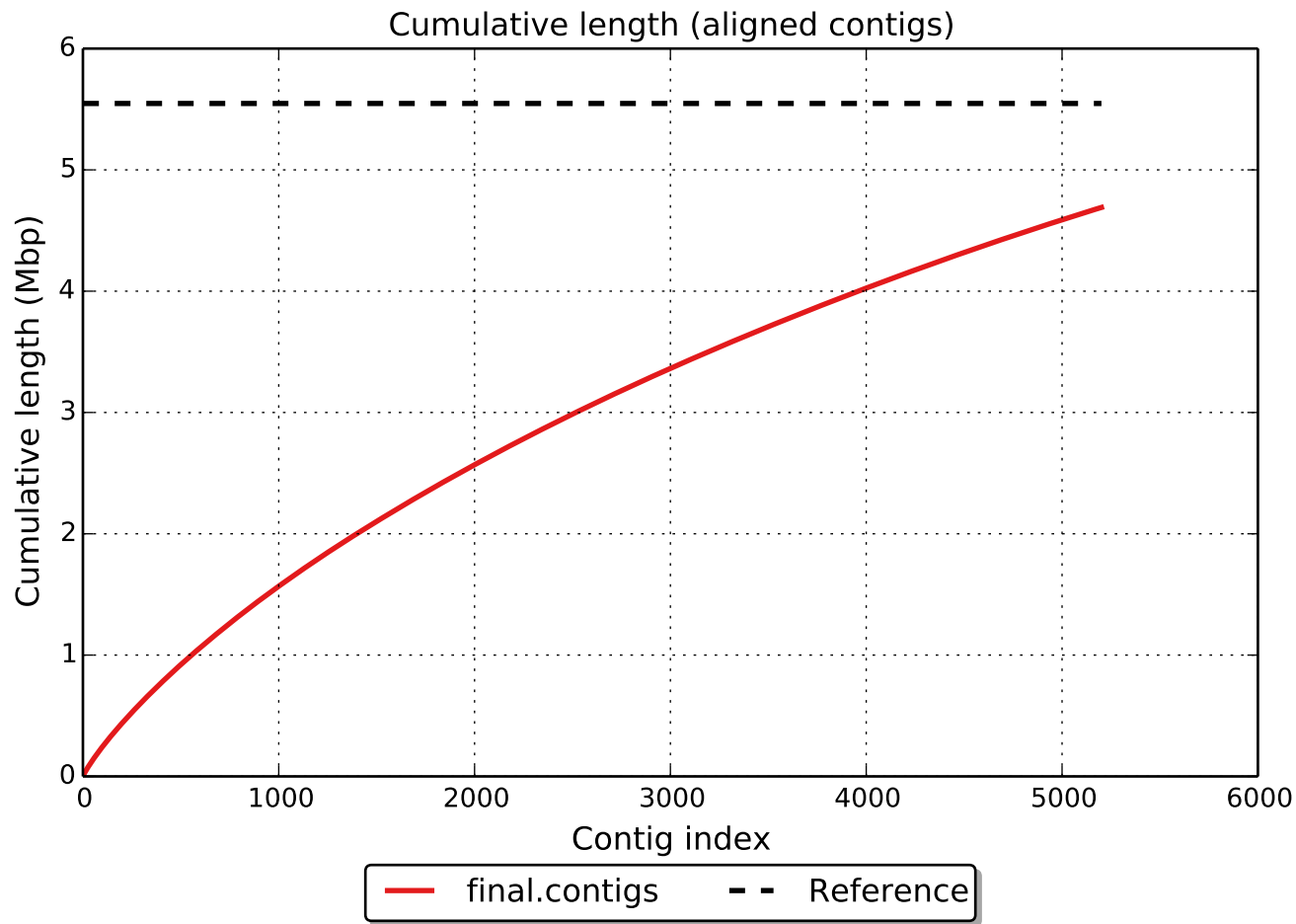




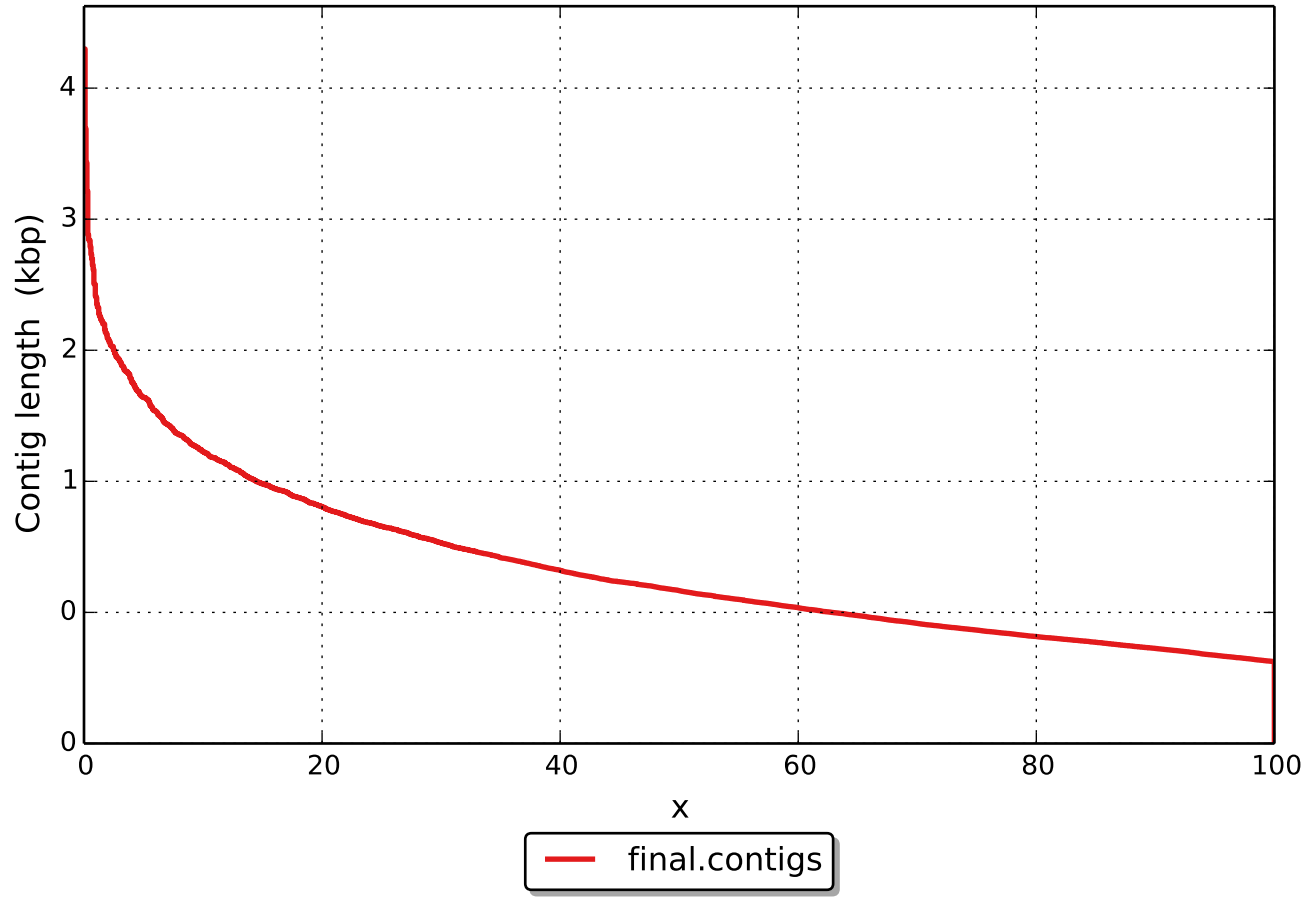
NGx







NAx



NGAx

