

Report

	final.contigs
# contigs (≥ 0 bp)	1516
# contigs (≥ 1000 bp)	1055
Total length (≥ 0 bp)	3801198
Total length (≥ 1000 bp)	3542742
# contigs	1312
Largest contig	15927
Total length	3735255
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.26
N50	4200
NG50	4118
N75	2277
NG75	2216
L50	284
LG50	290
L75	584
LG75	601
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6315
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.974
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.77
# indels per 100 kbp	0.00
Largest alignment	15927
NA50	4200
NGA50	4118
NA75	2277
NGA75	2216
LA50	284
LGA50	290
LA75	584
LGA75	601

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

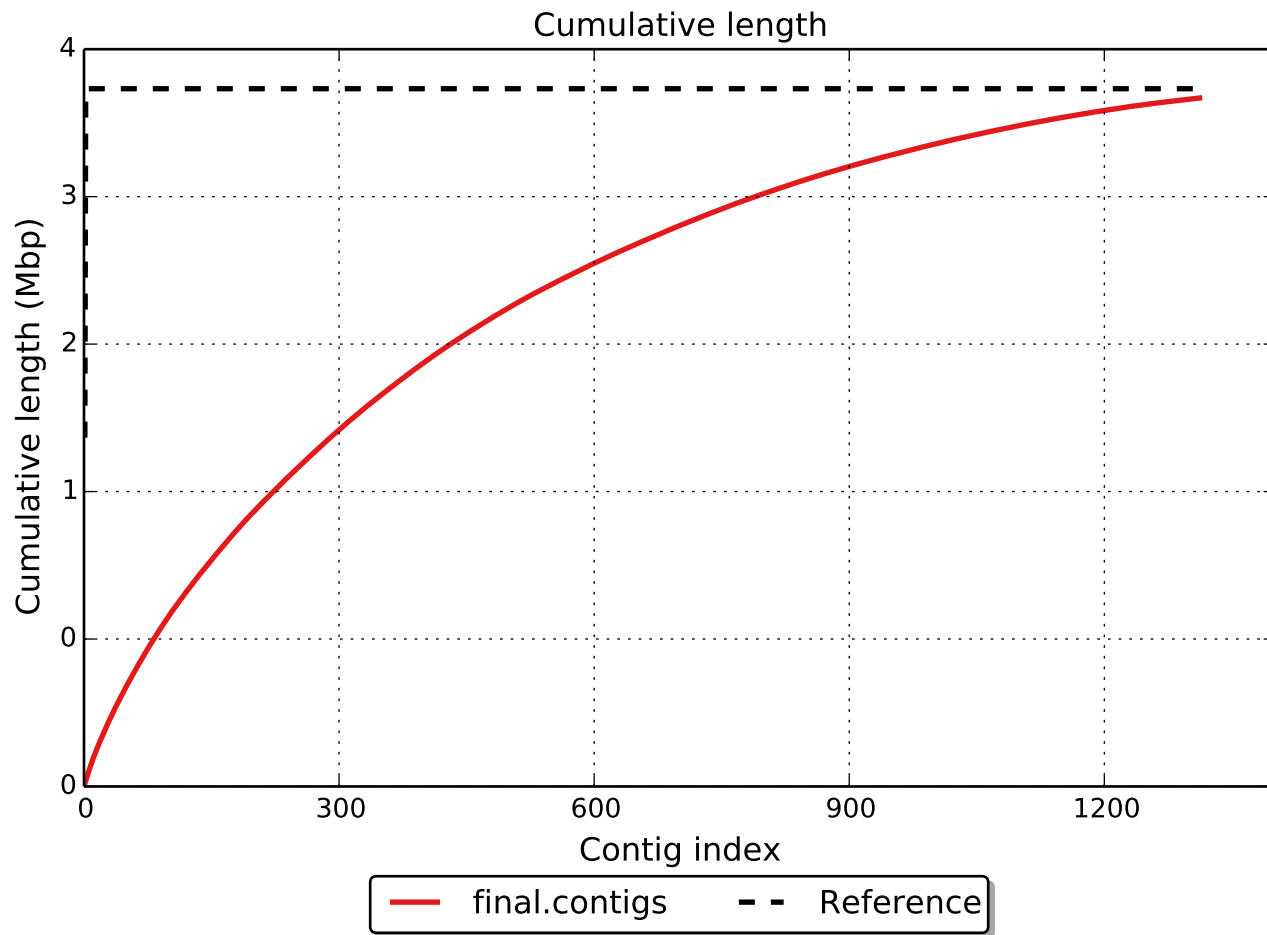
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	6315
# local misassemblies	0
# mismatches	1227
# indels	0
# short indels	0
# long indels	0
Indels length	0

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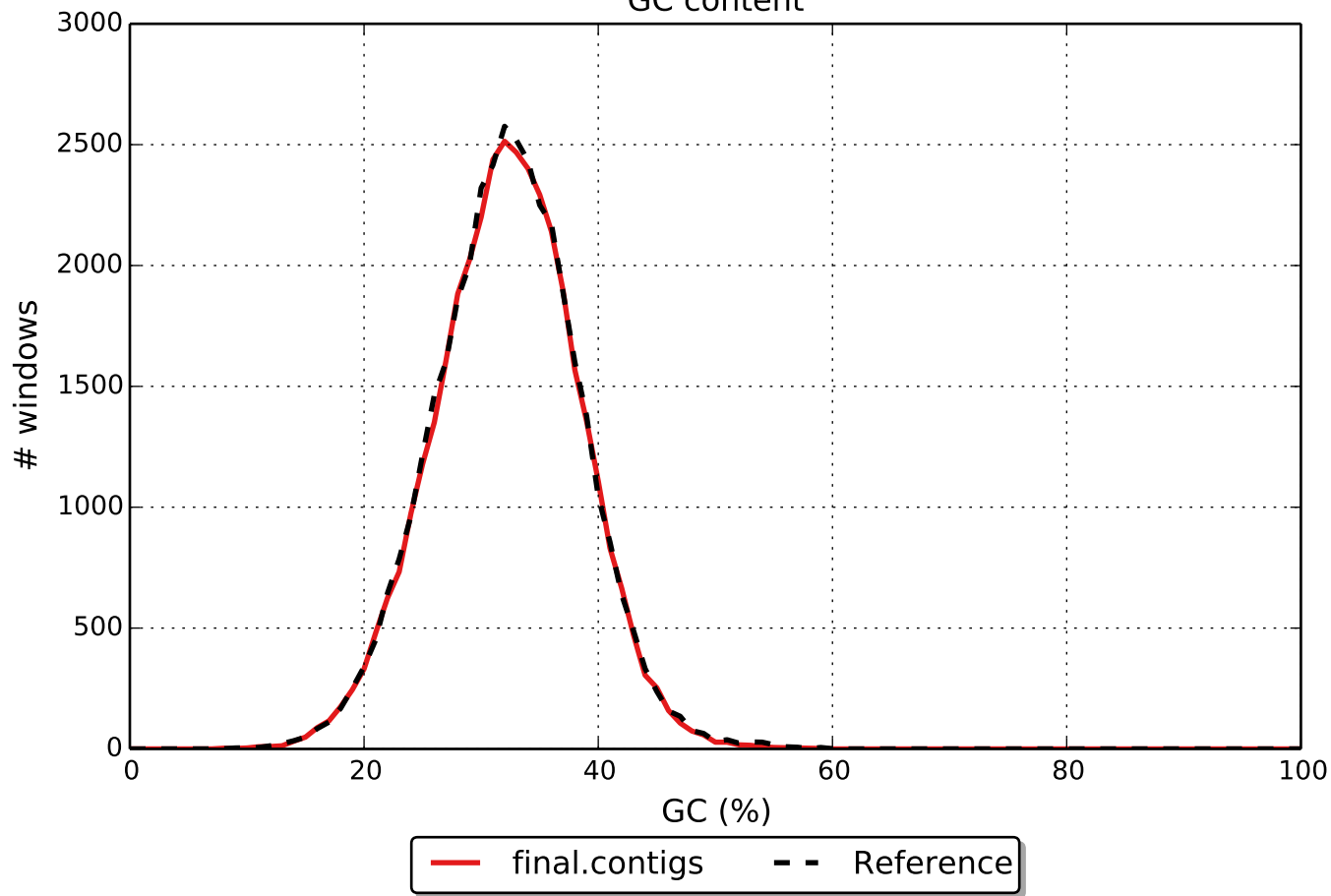
Unaligned report

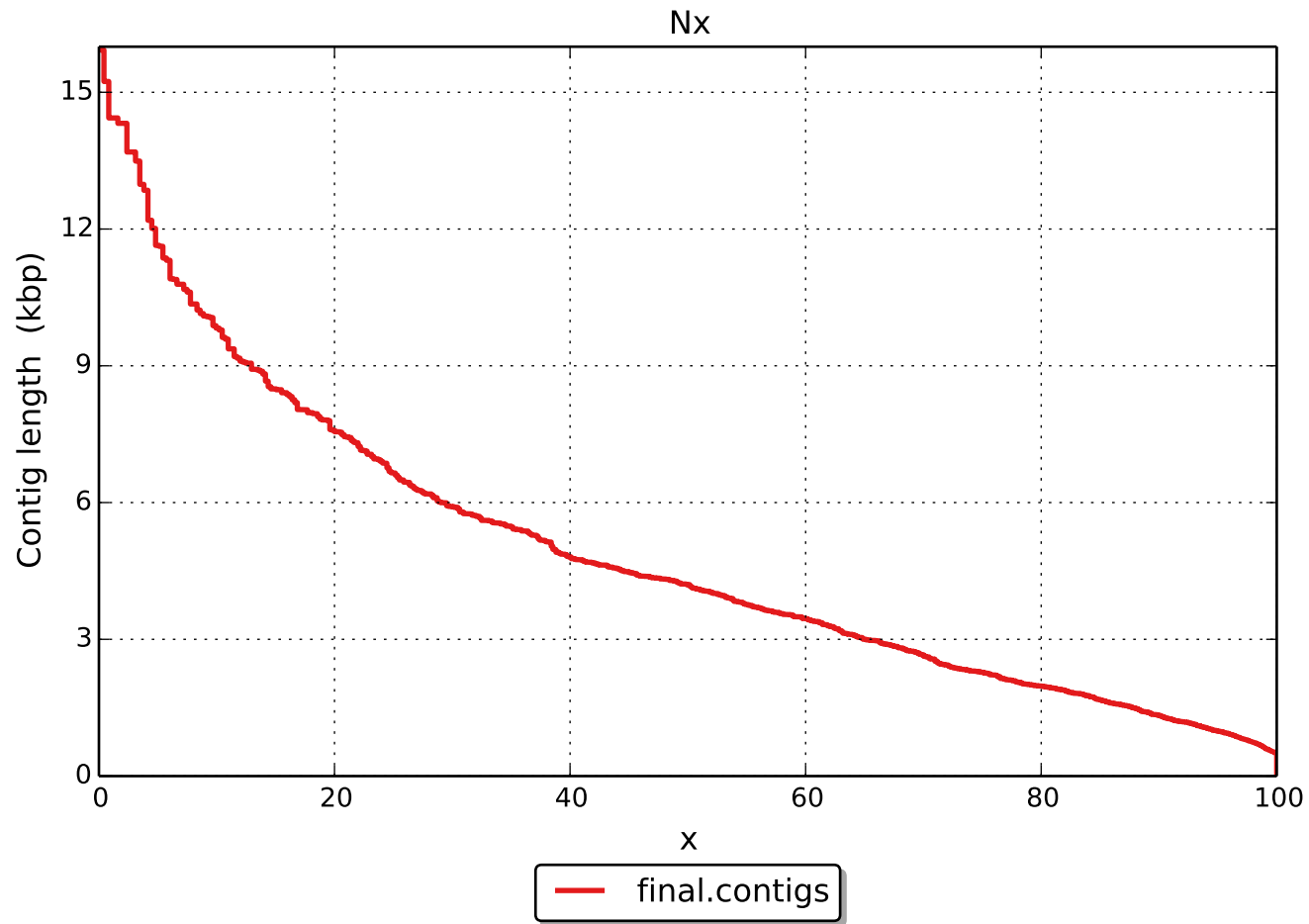
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

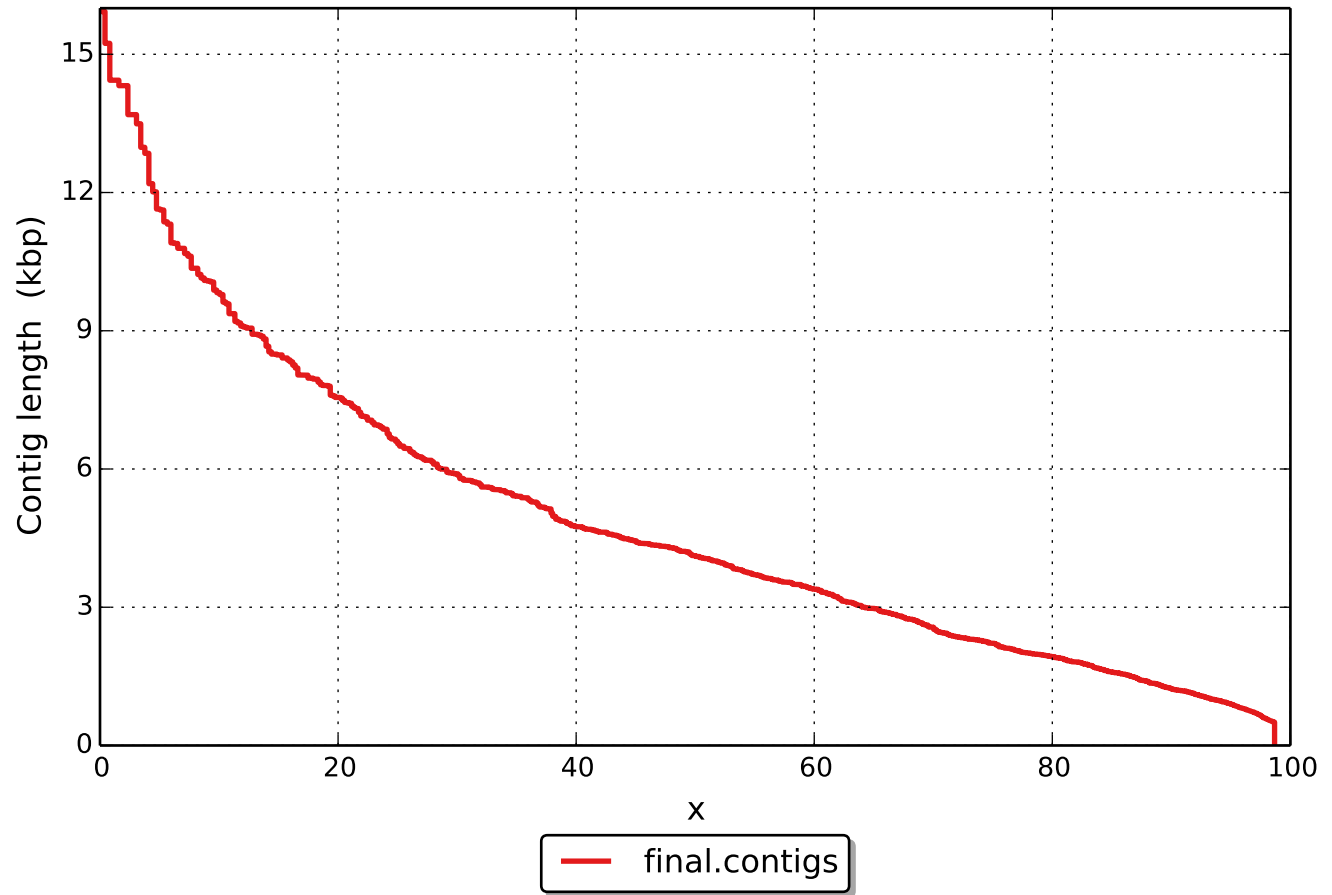


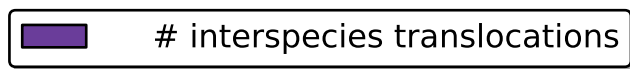
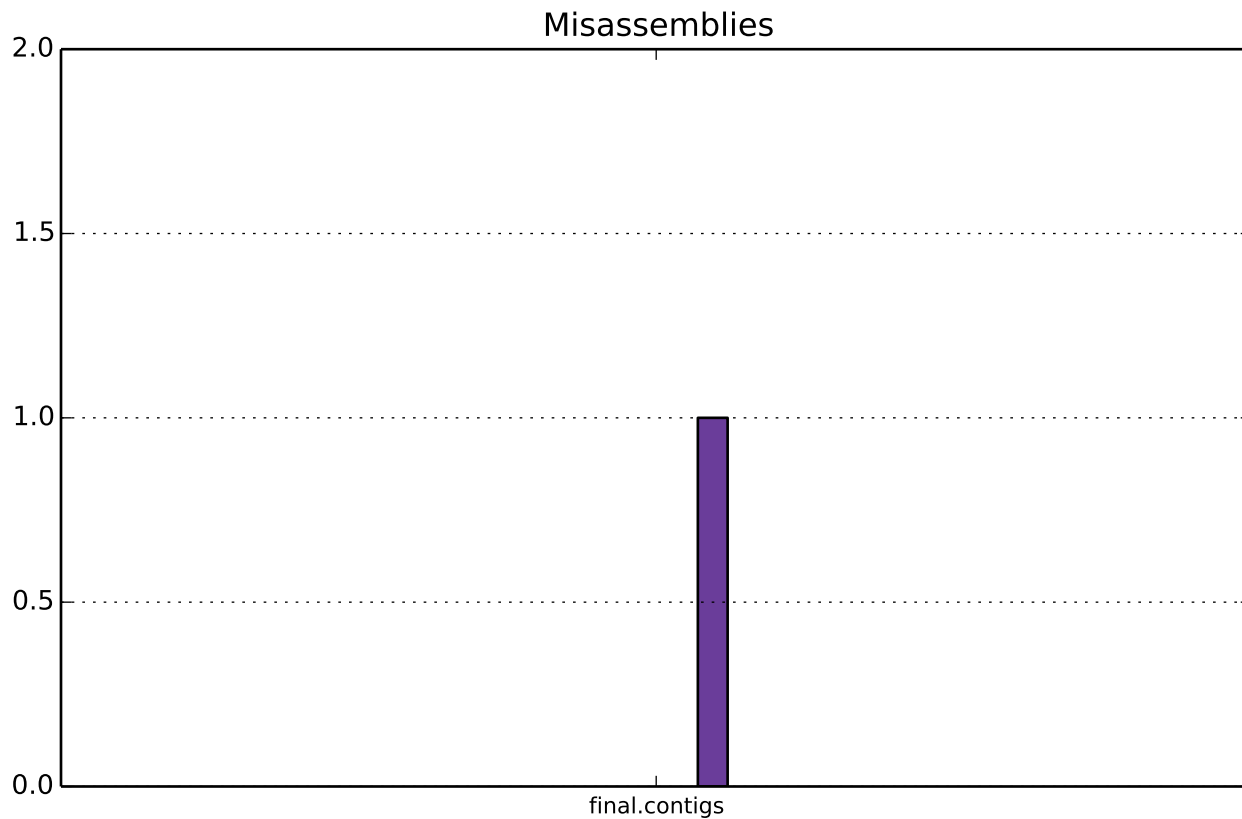
GC content

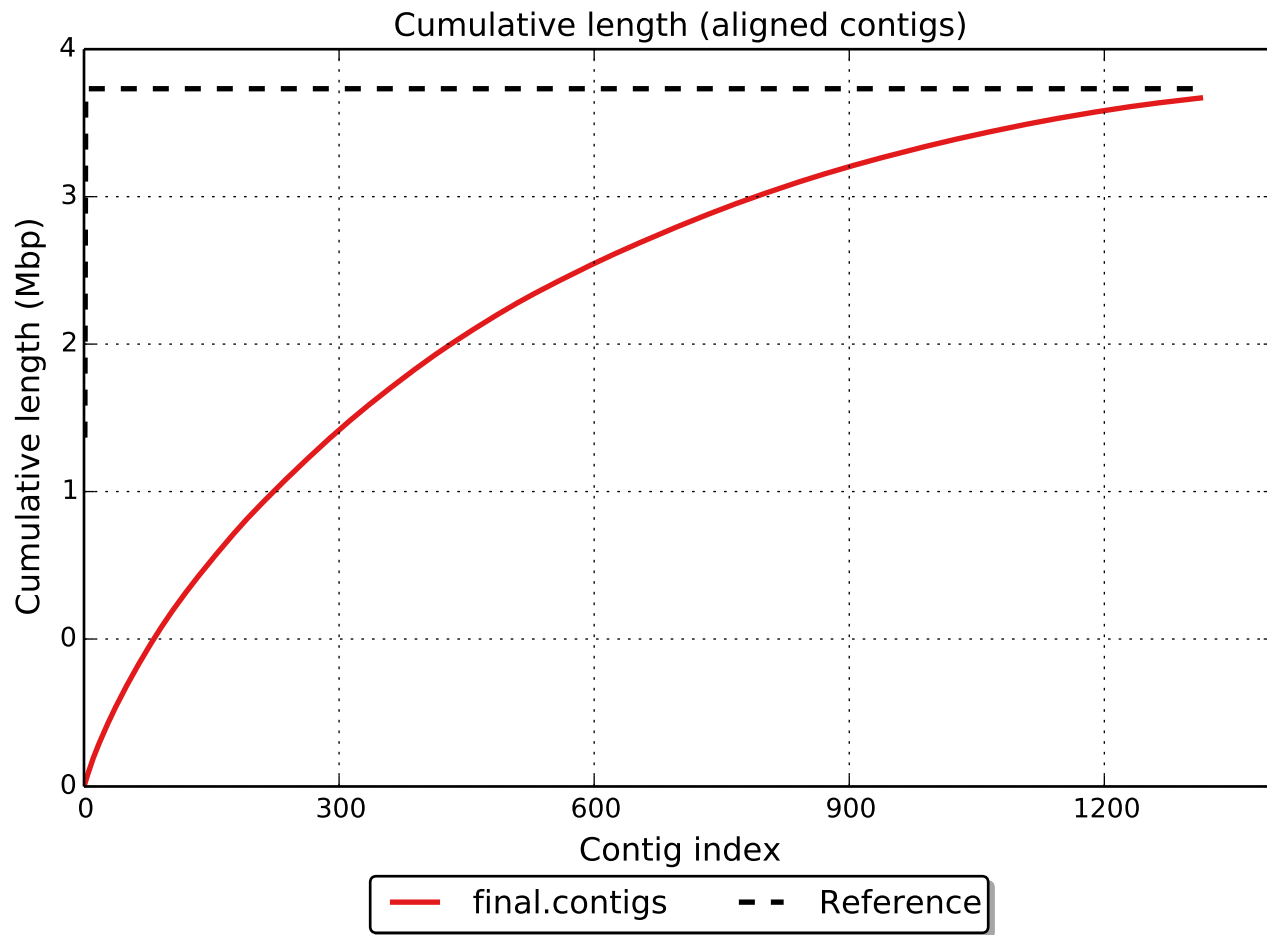


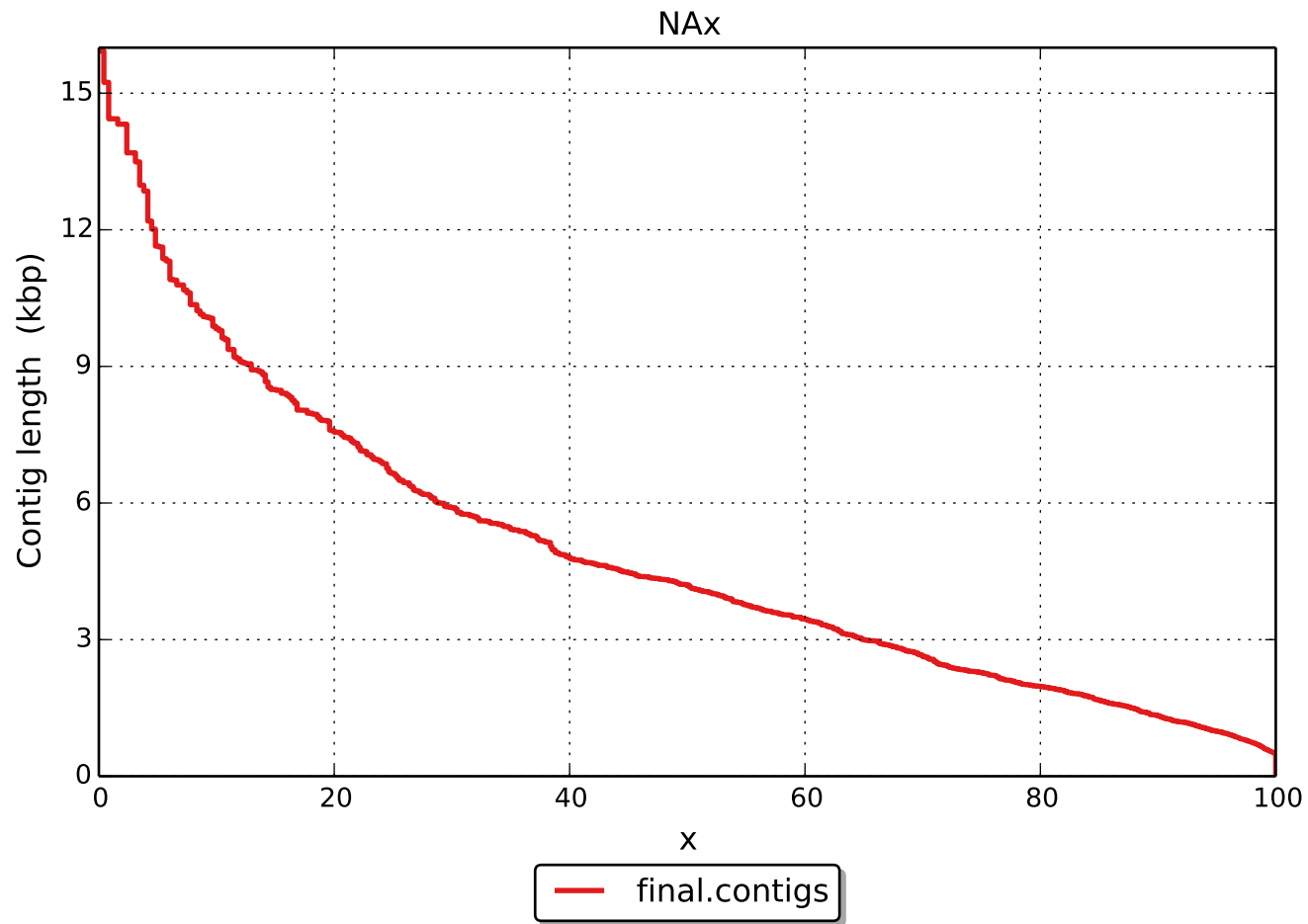


NGx









NGAx

