

Report

	final.contigs
# contigs (≥ 0 bp)	960
# contigs (≥ 1000 bp)	395
Total length (≥ 0 bp)	1125369
Total length (≥ 1000 bp)	730492
# contigs	960
Largest contig	5595
Total length	1125369
Reference length	615980
GC (%)	25.42
Reference GC (%)	25.35
N50	1358
NG50	2130
N75	829
NG75	1676
L50	253
LG50	104
L75	520
LG75	186
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	8535
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.789
Duplication ratio	1.969
# N's per 100 kbp	0.00
# mismatches per 100 kbp	936.38
# indels per 100 kbp	0.35
Largest alignment	5595
NA50	772
NGA50	1449
NGA75	969
LA50	386
LGA50	137
LGA75	270

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

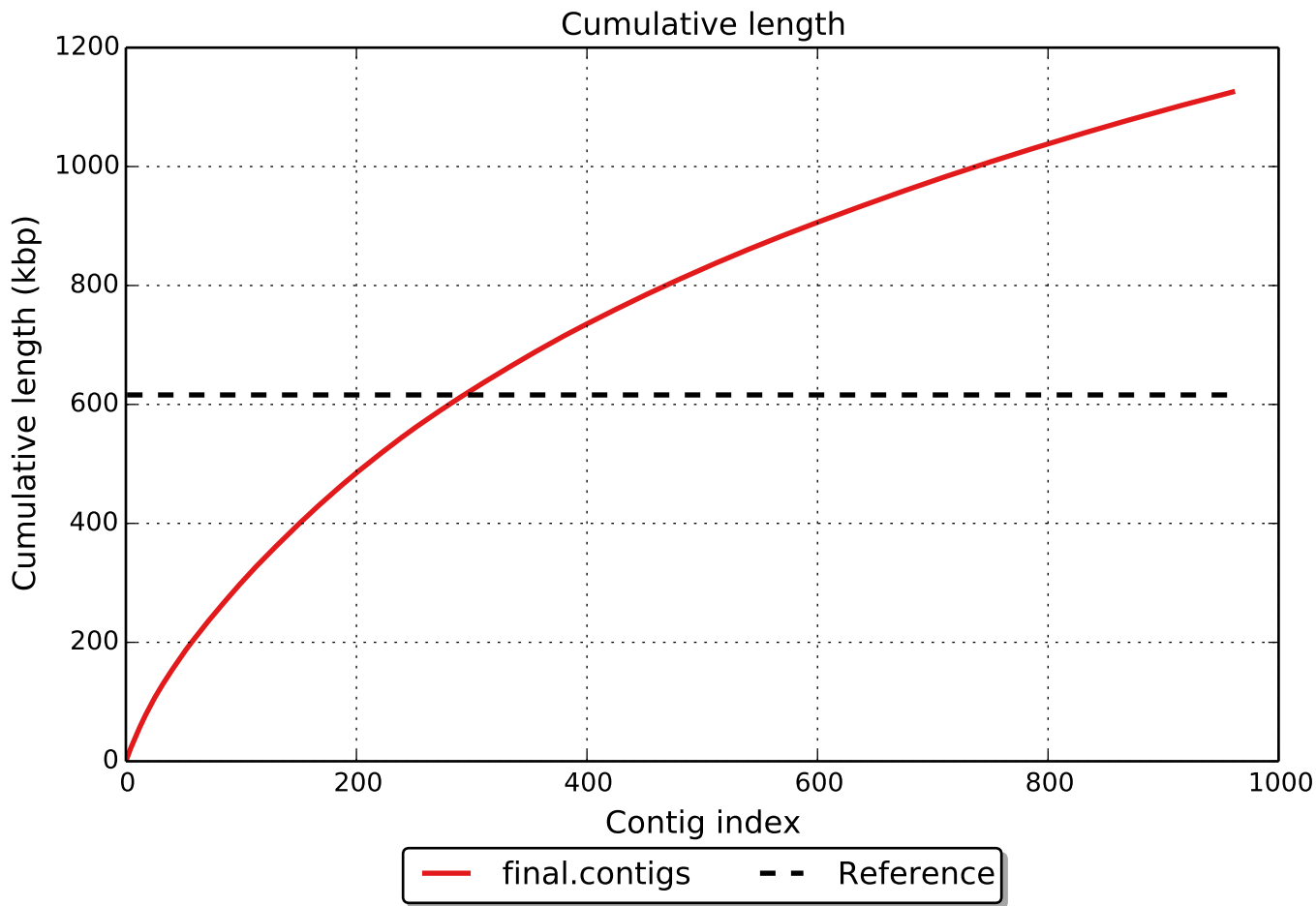
	final.contigs
# misassemblies	9
# relocations	9
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	9
Misassembled contigs length	8535
# local misassemblies	0
# mismatches	5352
# indels	2
# short indels	2
# long indels	0
Indels length	2

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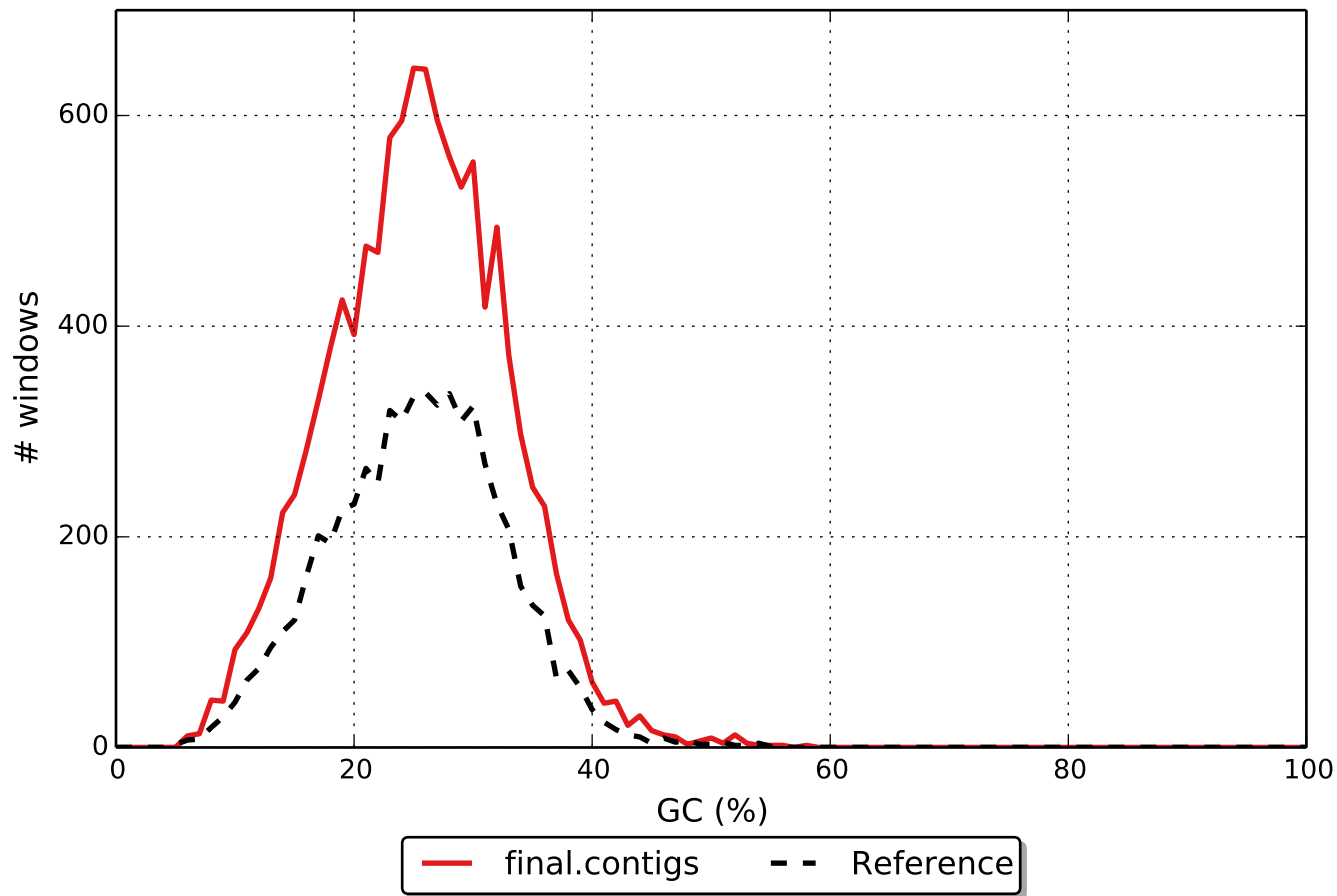
Unaligned report

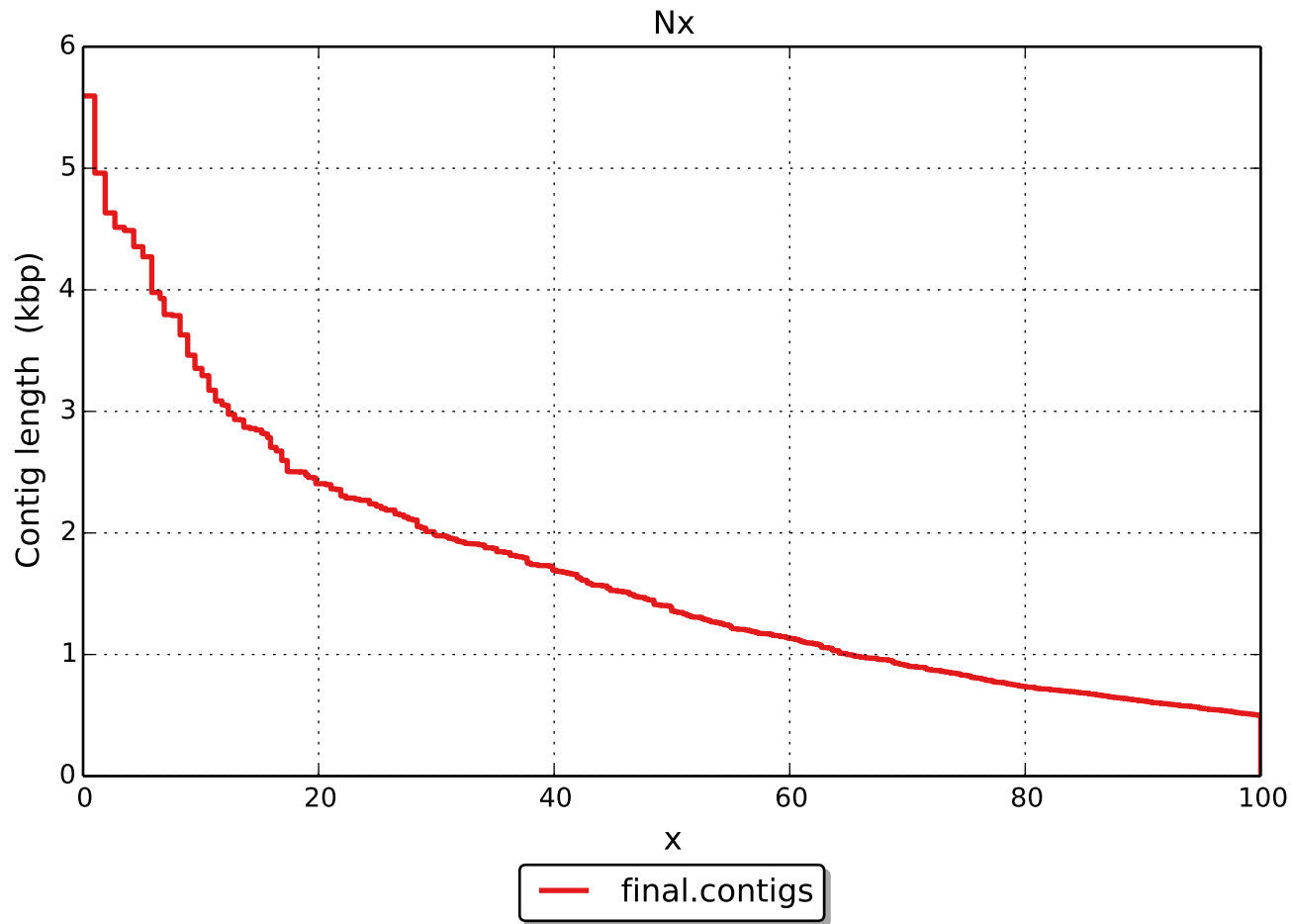
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

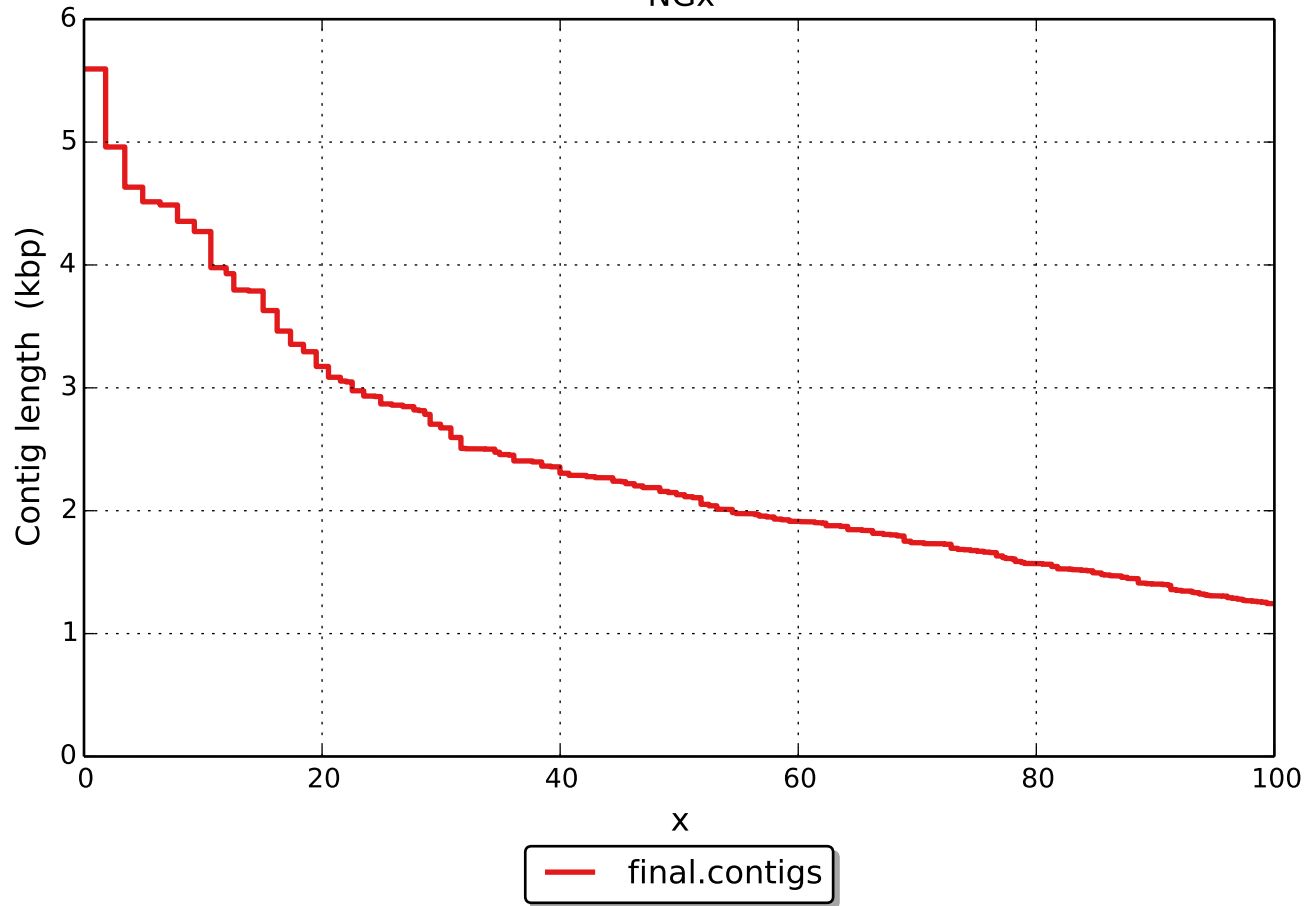


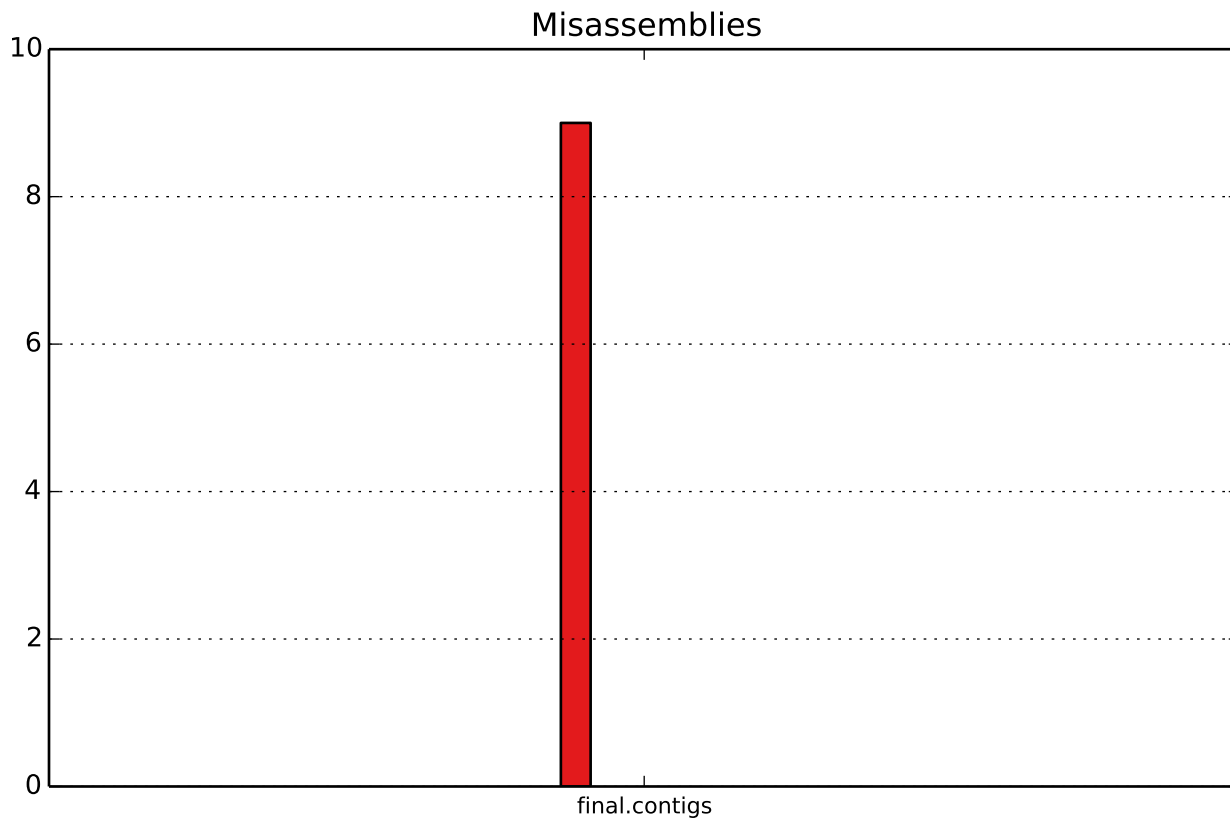
GC content

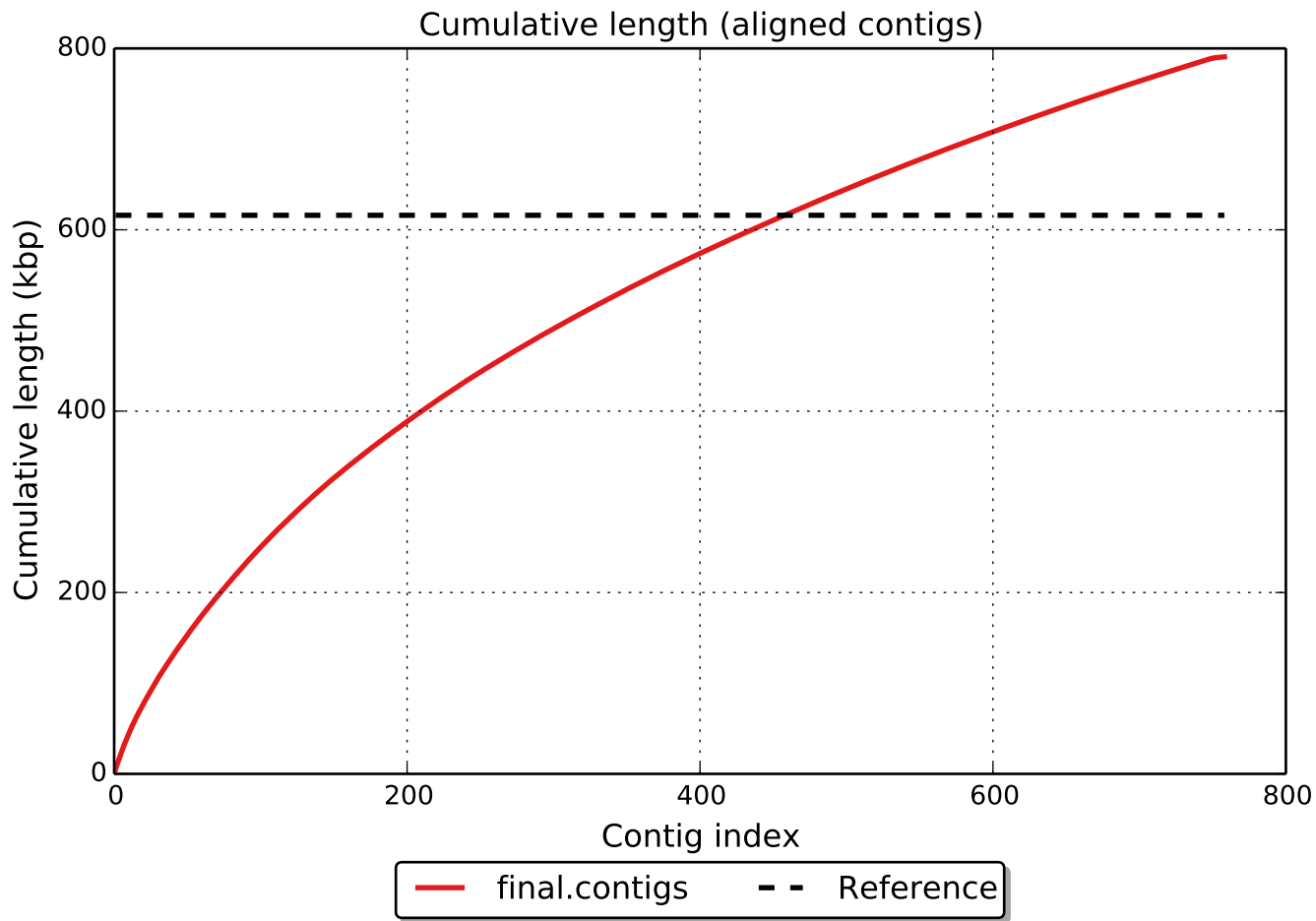


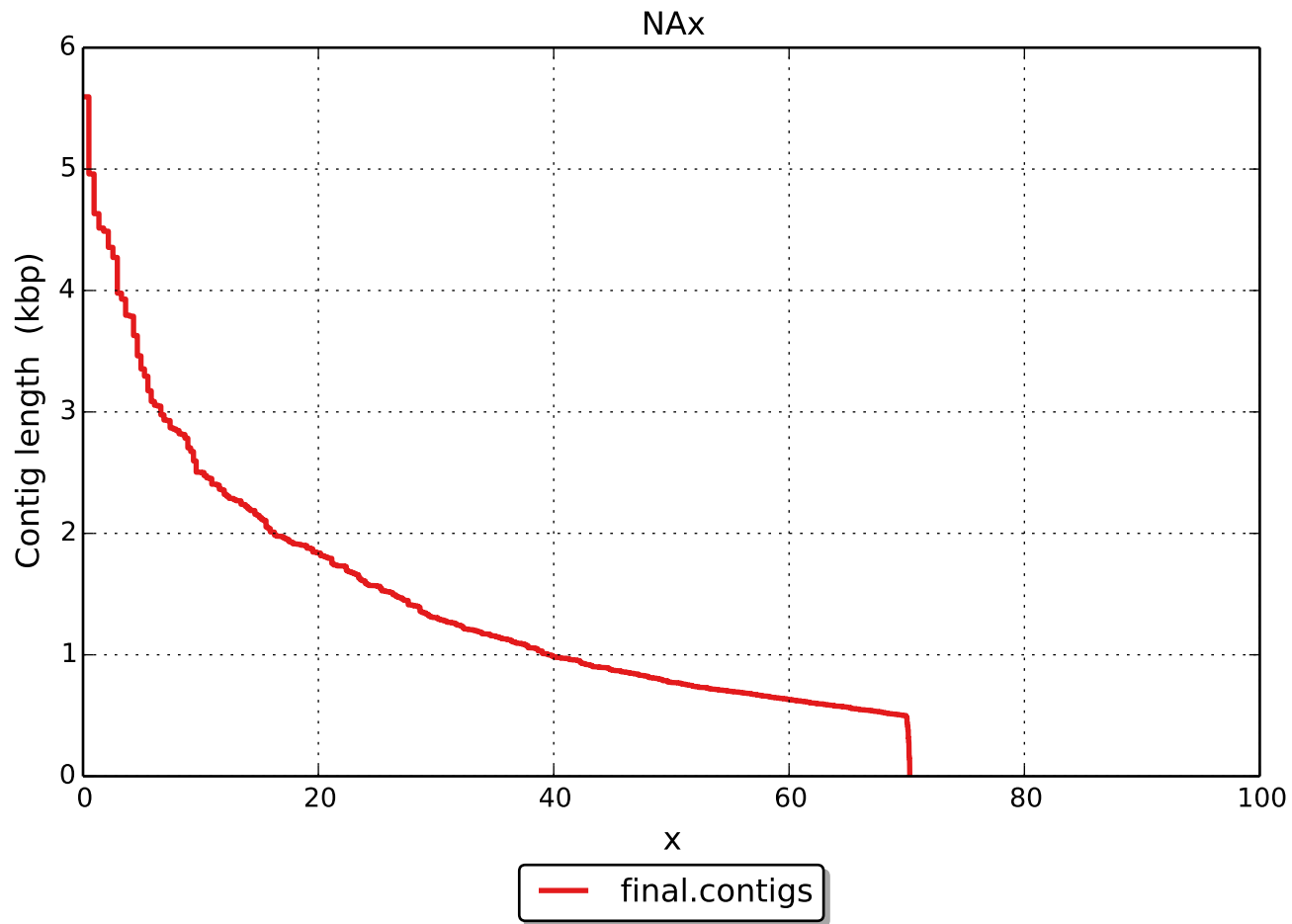


NGx









NGAx

