

Report

	final.contigs
# contigs (≥ 0 bp)	1082
# contigs (≥ 1000 bp)	522
Total length (≥ 0 bp)	10903304
Total length (≥ 1000 bp)	10700615
# contigs	617
Largest contig	168092
Total length	10764388
Reference length	11094646
GC (%)	50.40
Reference GC (%)	50.48
N50	40236
NG50	39095
N75	21021
NG75	20040
L50	83
LG50	87
L75	175
LG75	187
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	16523
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.659
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.11
# indels per 100 kbp	0.35
Largest alignment	168092
NA50	40236
NGA50	39095
NA75	21021
NGA75	20040
LA50	83
LGA50	87
LA75	175
LGA75	187

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

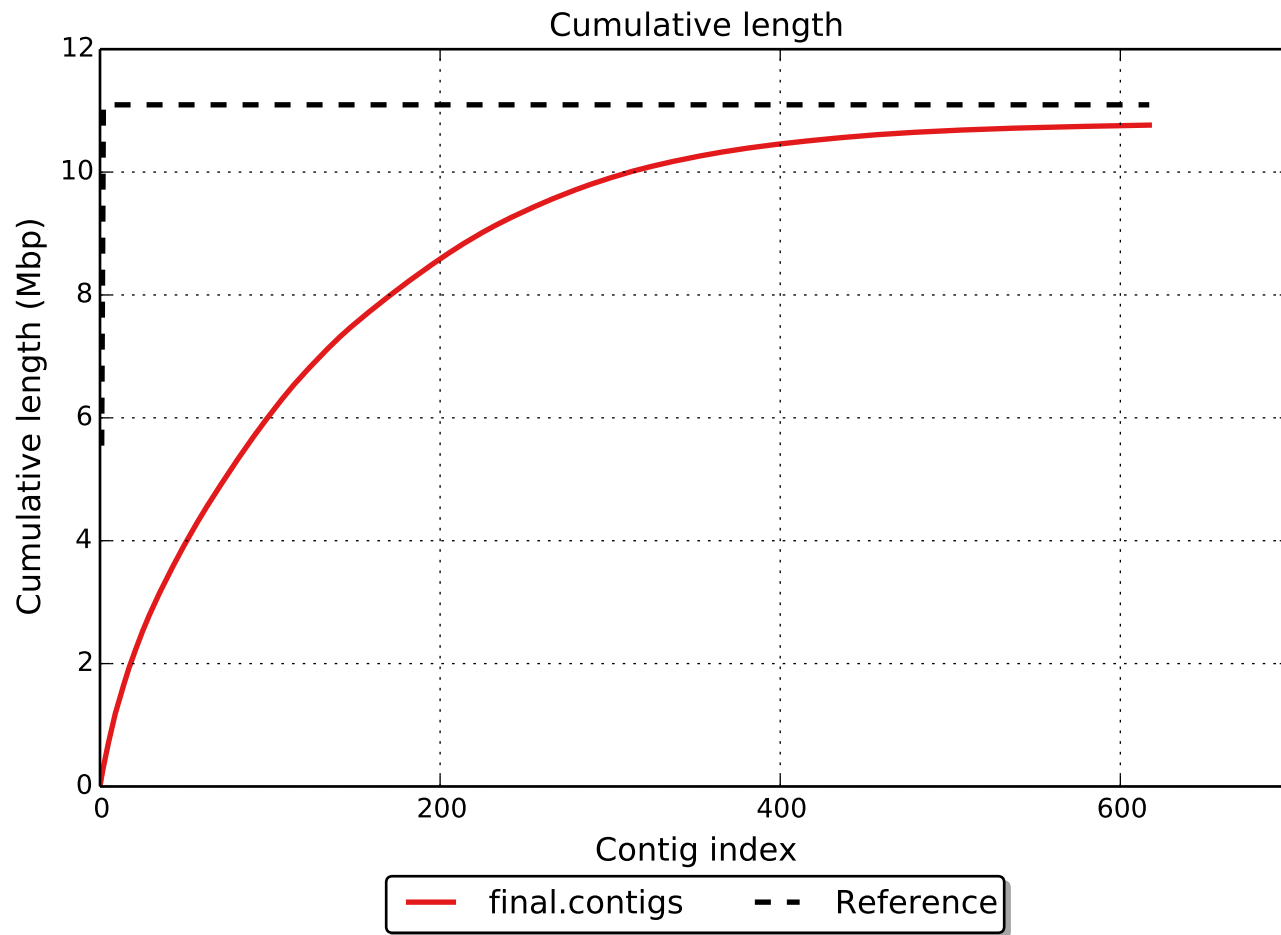
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	16523
# local misassemblies	3
# mismatches	1529
# indels	38
# short indels	34
# long indels	4
Indels length	86

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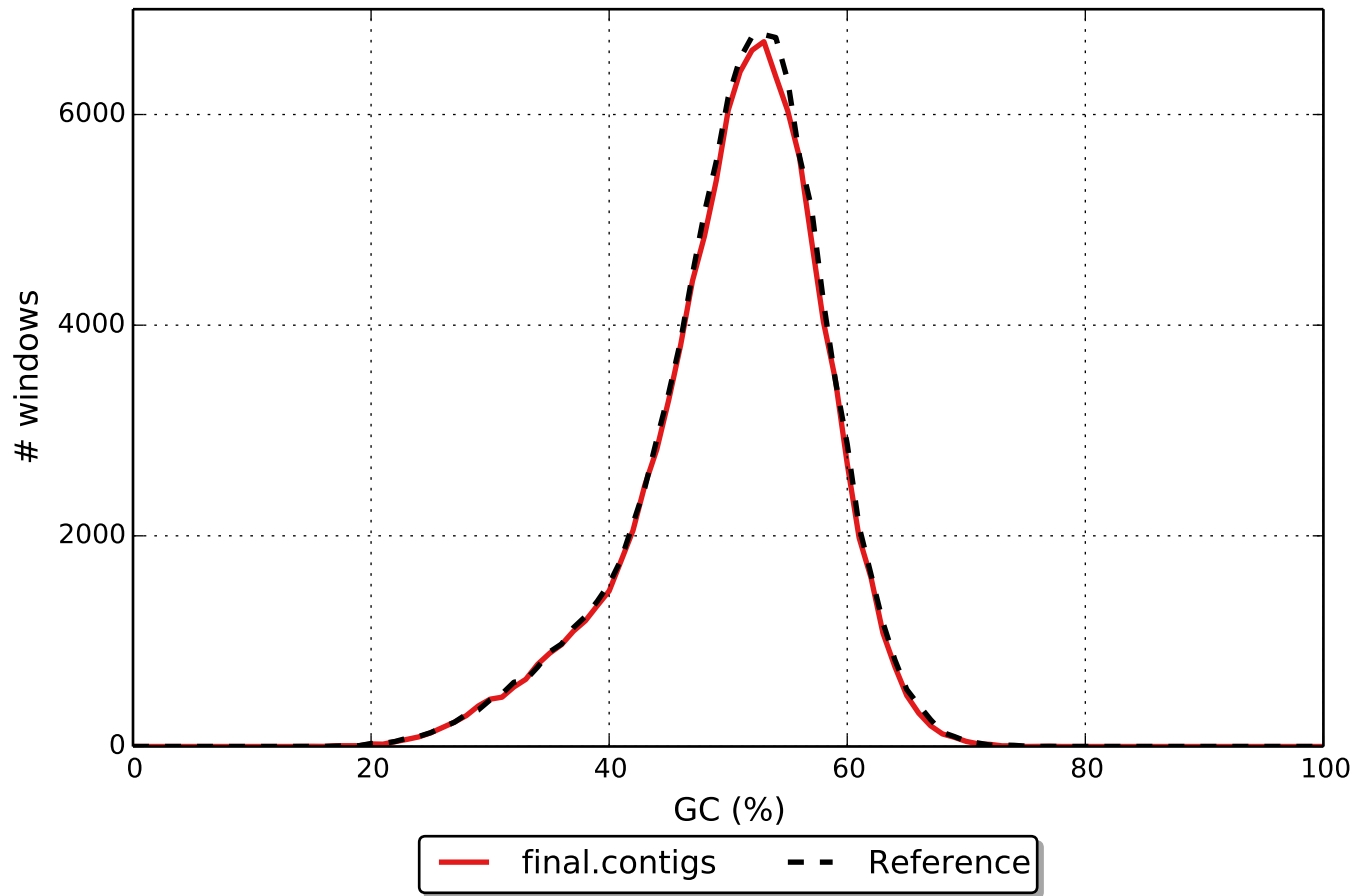
Unaligned report

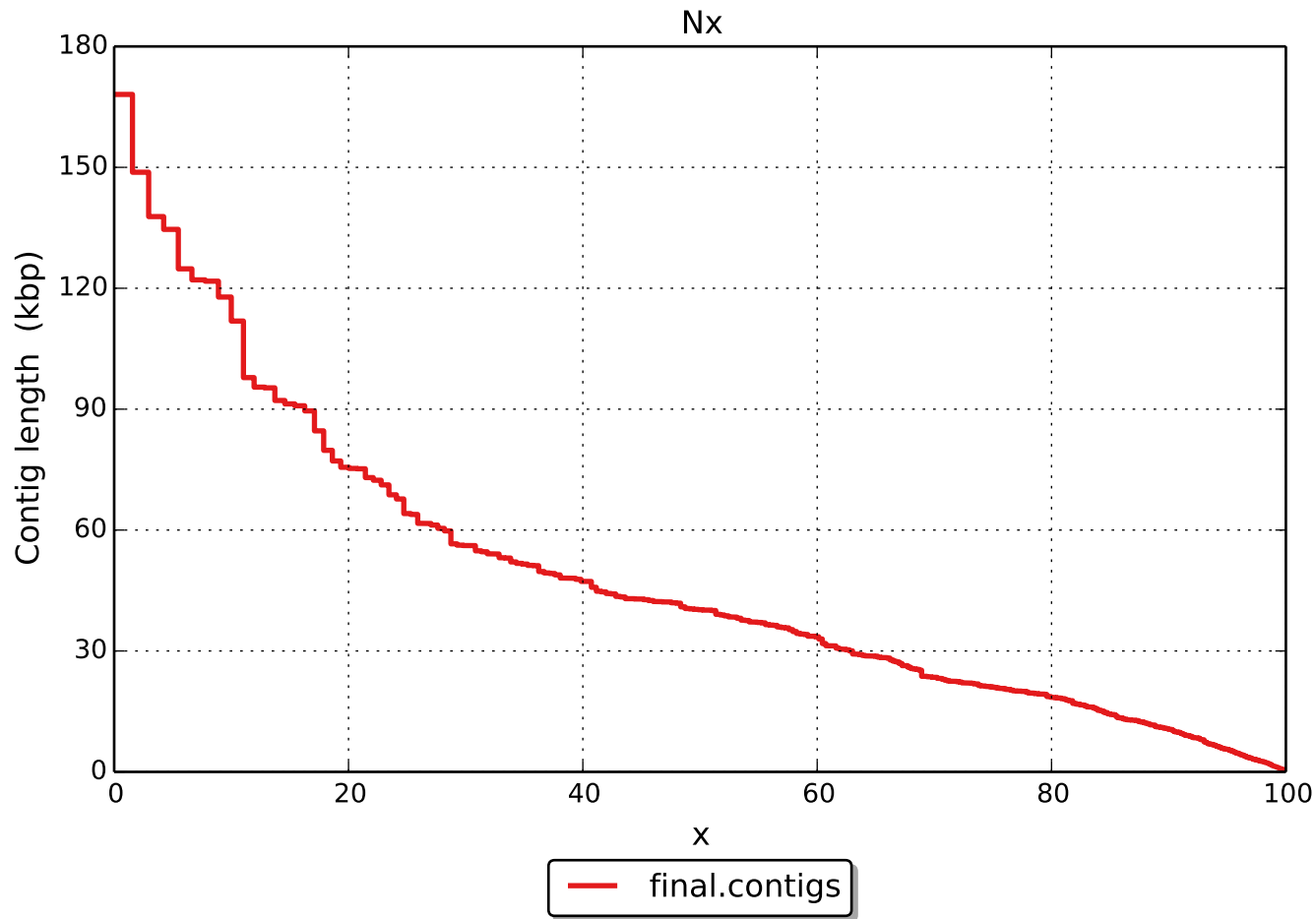
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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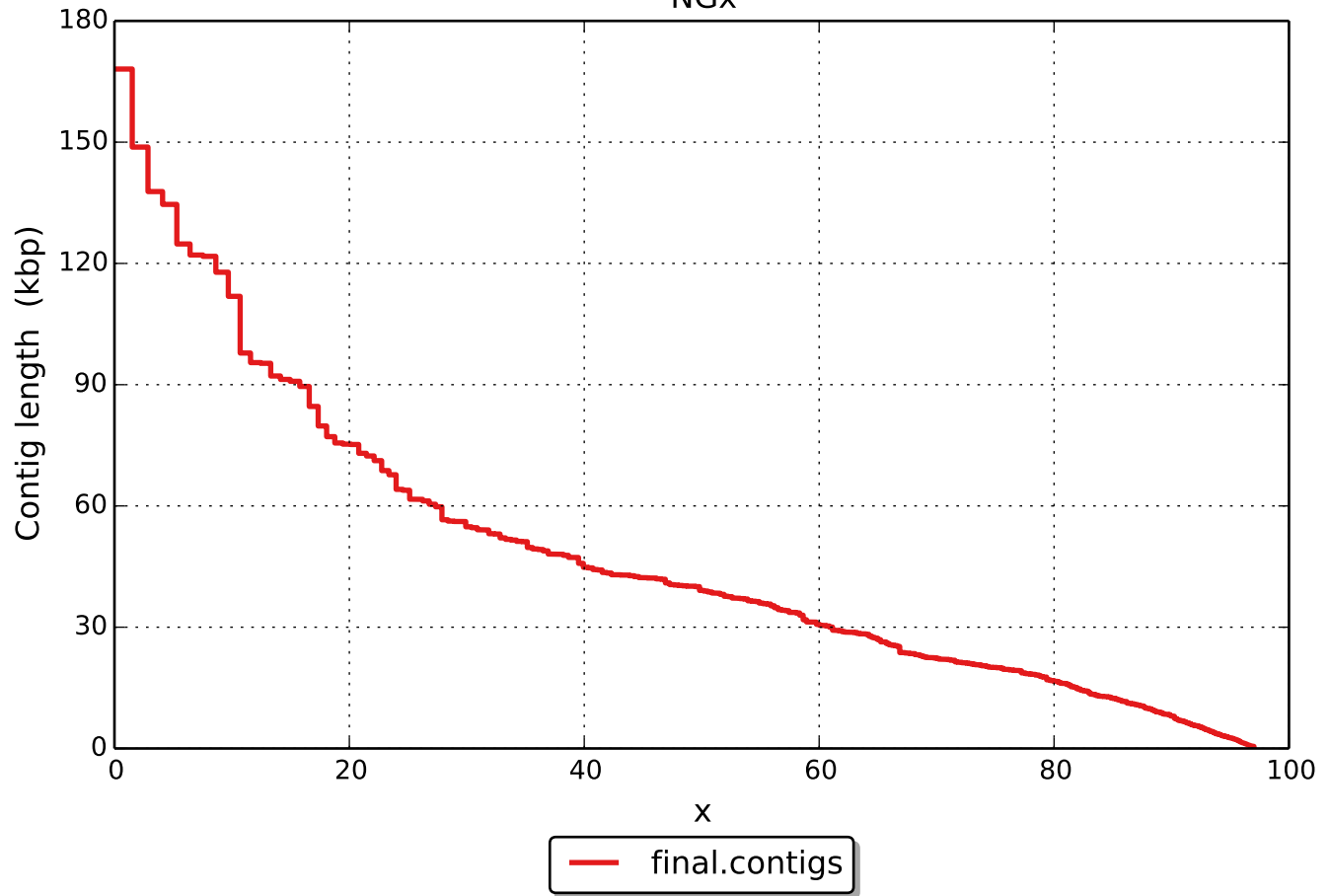


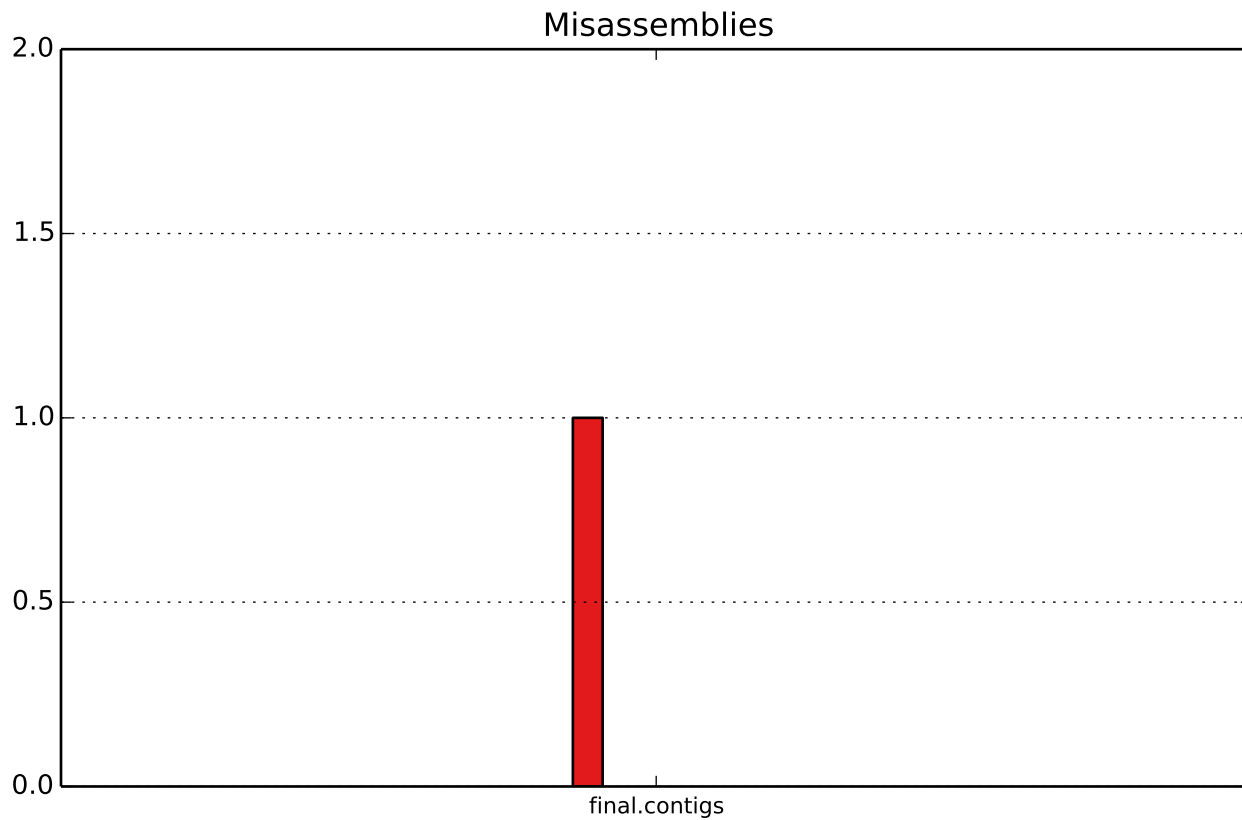
GC content

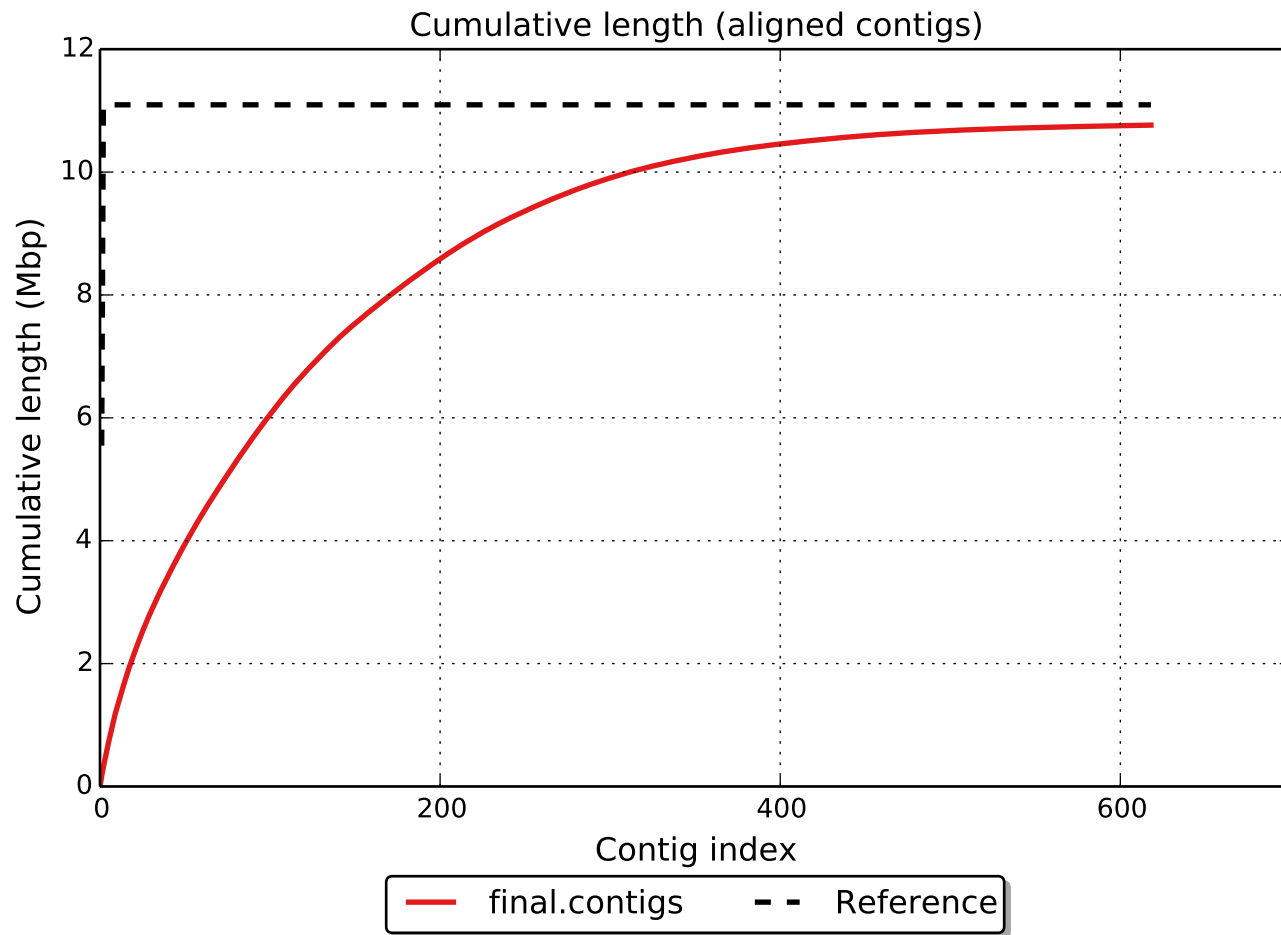




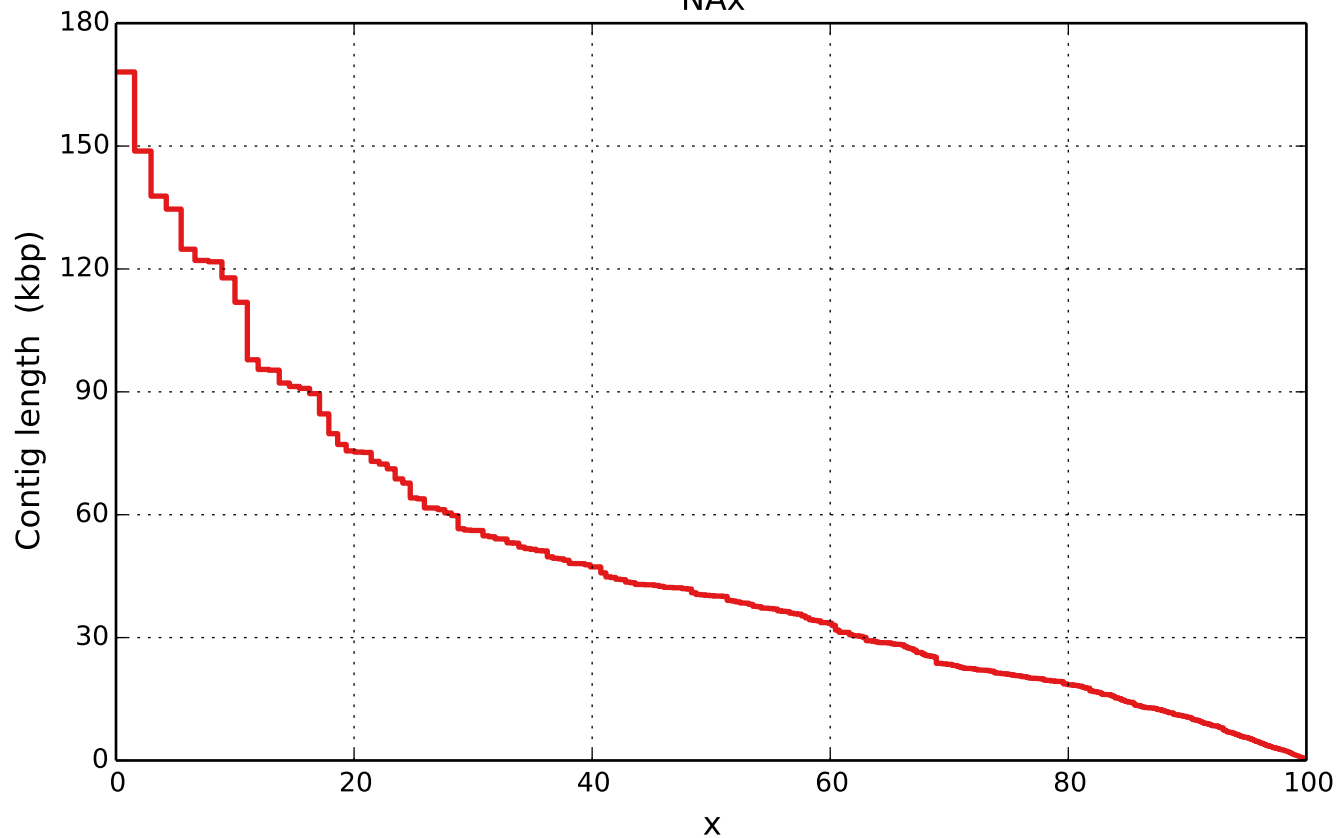
NGx







NAx



— final.contigs

NGAx

