

Report

	final.contigs
# contigs (≥ 0 bp)	1026
# contigs (≥ 1000 bp)	500
Total length (≥ 0 bp)	10842243
Total length (≥ 1000 bp)	10636158
# contigs	615
Largest contig	194428
Total length	10717378
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.50
N50	41387
NG50	40875
N75	22863
NG75	22265
L50	75
LG50	78
L75	161
LG75	169
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	263648
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.986
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.12
# indels per 100 kbp	0.11
Largest alignment	166181
NA50	40875
NGA50	40343
NA75	22863
NGA75	22265
LA50	77
LGA50	79
LA75	163
LGA75	171

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

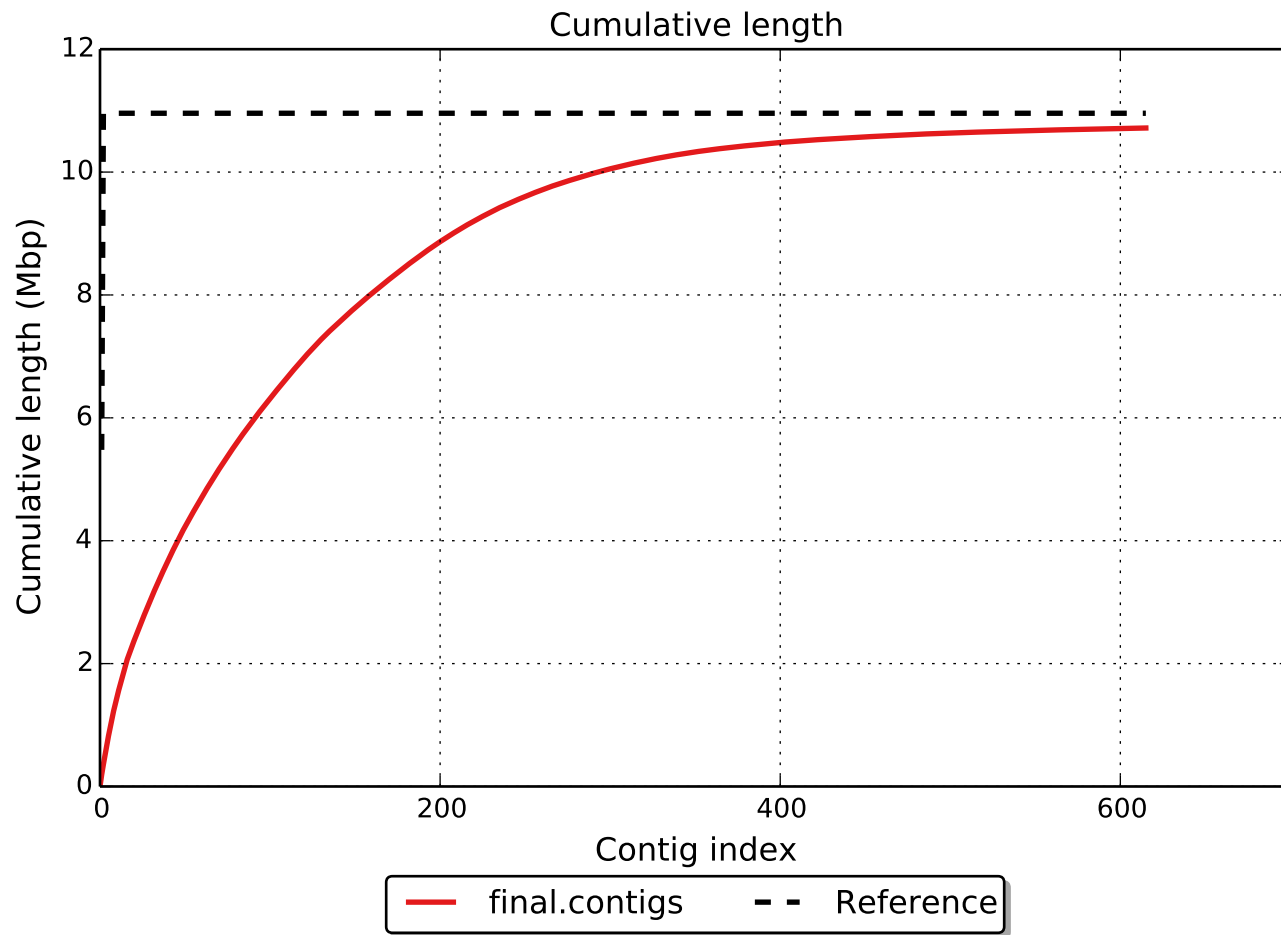
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	263648
# local misassemblies	0
# mismatches	1516
# indels	12
# short indels	10
# long indels	2
Indels length	37

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).

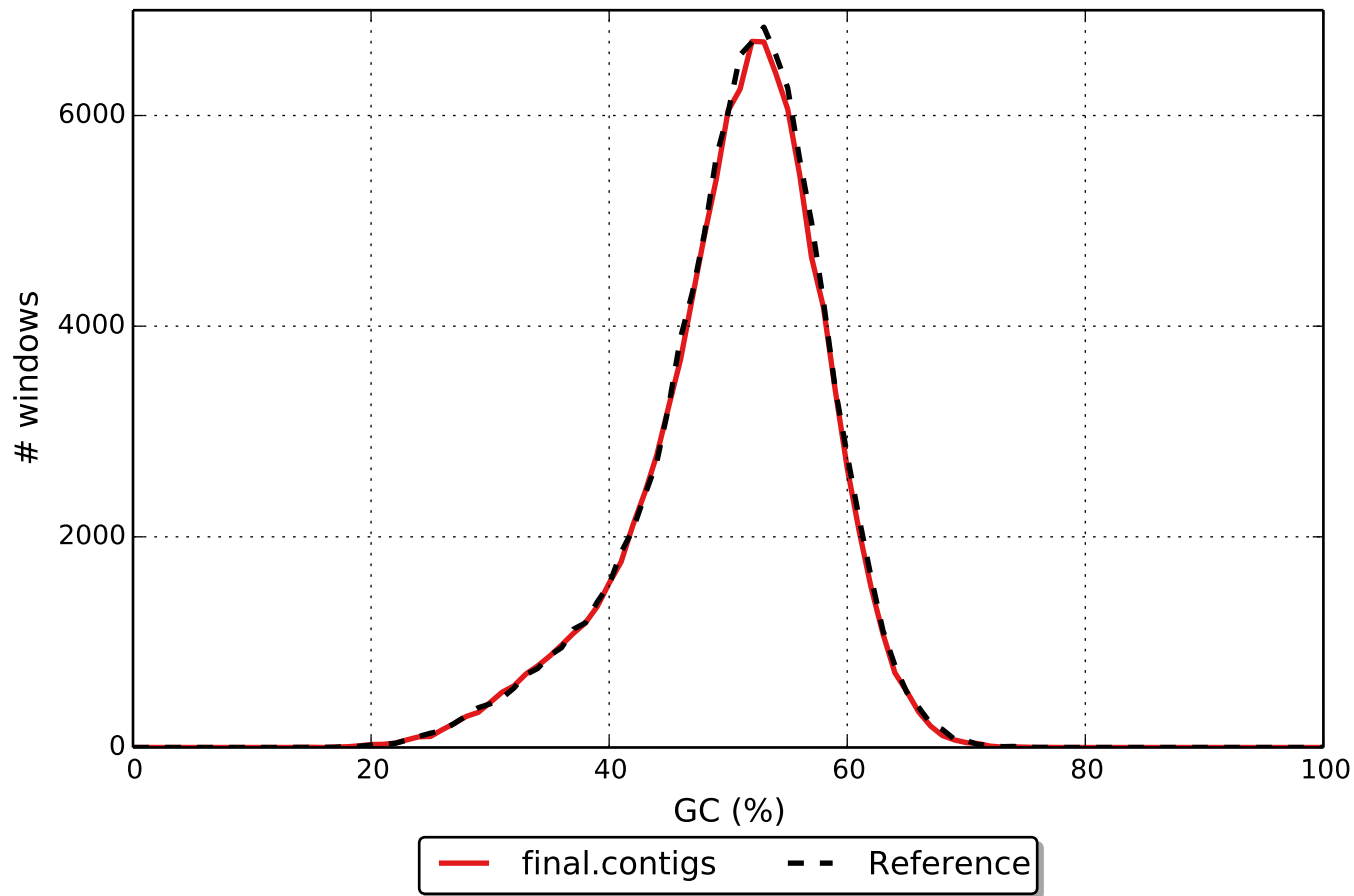
Unaligned report

	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

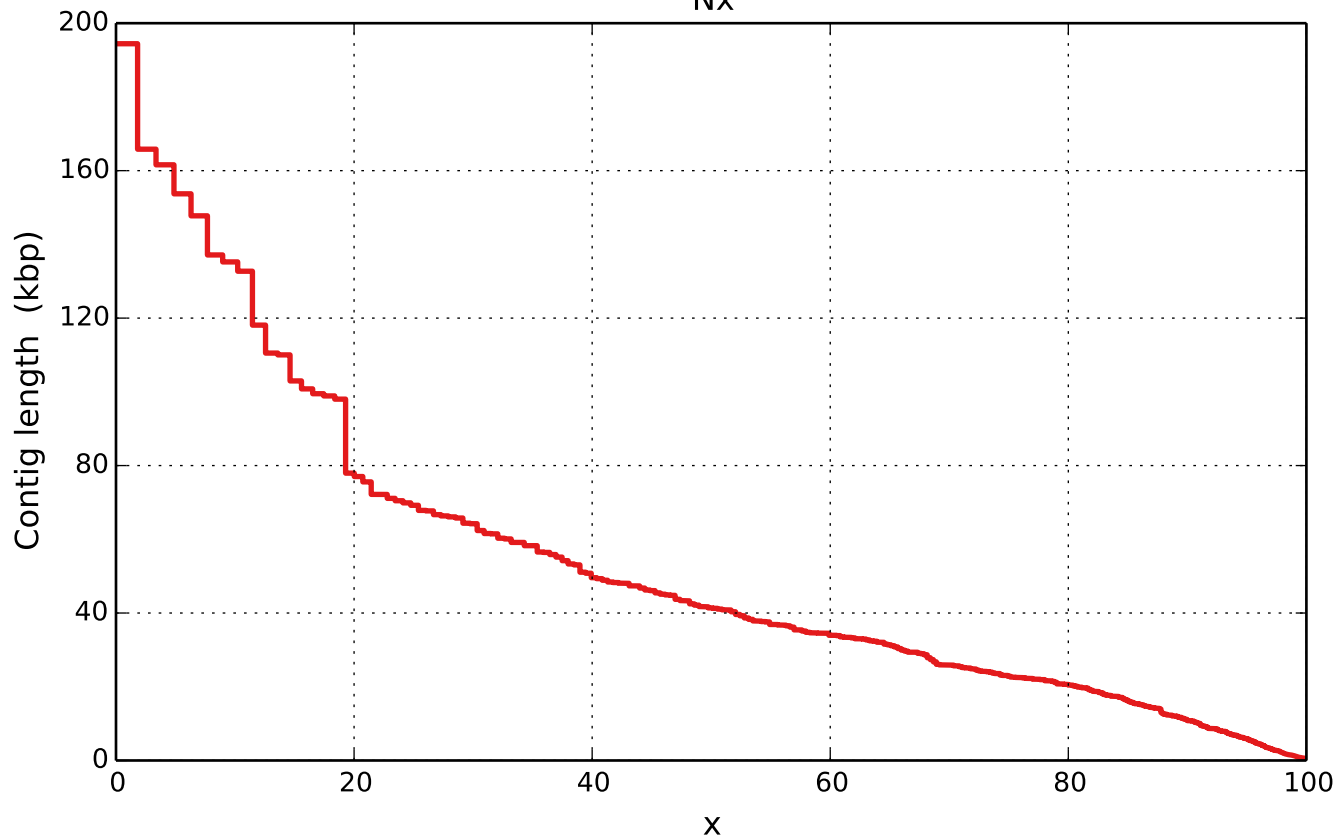
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

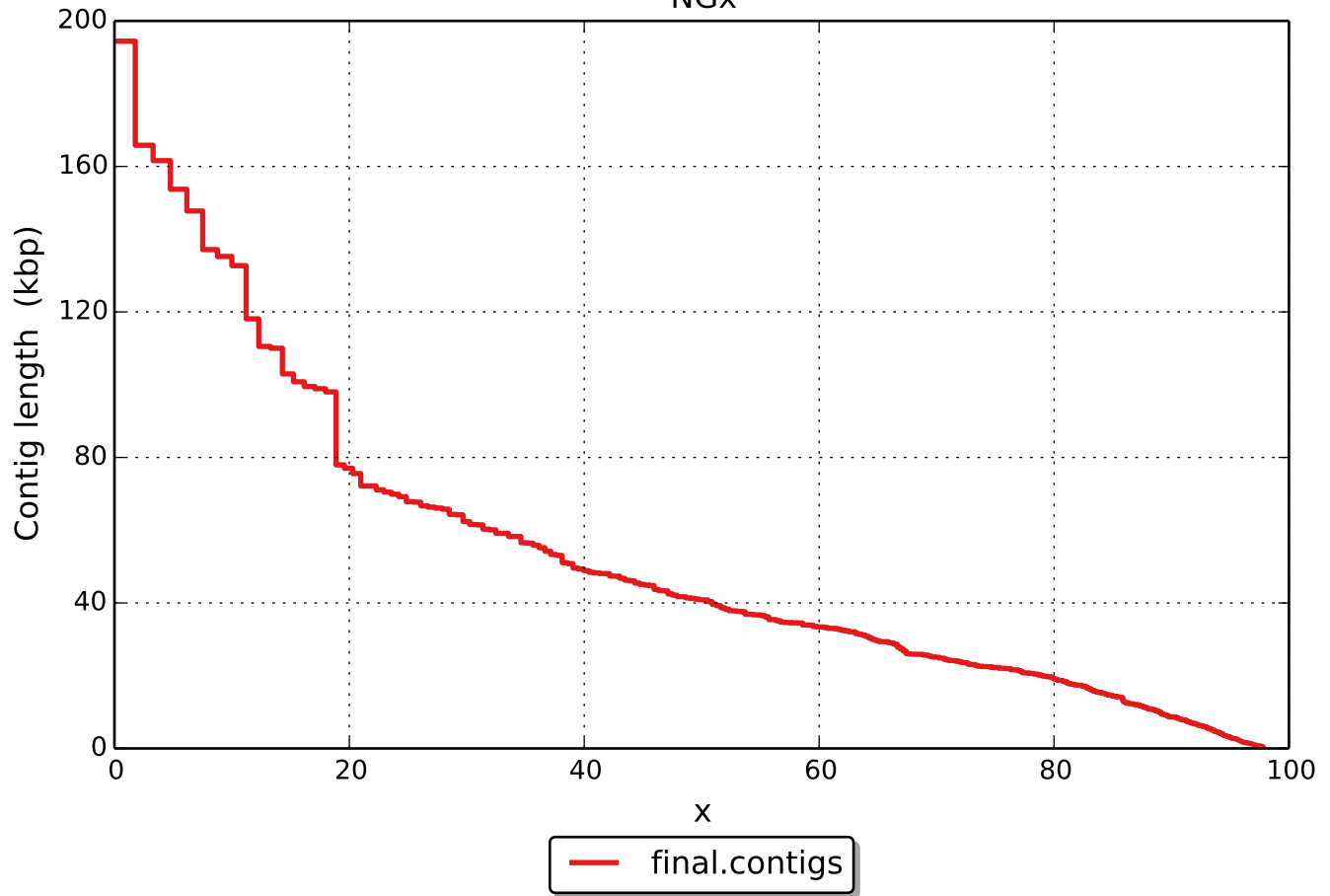


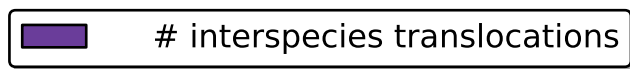
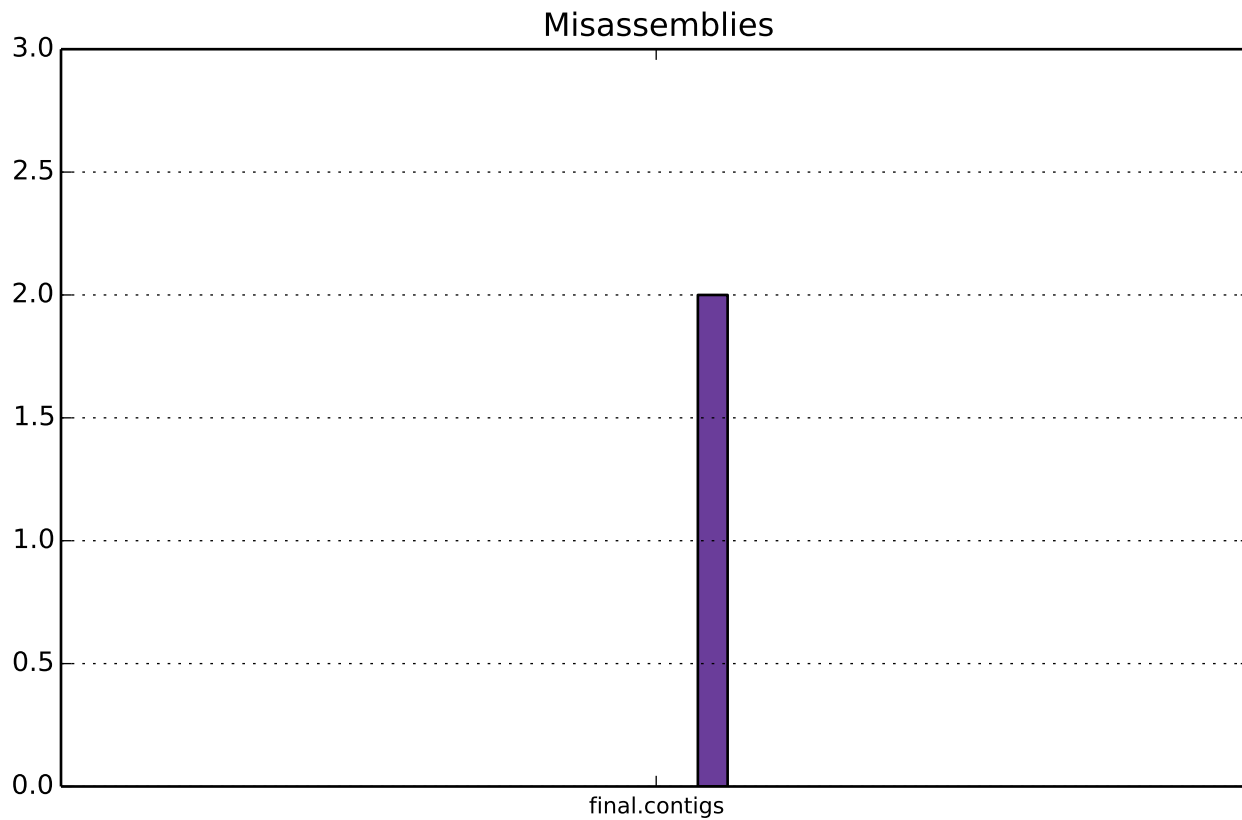
Nx

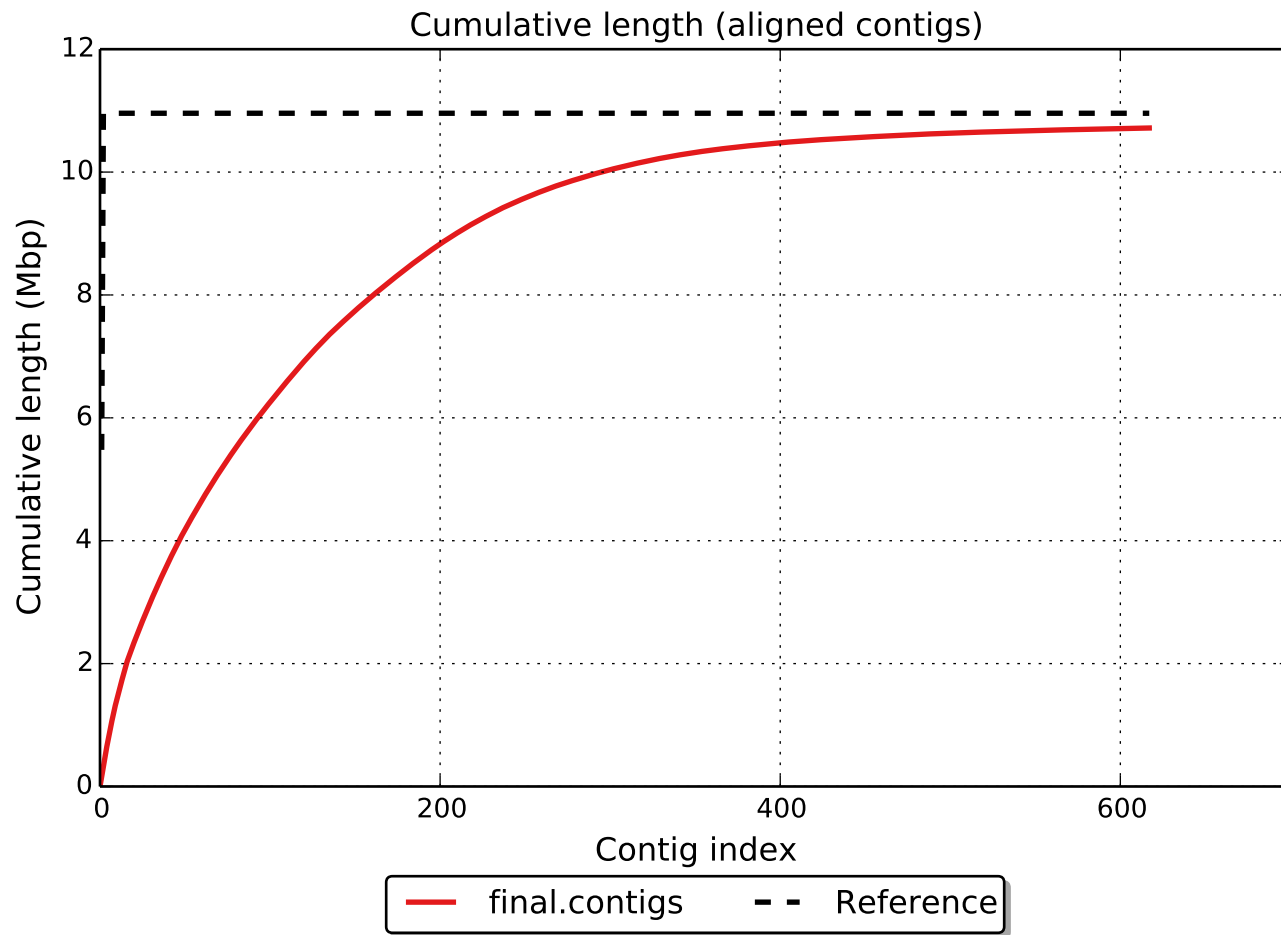


— final.contigs

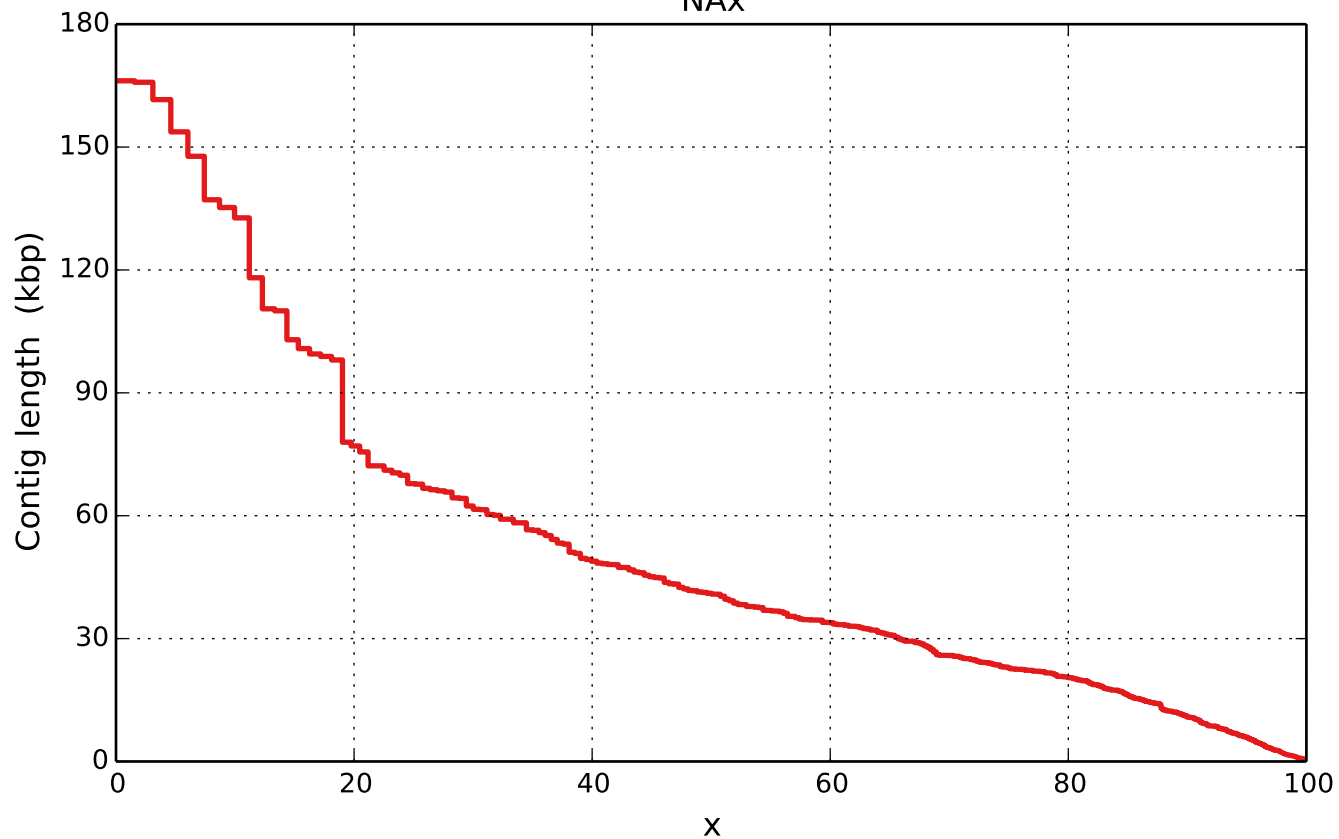
NGx





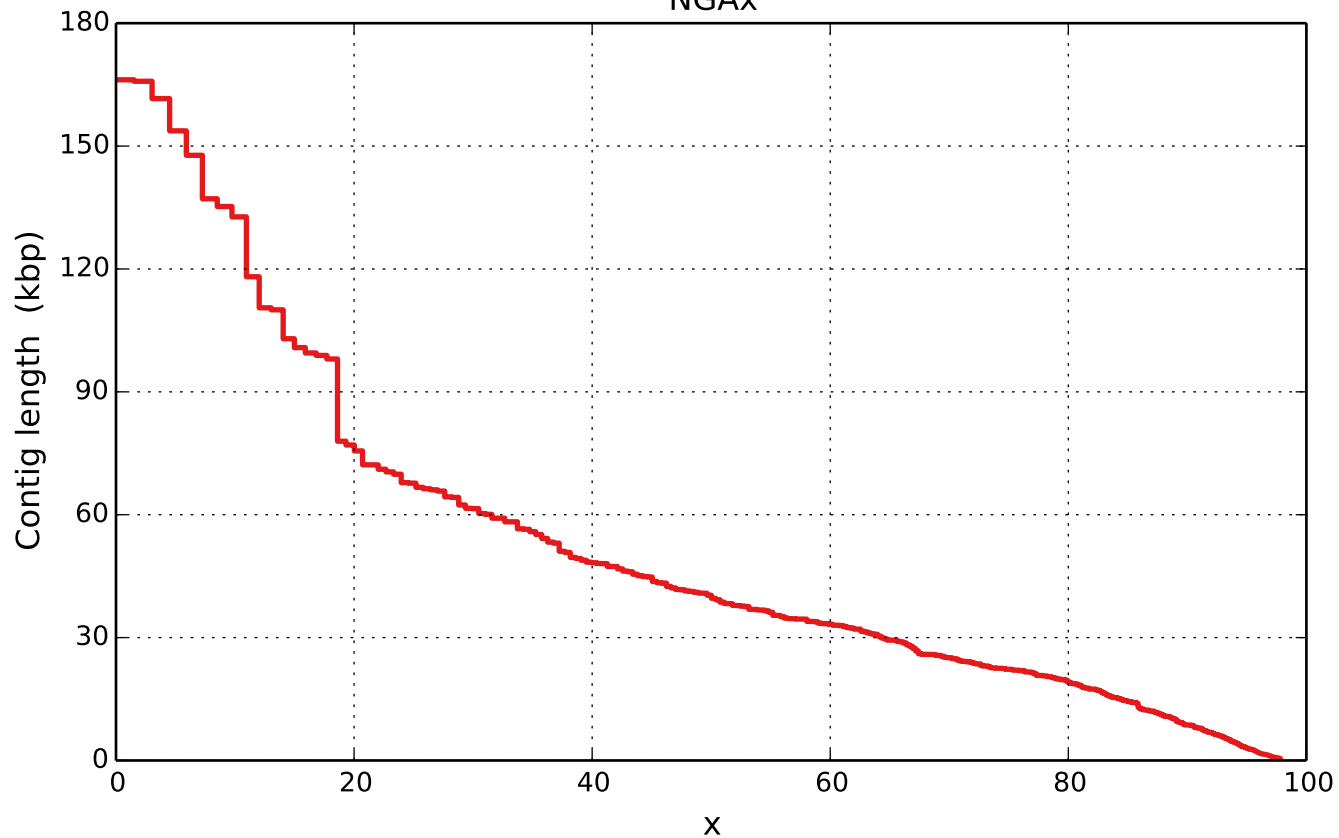


NAx



— final.contigs

NGAx



— final.contigs