

Report

	final.contigs
# contigs (≥ 0 bp)	5100
# contigs (≥ 1000 bp)	795
Total length (≥ 0 bp)	3436600
Total length (≥ 1000 bp)	1132122
# contigs	3004
Largest contig	3974
Total length	2682035
Reference length	3785550
GC (%)	32.30
Reference GC (%)	32.26
N50	914
NG50	723
N75	682
L50	1014
LG50	1694
L75	1863
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	77.719
Duplication ratio	1.064
# N's per 100 kbp	0.00
# mismatches per 100 kbp	283.68
# indels per 100 kbp	0.00
Largest alignment	3974
NA50	914
NGA50	723
NA75	682
LA50	1014
LGA50	1694
LA75	1863

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

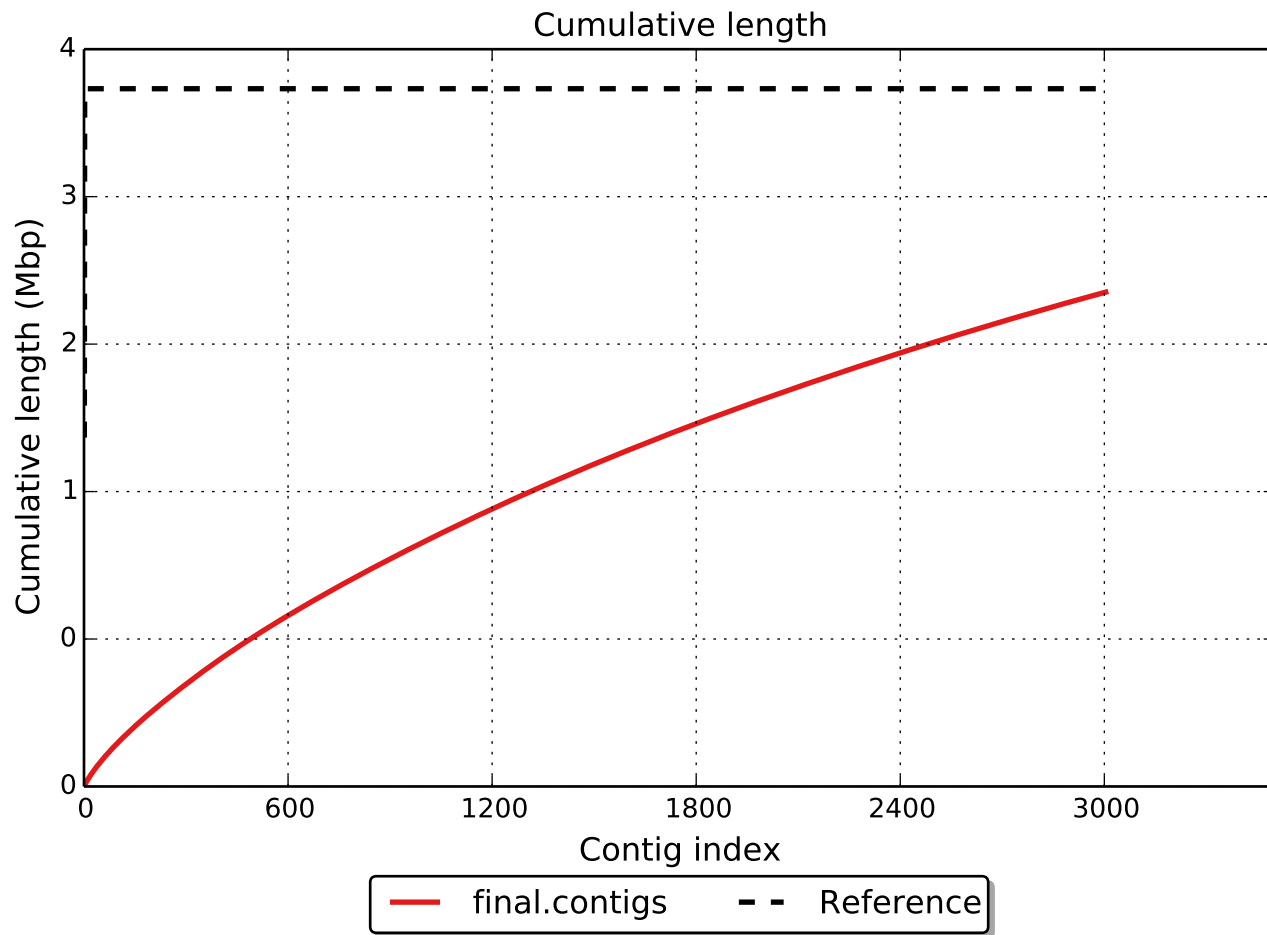
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	8346
# indels	0
# short indels	0
# long indels	0
Indels length	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).

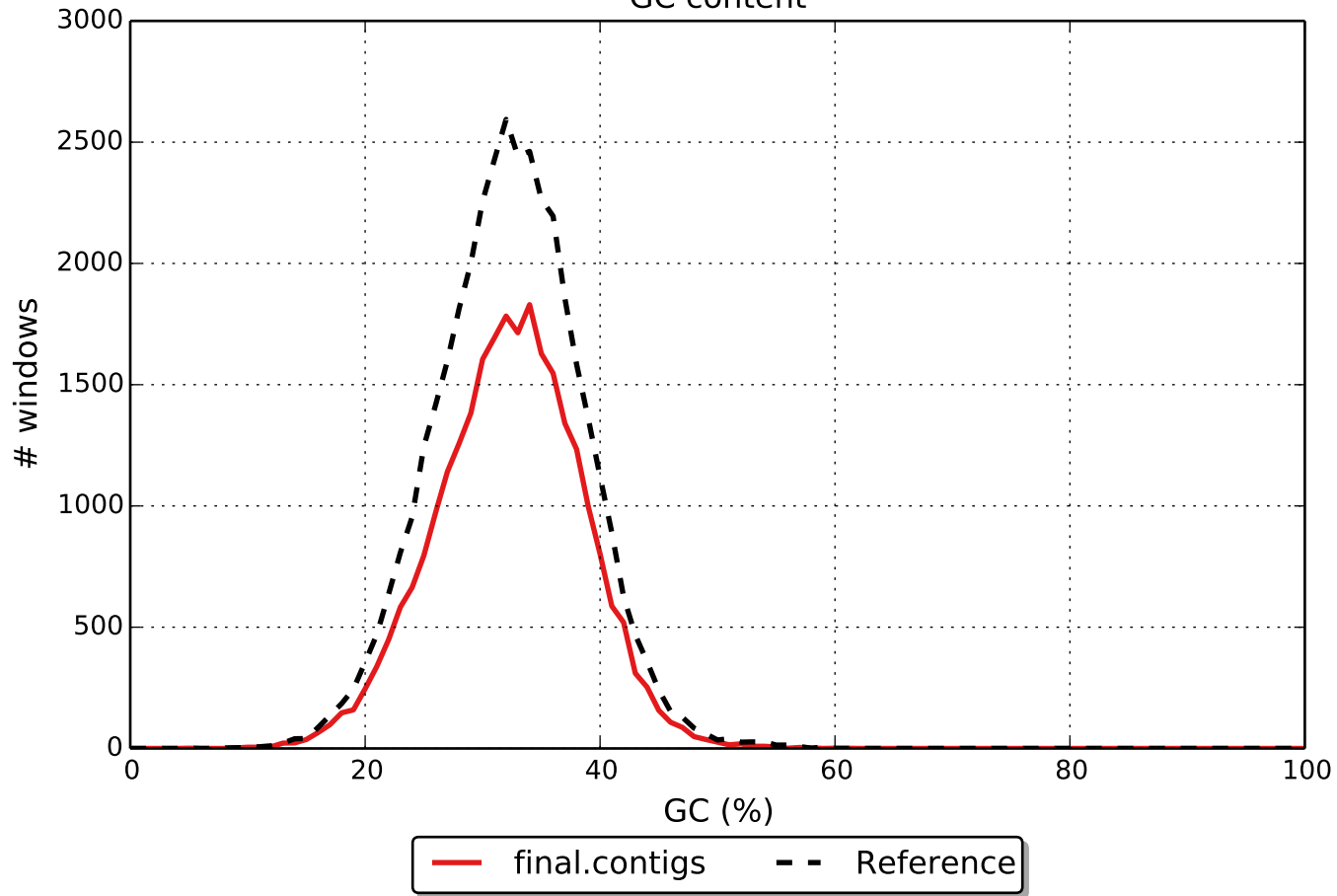
Unaligned report

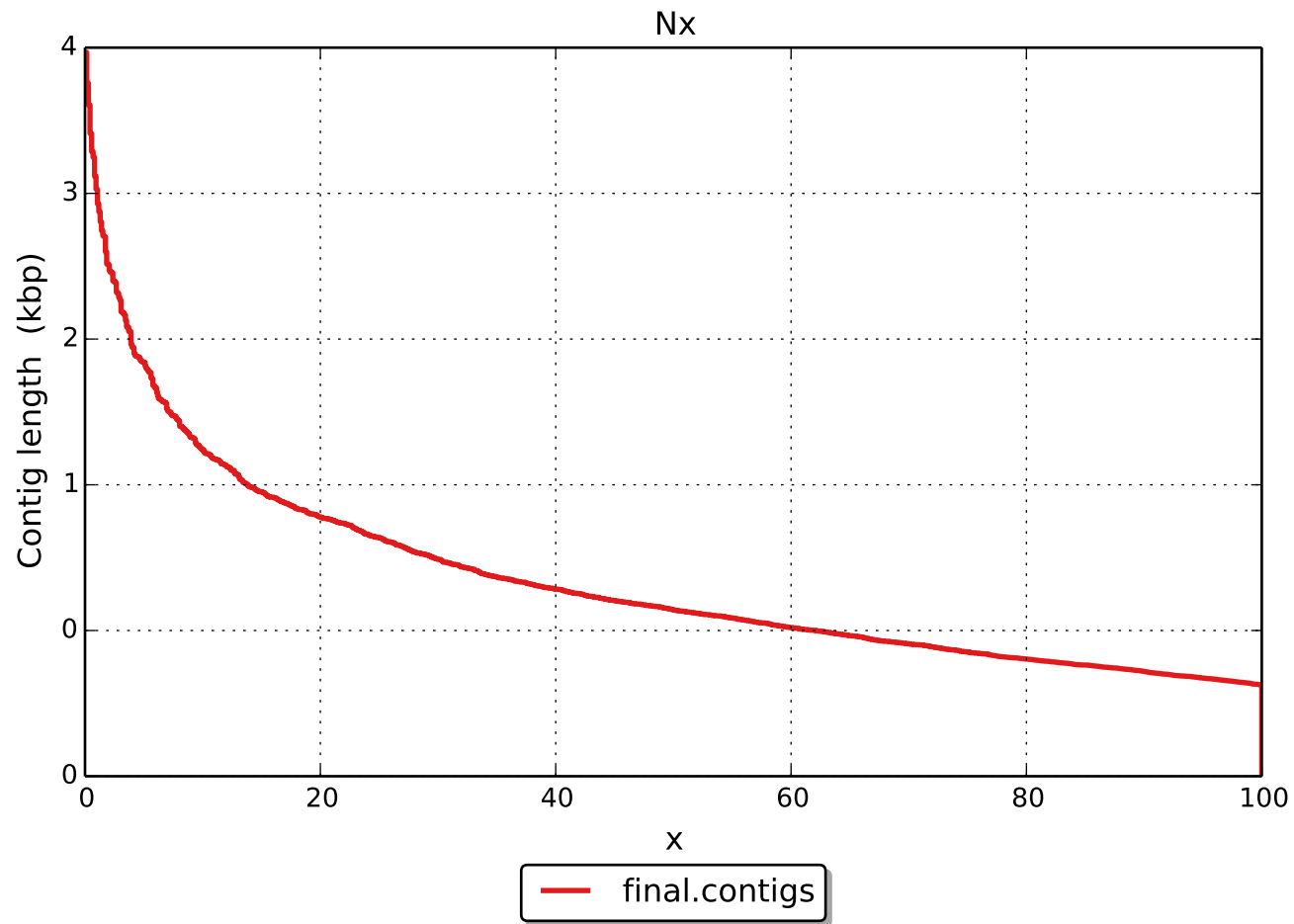
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

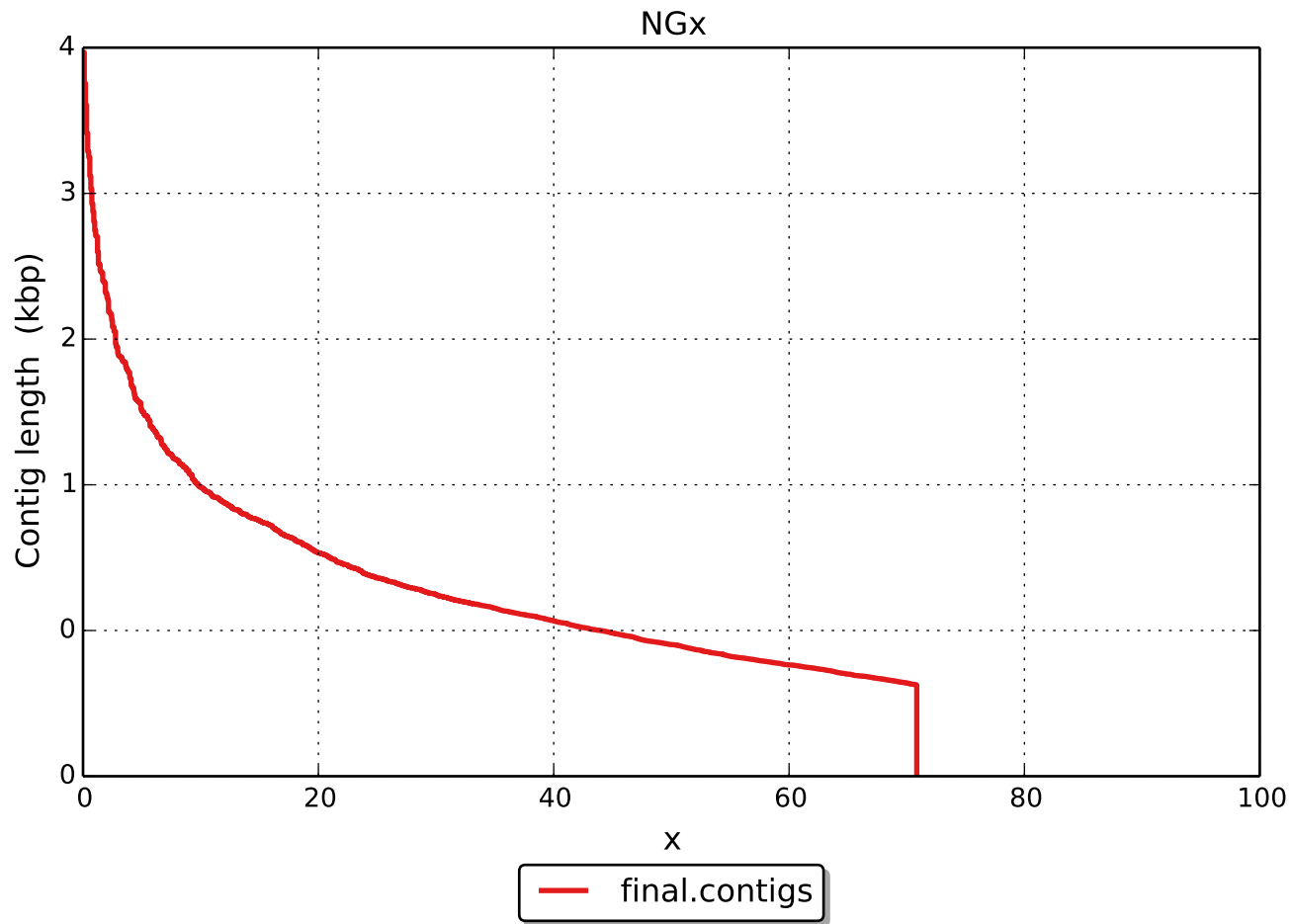
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

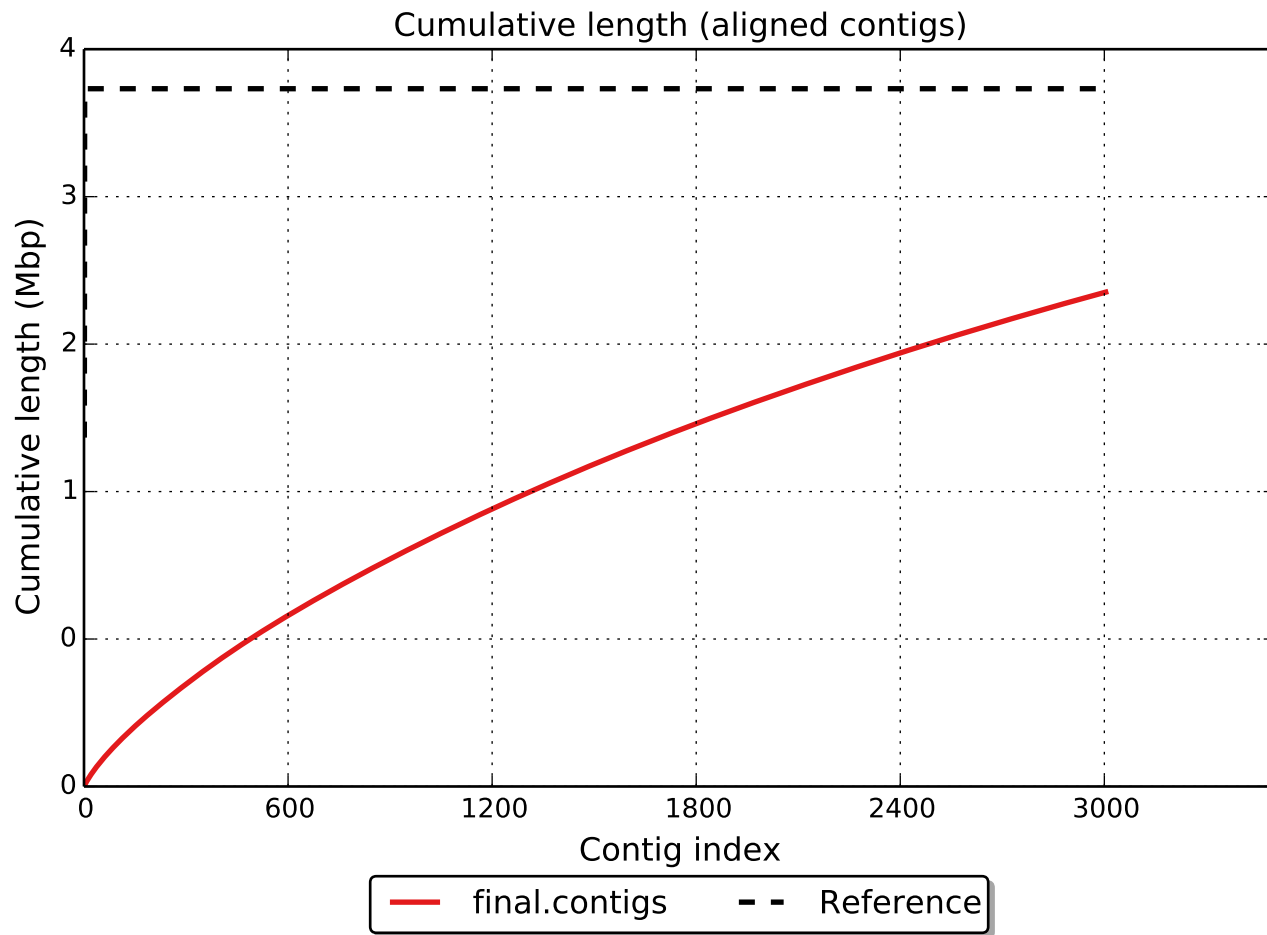


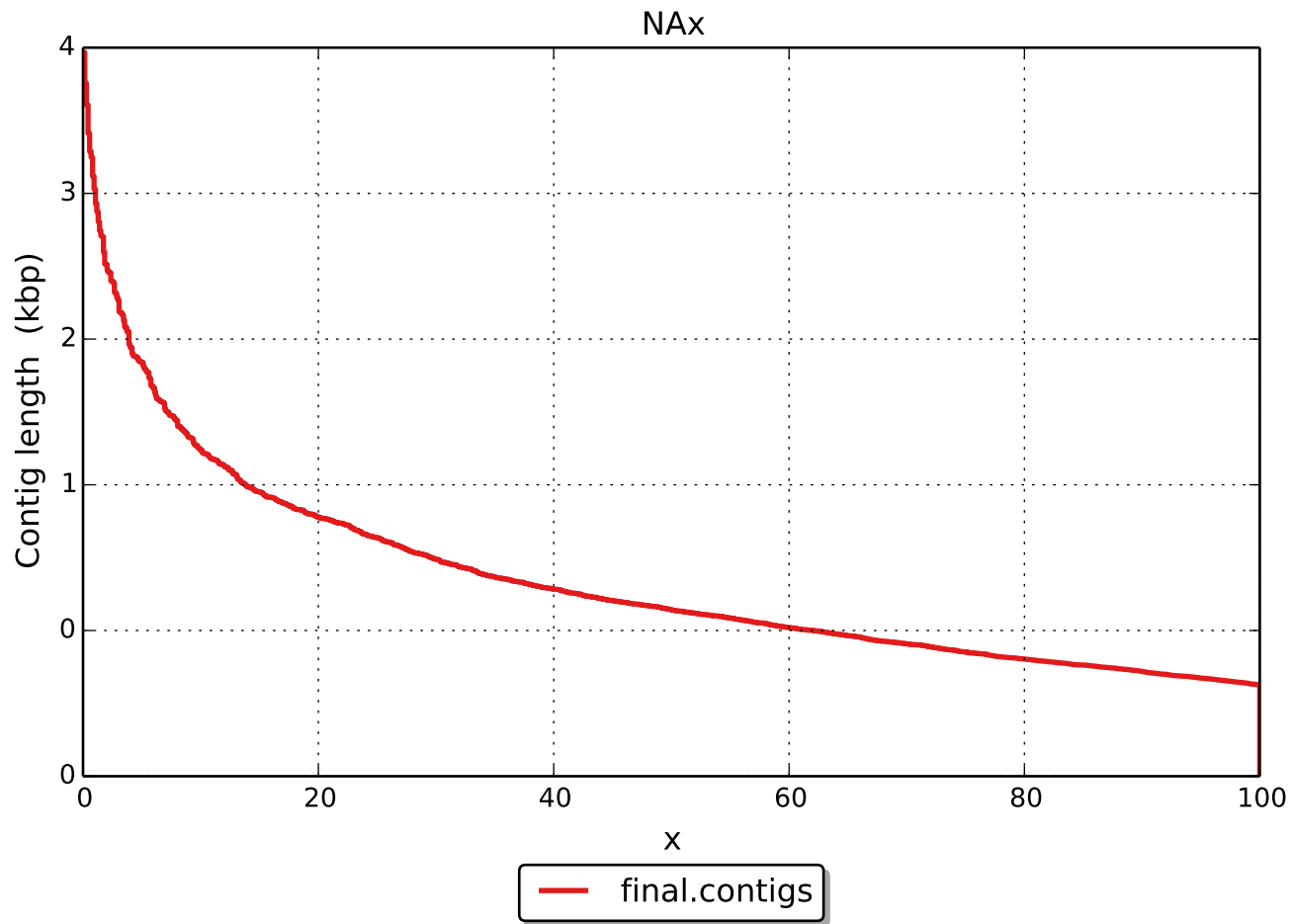




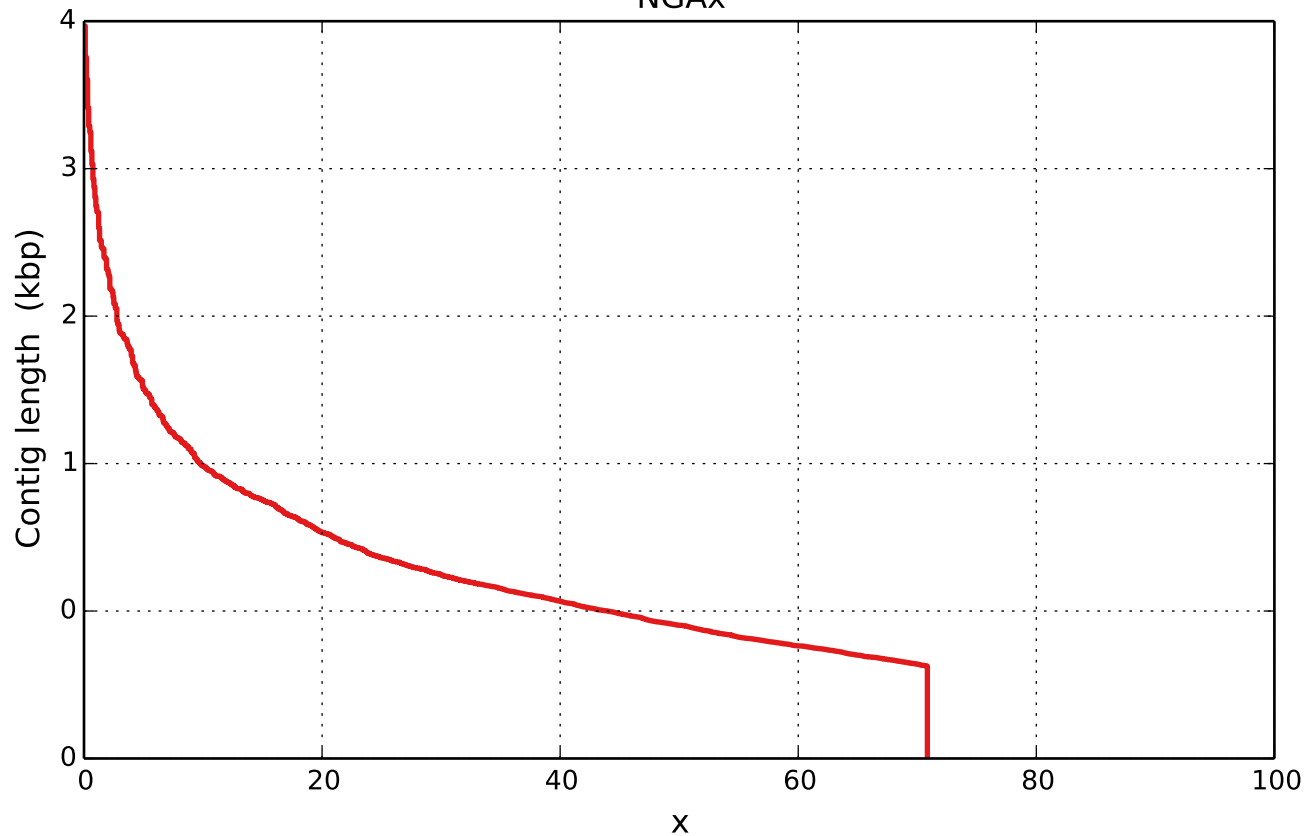
Misassemblies







NGAx



— final.contigs