

Report

	final.contigs
# contigs (>= 0 bp)	4338
# contigs (>= 1000 bp)	1886
Total length (>= 0 bp)	4807731
Total length (>= 1000 bp)	3054881
# contigs	4338
Largest contig	5549
Total length	4807731
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	1223
NG50	1091
N75	829
NG75	676
L50	1297
LG50	1617
L75	2491
LG75	3233
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.235
Duplication ratio	1.054
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.06
# indels per 100 kbp	0.07
Largest alignment	5549
NA50	1223
NGA50	1091
NA75	829
NGA75	676
LA50	1297
LGA50	1617
LA75	2491
LGA75	3233

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

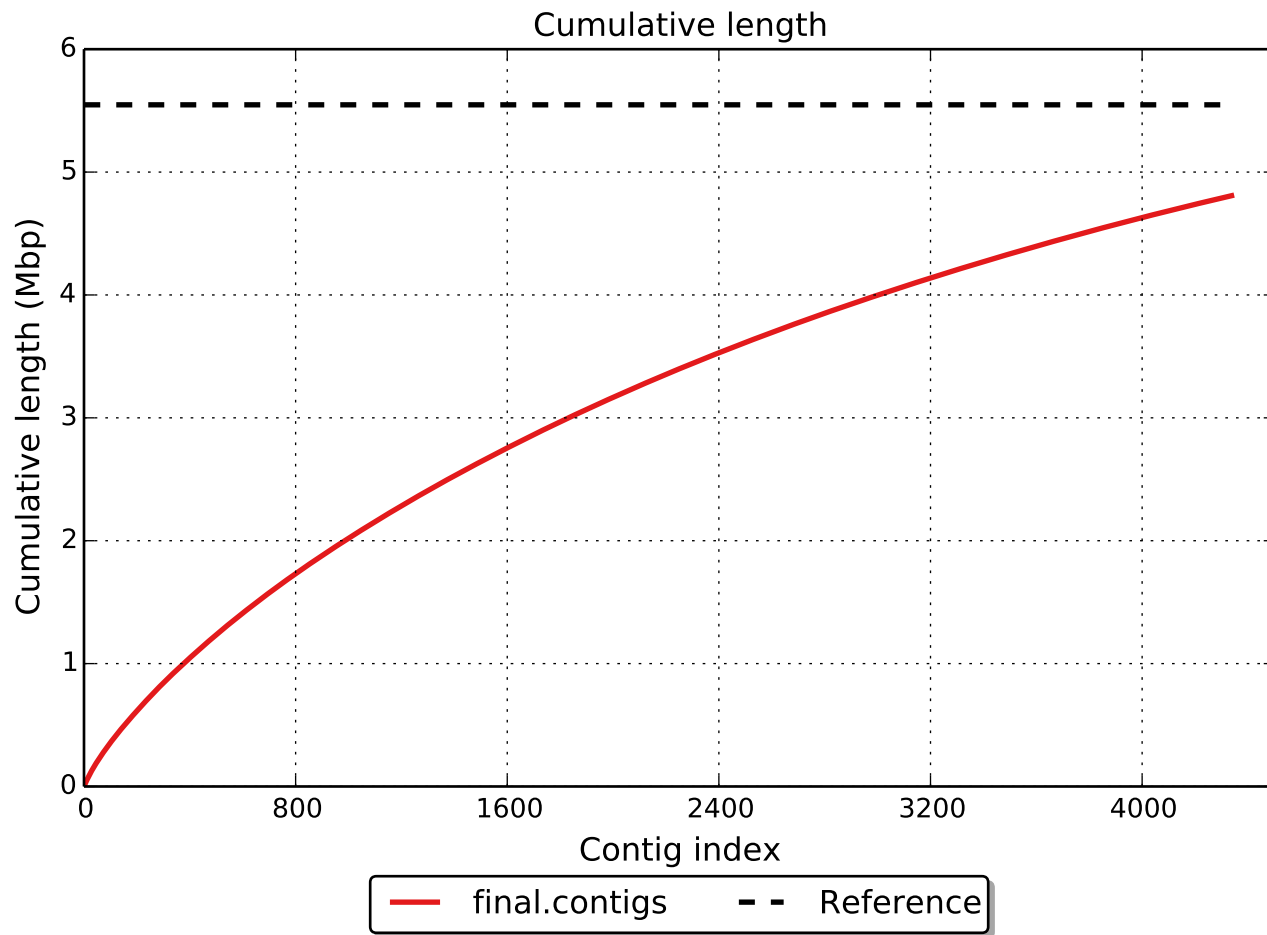
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3926
# indels	3
# short indels	2
# long indels	1
Indels length	8

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).

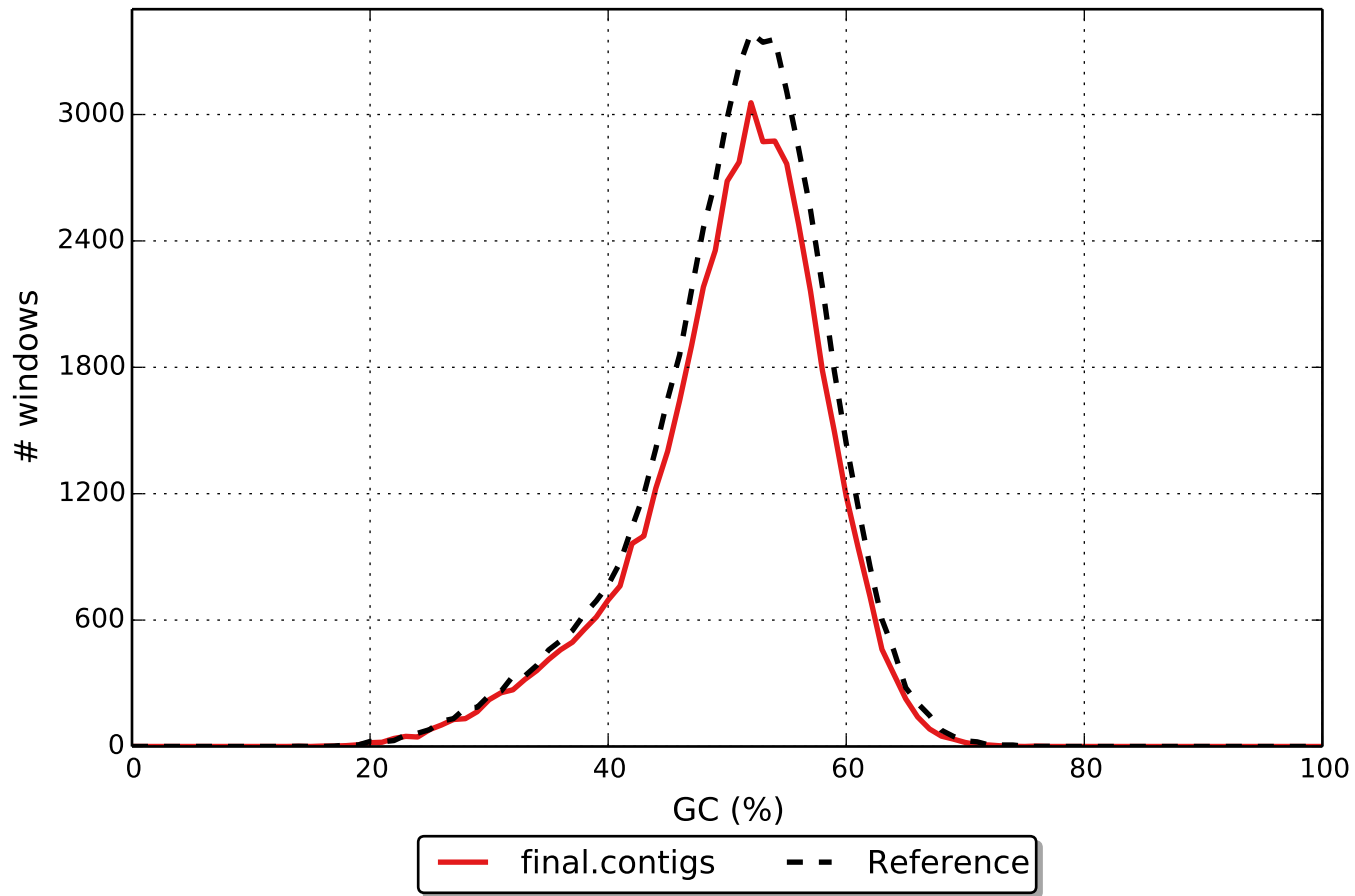
Unaligned report

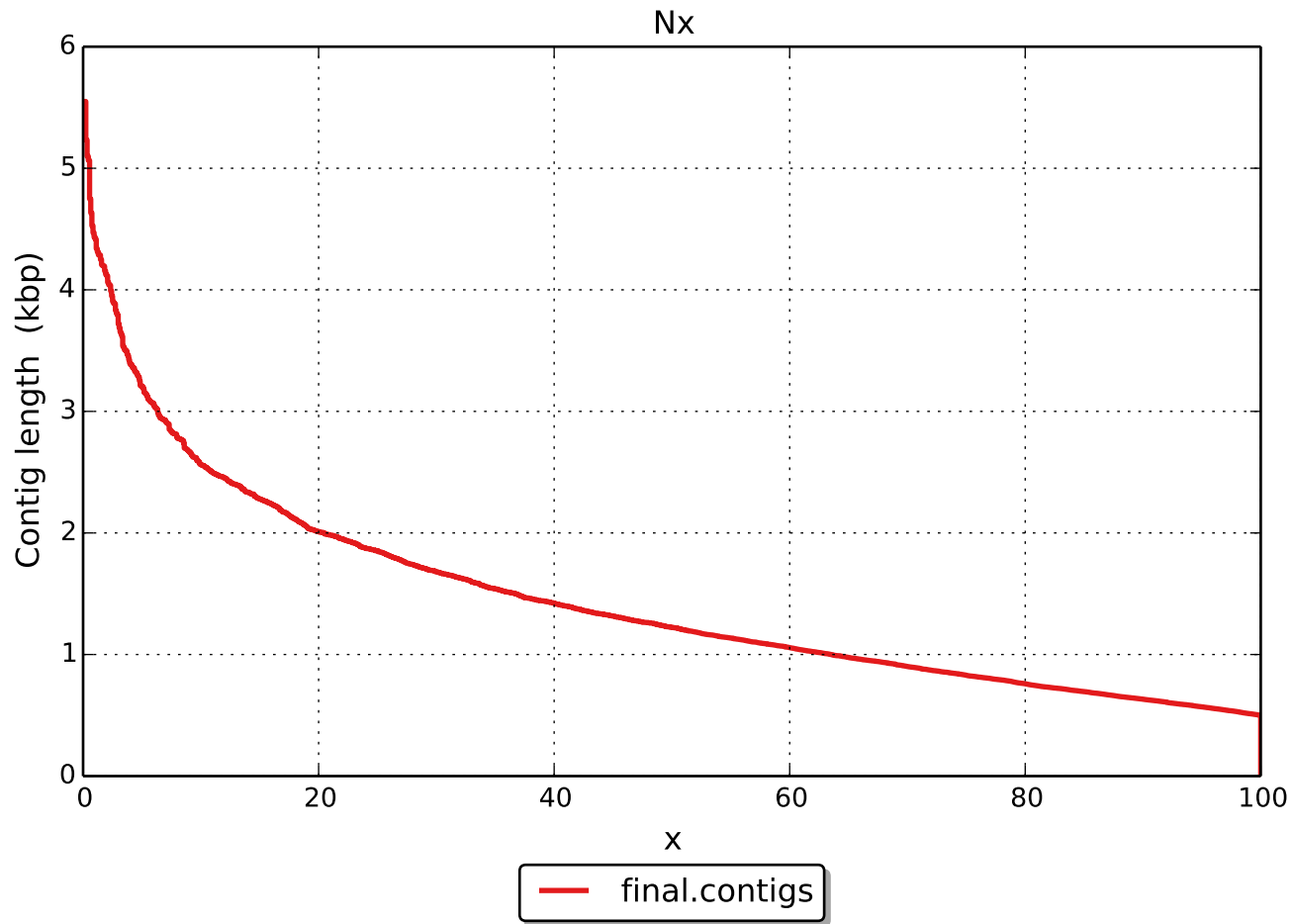
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

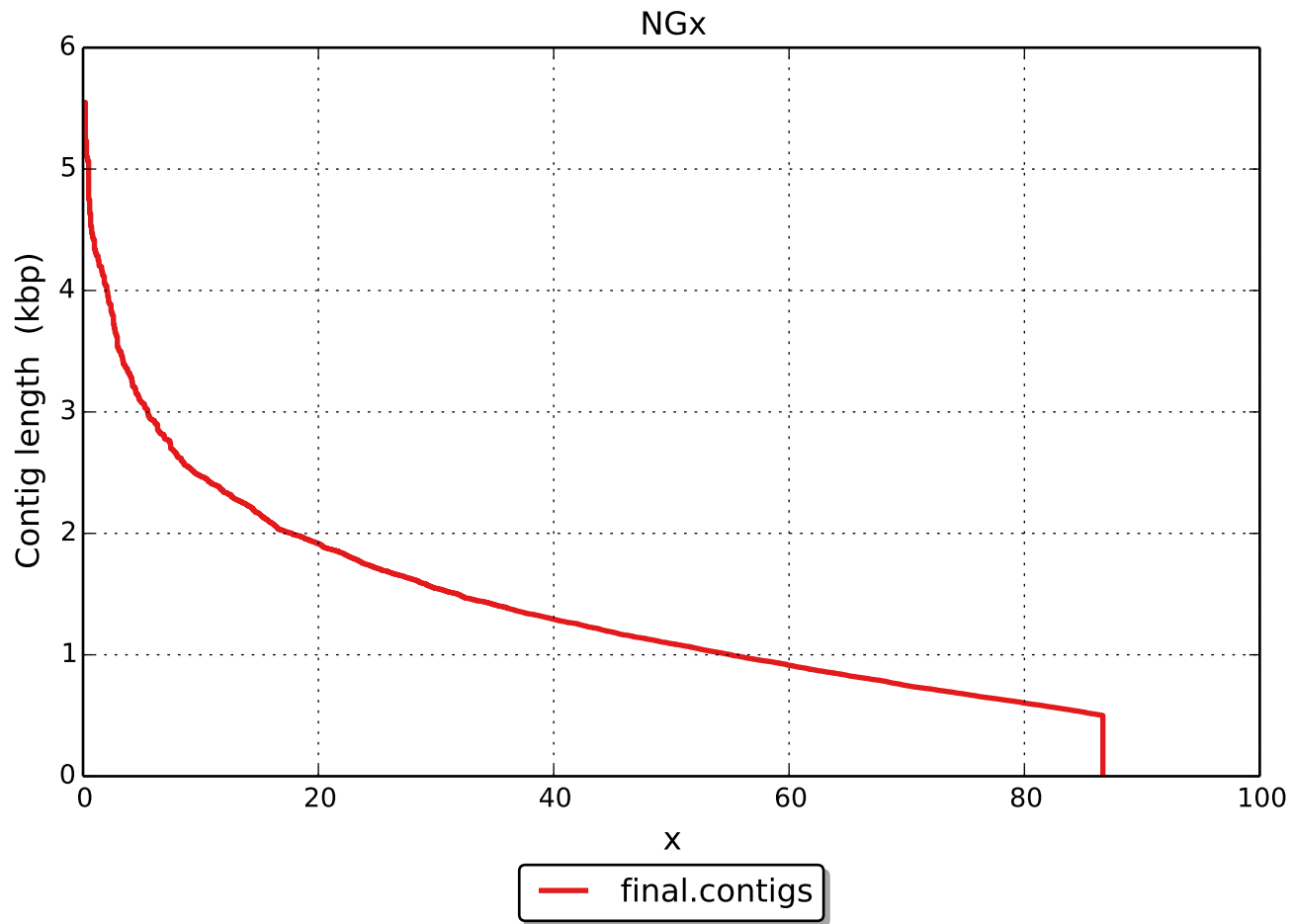
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

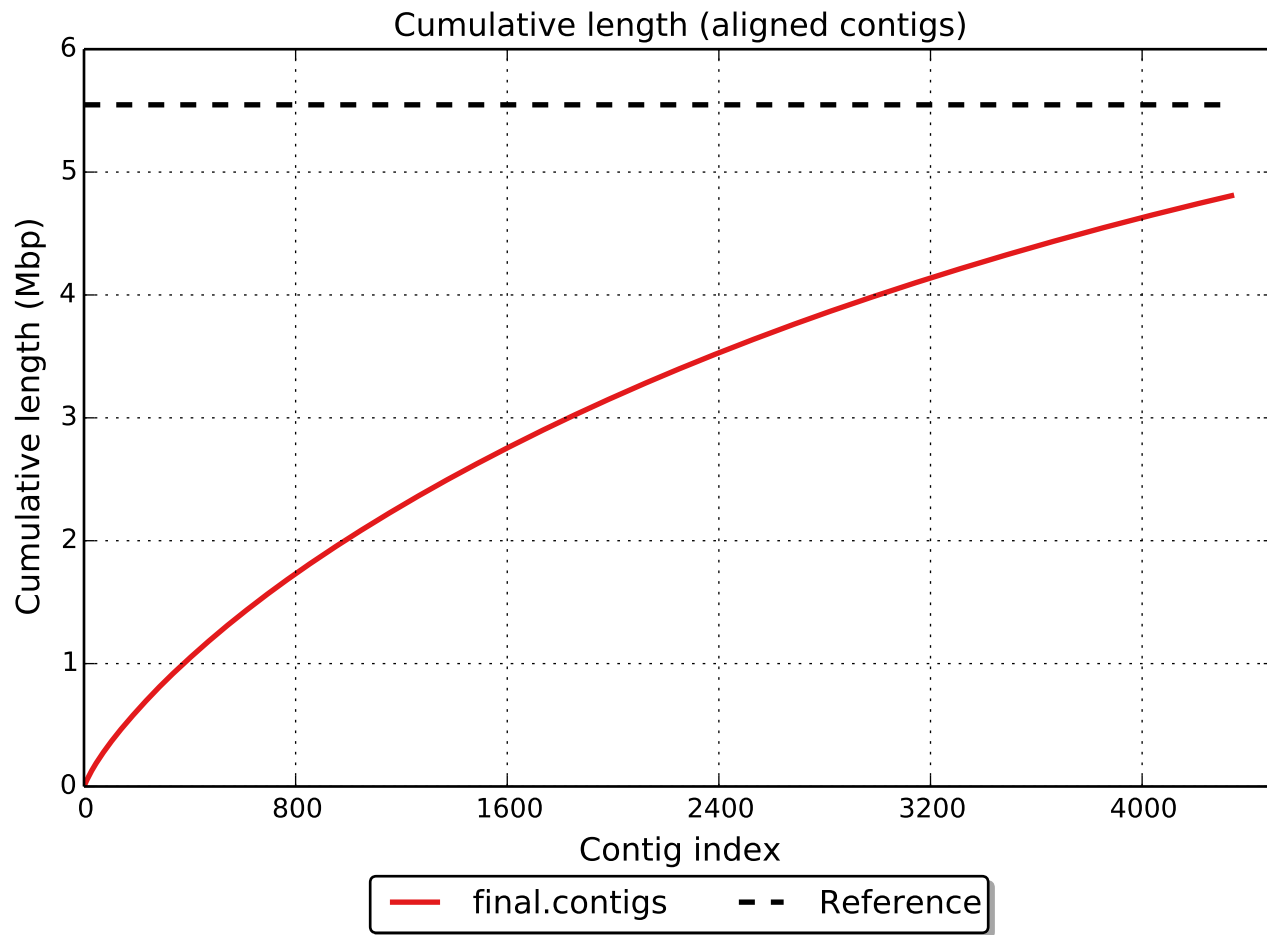


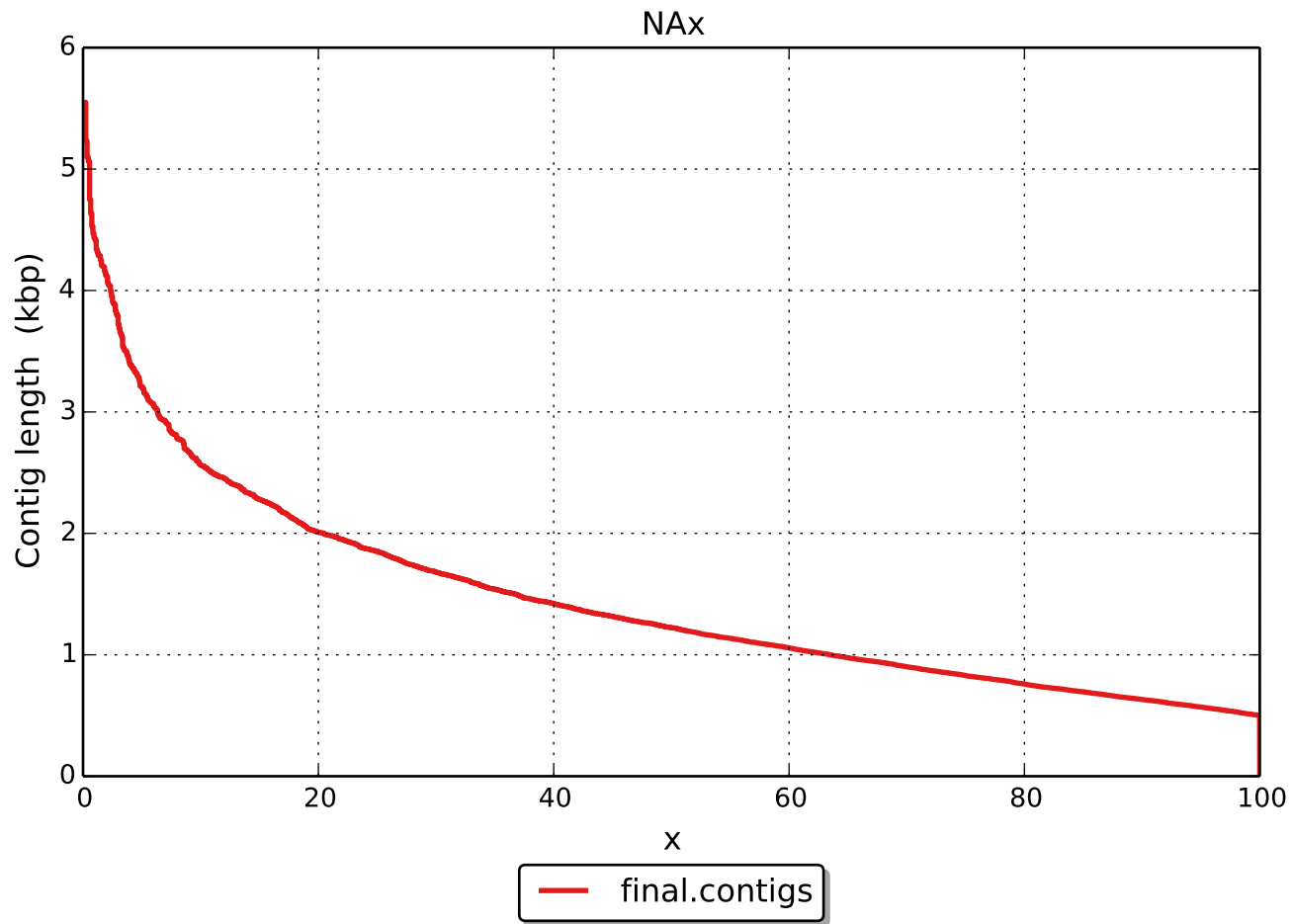




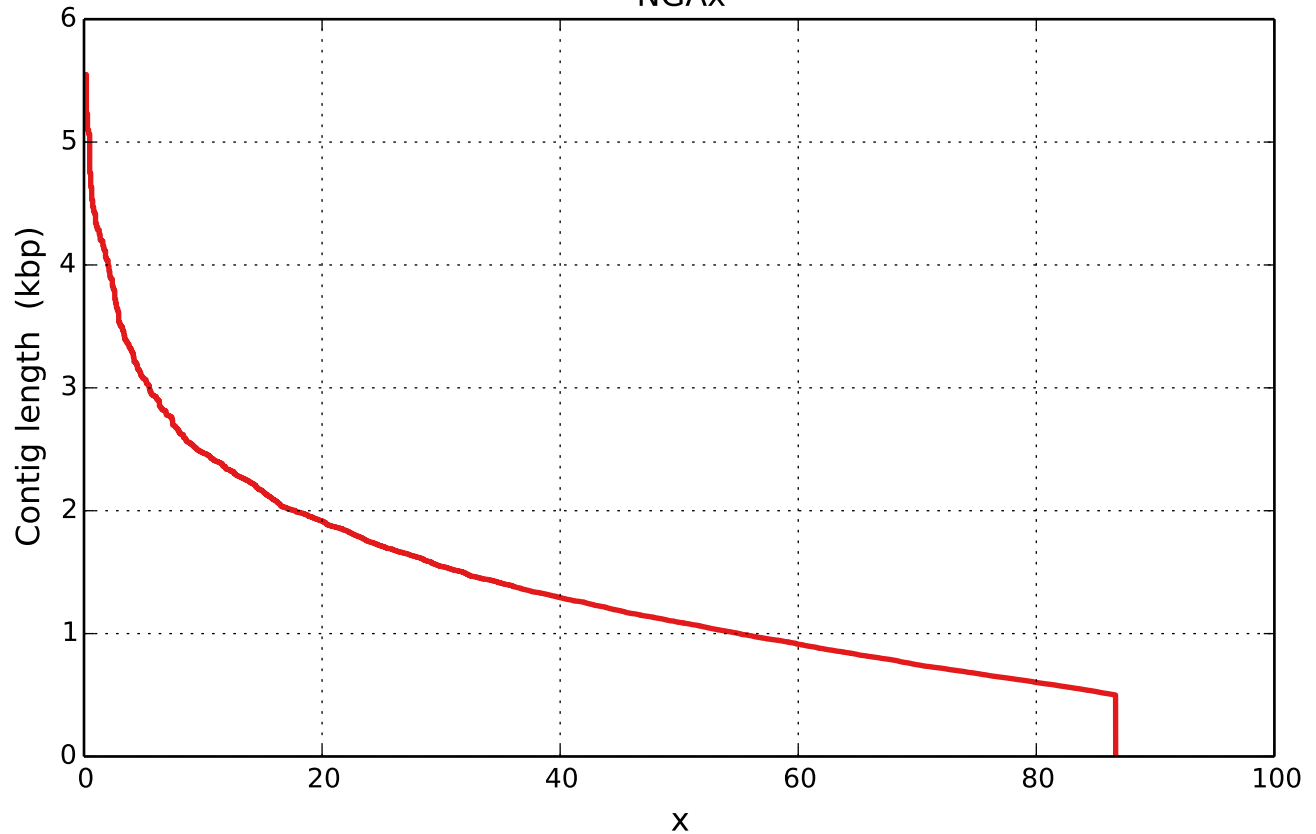
Misassemblies







NGAx



— final.contigs