

Report

	final.contigs
# contigs (≥ 0 bp)	3004
# contigs (≥ 1000 bp)	795
Total length (≥ 0 bp)	2682035
Total length (≥ 1000 bp)	1132122
# contigs	3004
Largest contig	3974
Total length	2682035
Reference length	1892775
GC (%)	32.30
Reference GC (%)	32.26
N50	914
NG50	1088
N75	682
NG75	887
L50	1014
LG50	617
L75	1863
LG75	1102
# misassemblies	38
# misassembled contigs	37
Misassembled contigs length	39714
# local misassemblies	0
# unaligned contigs	1 + 1 part
Unaligned length	915
Genome fraction (%)	85.819
Duplication ratio	1.651
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1167.23
# indels per 100 kbp	0.37
Largest alignment	3974
NA50	907
NGA50	1082
NA75	678
NGA75	882
LA50	1022
LGA50	622
LA75	1875
LGA75	1109

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	38
# relocations	38
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	37
Misassembled contigs length	39714
# local misassemblies	0
# mismatches	18960
# indels	6
# short indels	6
# long indels	0
Indels length	6

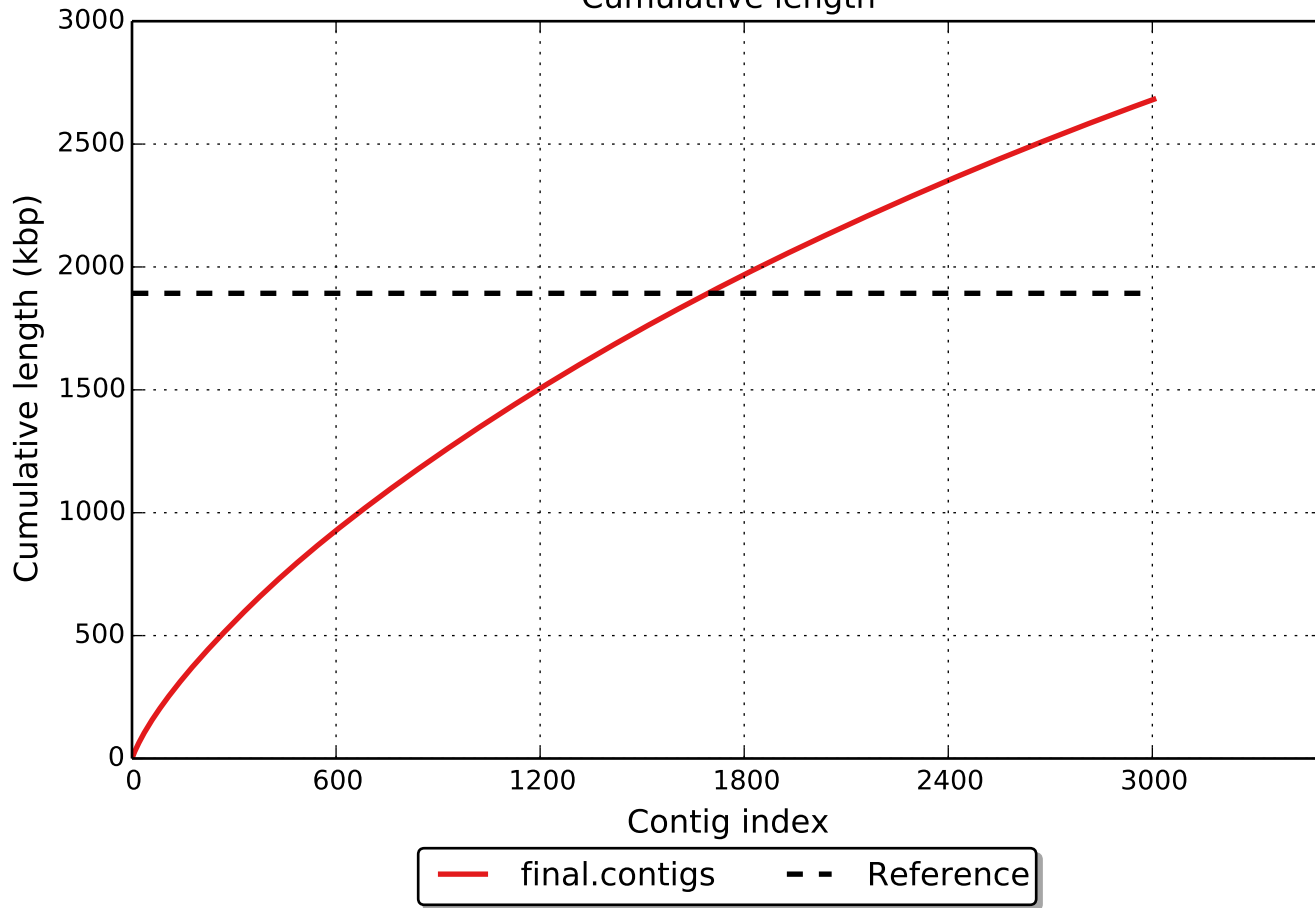
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

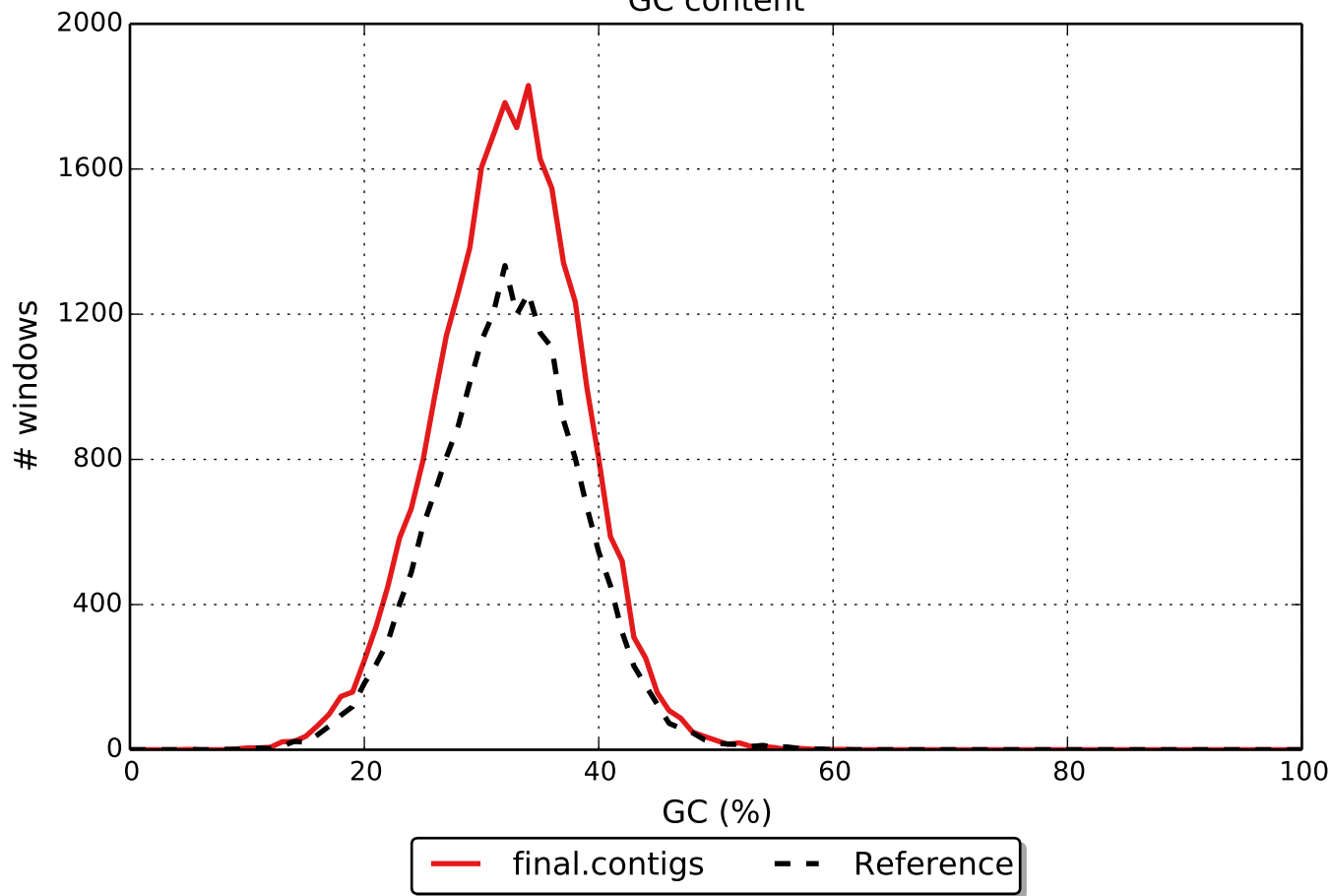
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	529
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	386
# N's	0

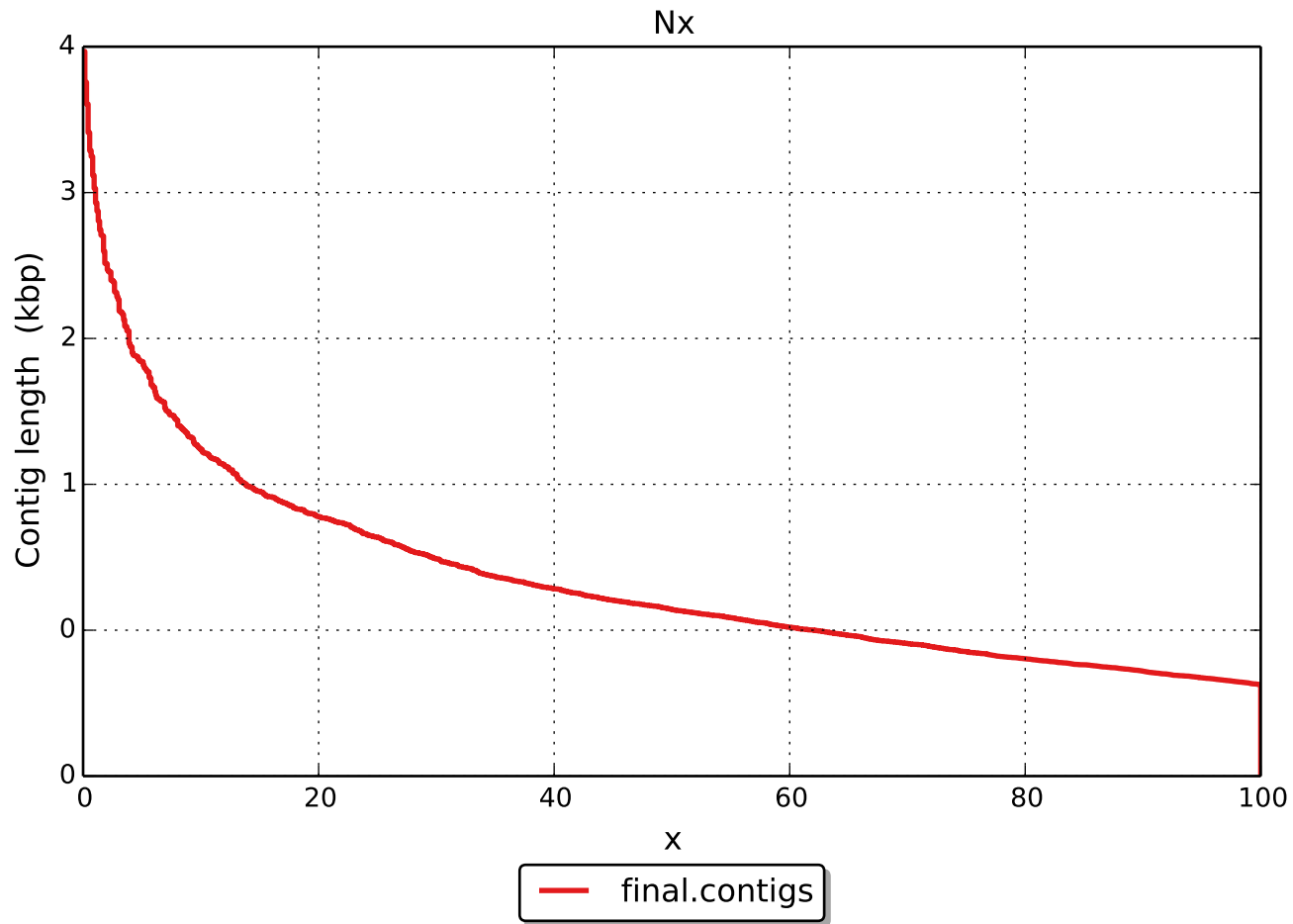
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

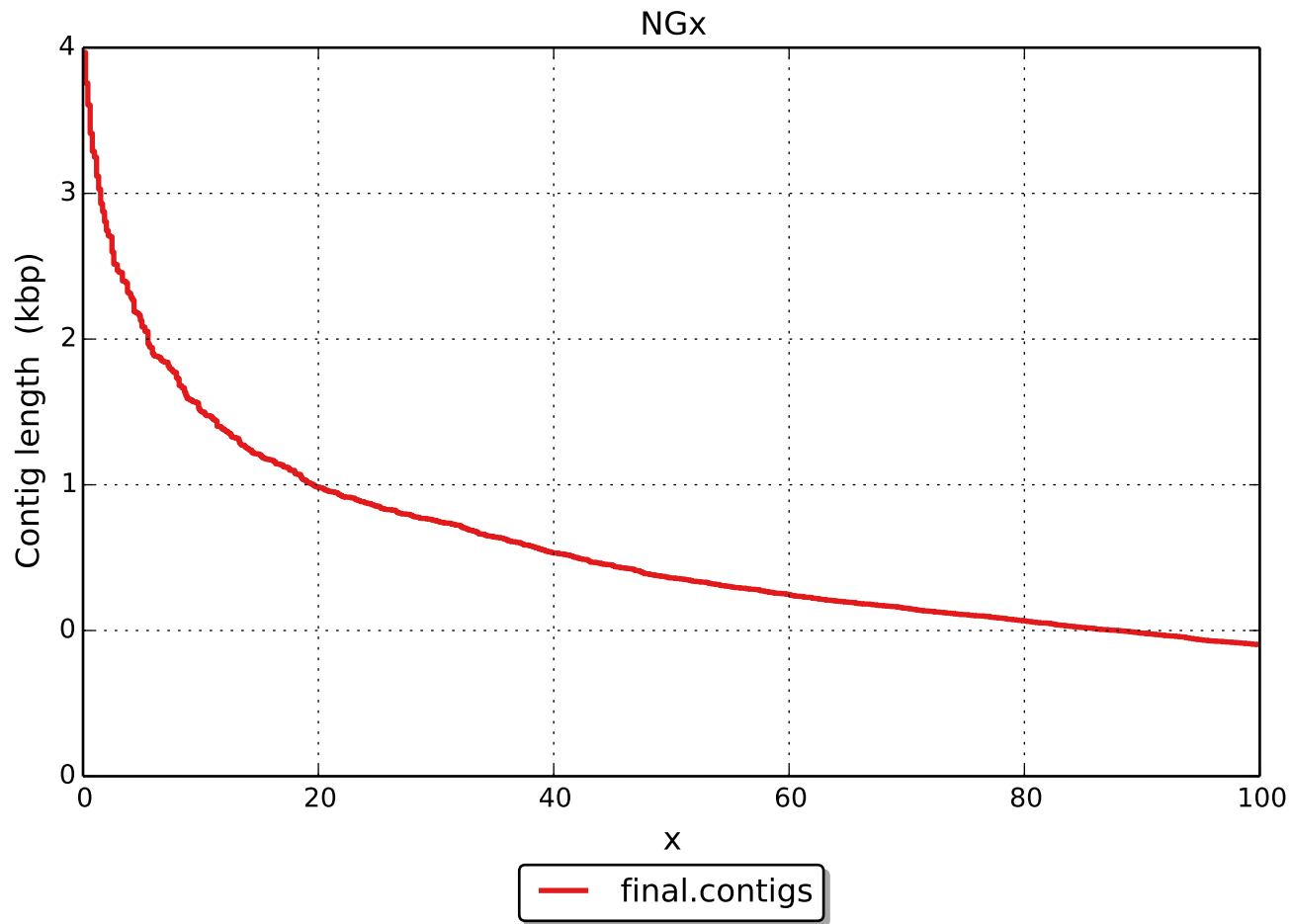
Cumulative length



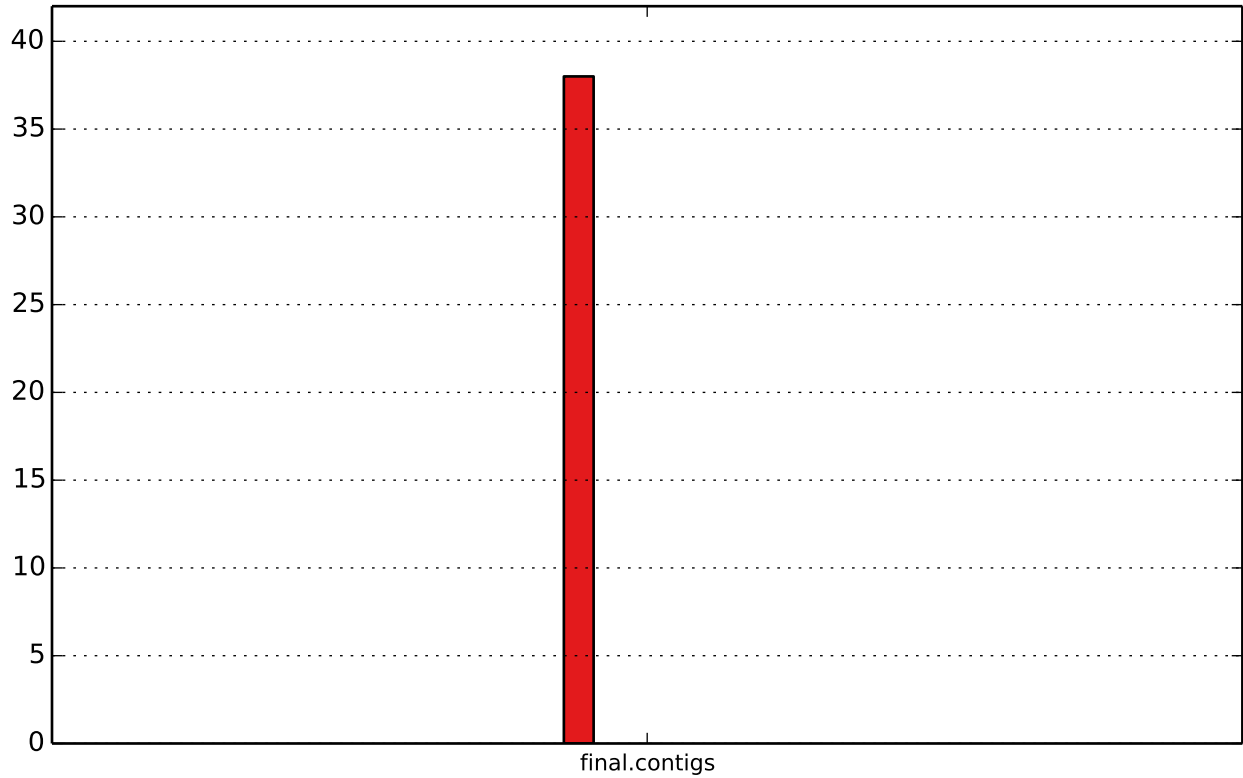
GC content





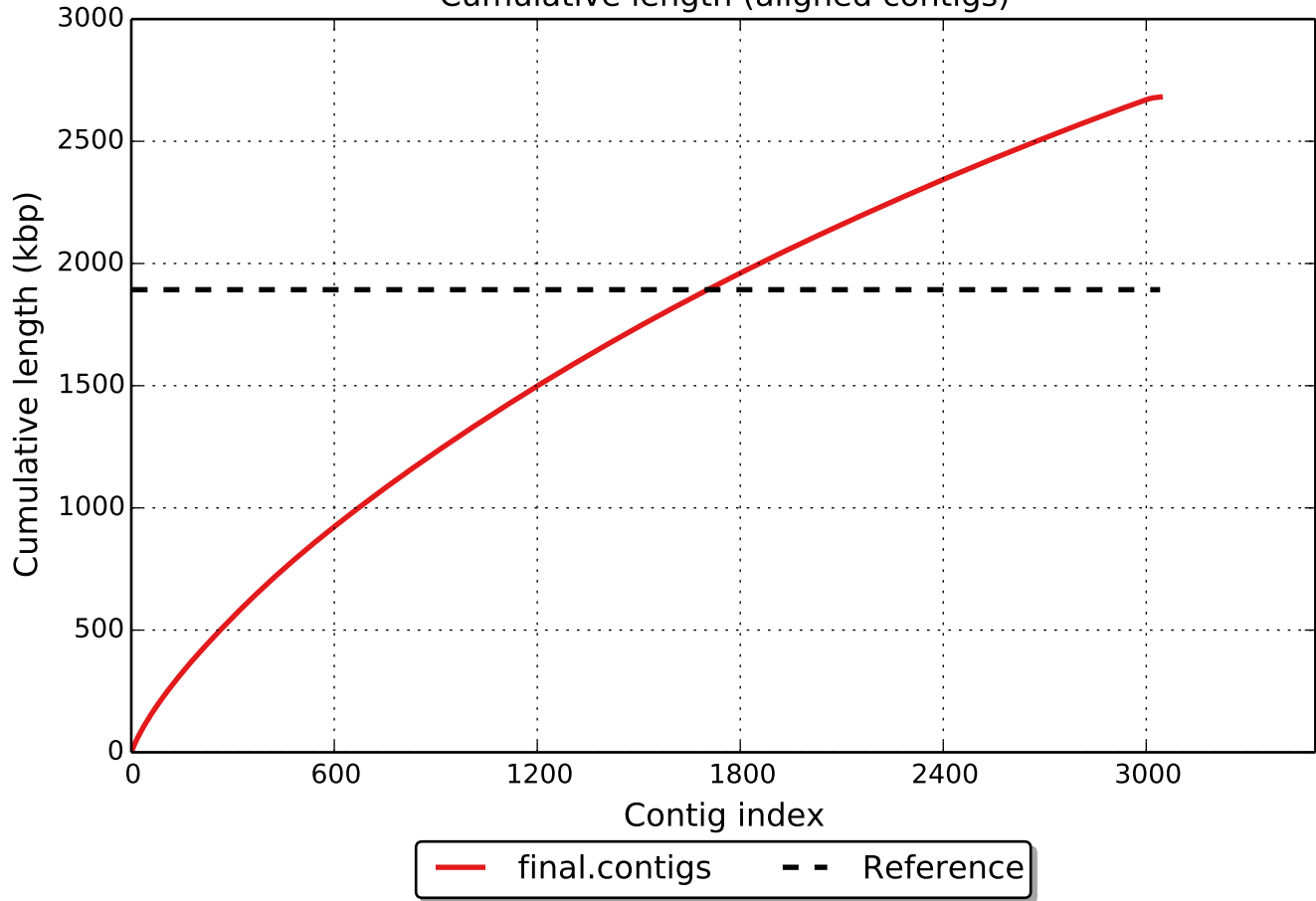


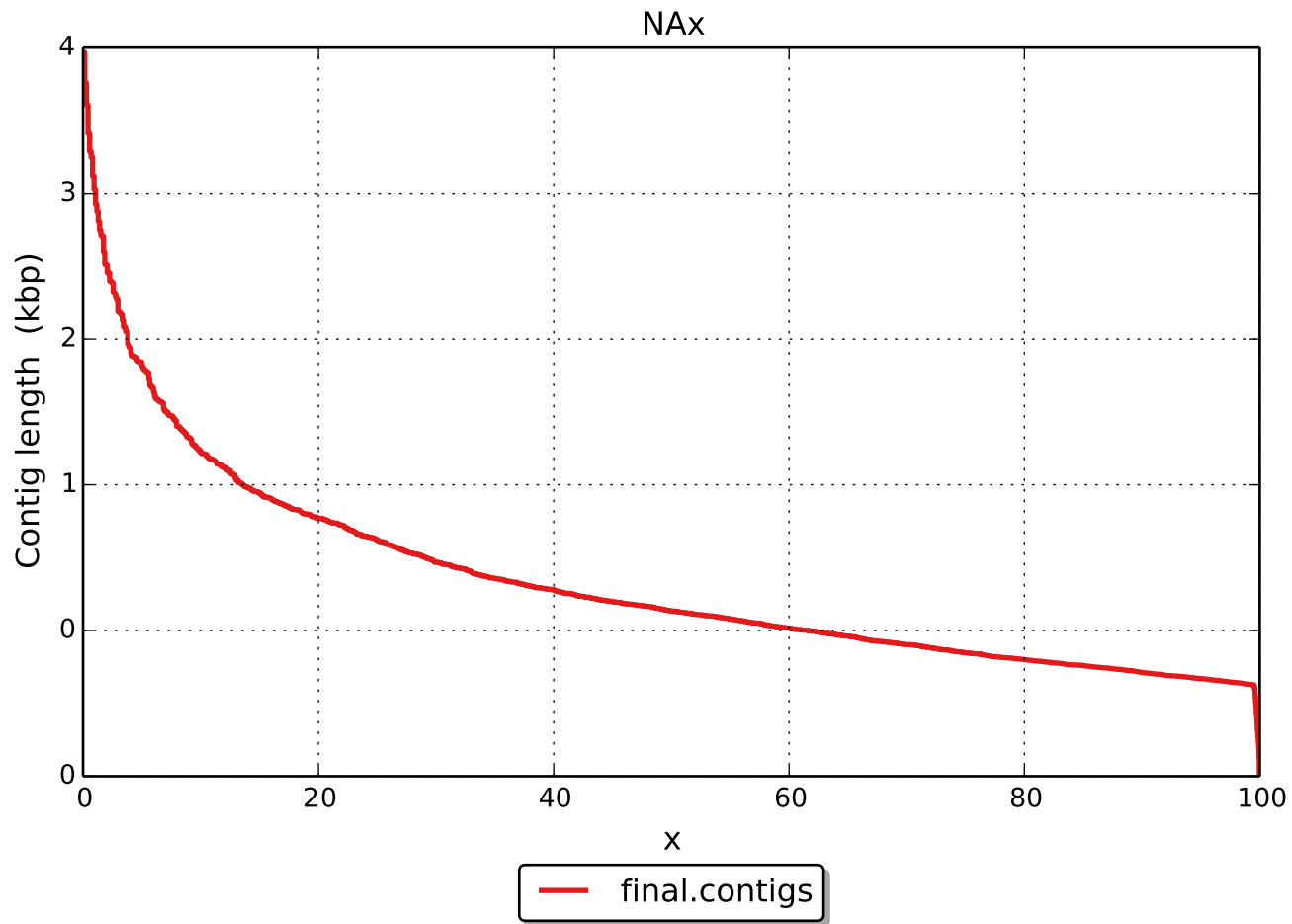
Misassemblies



 # relocations

Cumulative length (aligned contigs)





NGAx

