

Report

	final.contigs
# contigs (≥ 0 bp)	1210
# contigs (≥ 1000 bp)	253
Total length (≥ 0 bp)	961469
Total length (≥ 1000 bp)	446581
# contigs	749
Largest contig	5595
Total length	790680
Reference length	1231960
GC (%)	25.38
Reference GC (%)	25.34
N50	1155
NG50	707
N75	732
L50	206
LG50	457
L75	425
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.361
Duplication ratio	1.070
# N's per 100 kbp	0.00
# mismatches per 100 kbp	513.78
# indels per 100 kbp	0.19
Largest alignment	5595
NA50	1155
NGA50	707
NA75	732
LA50	206
LGA50	457
LA75	425

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	0
# mismatches	5403
# indels	2
# short indels	2
# long indels	0
Indels length	2

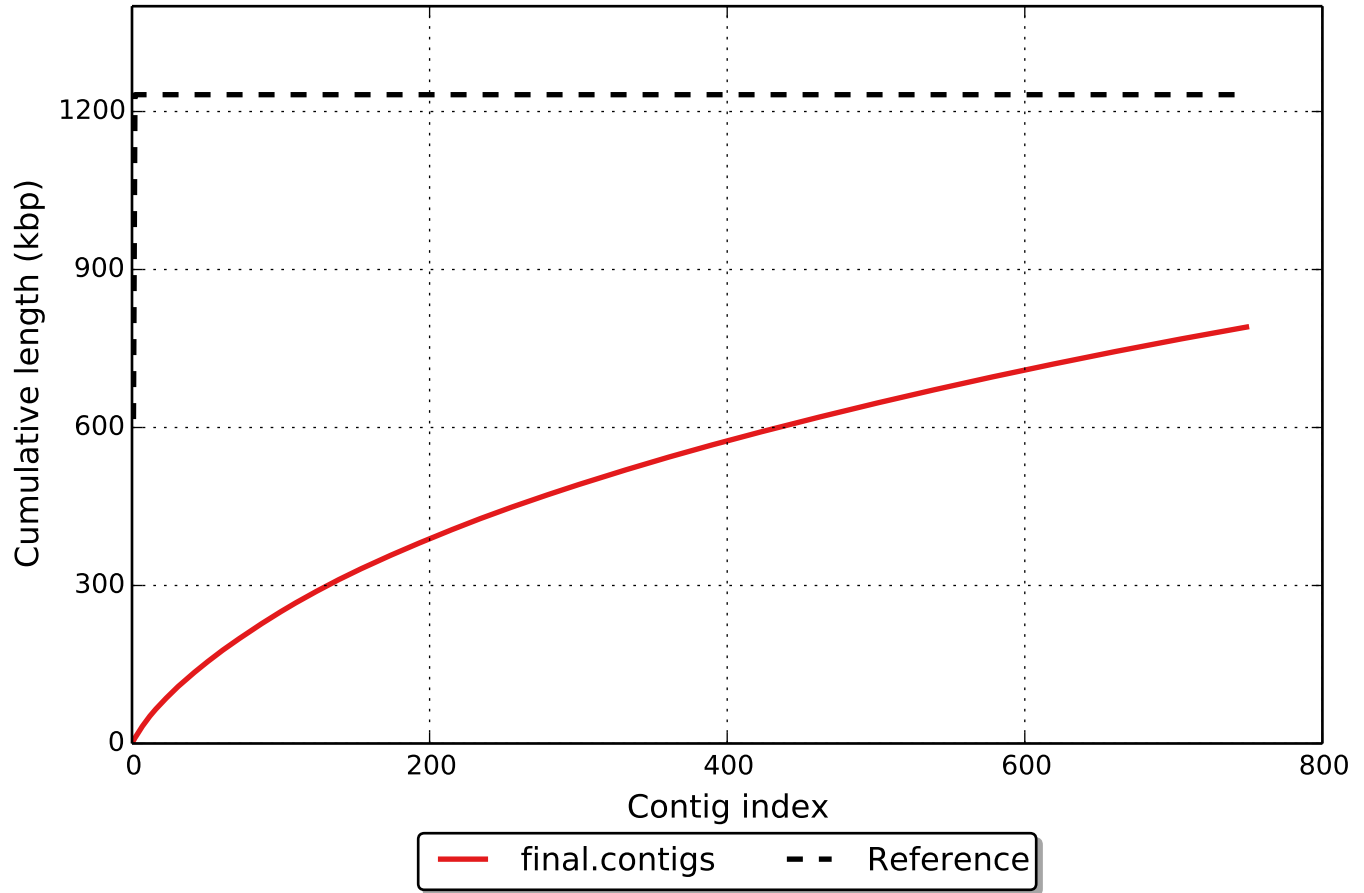
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

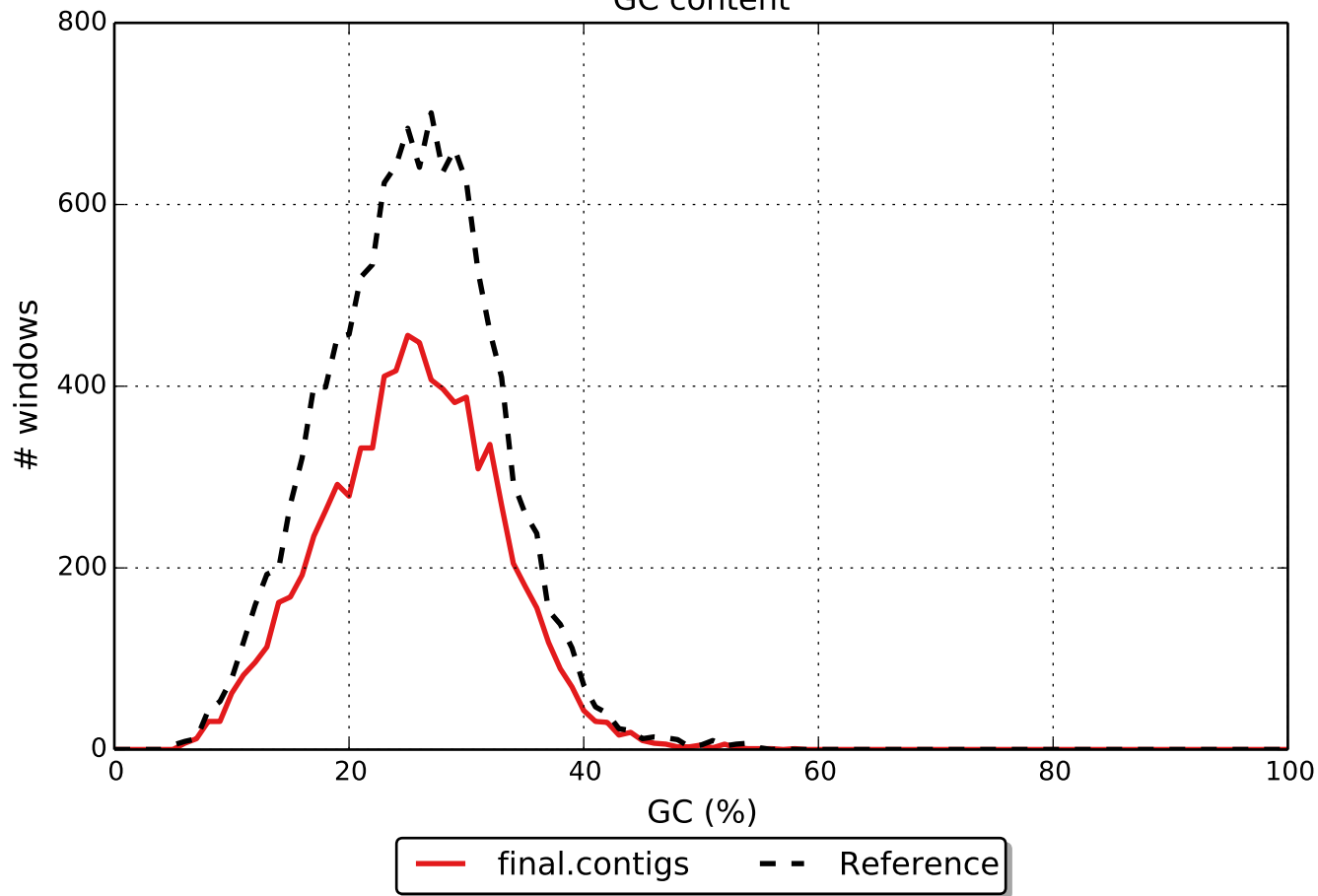
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

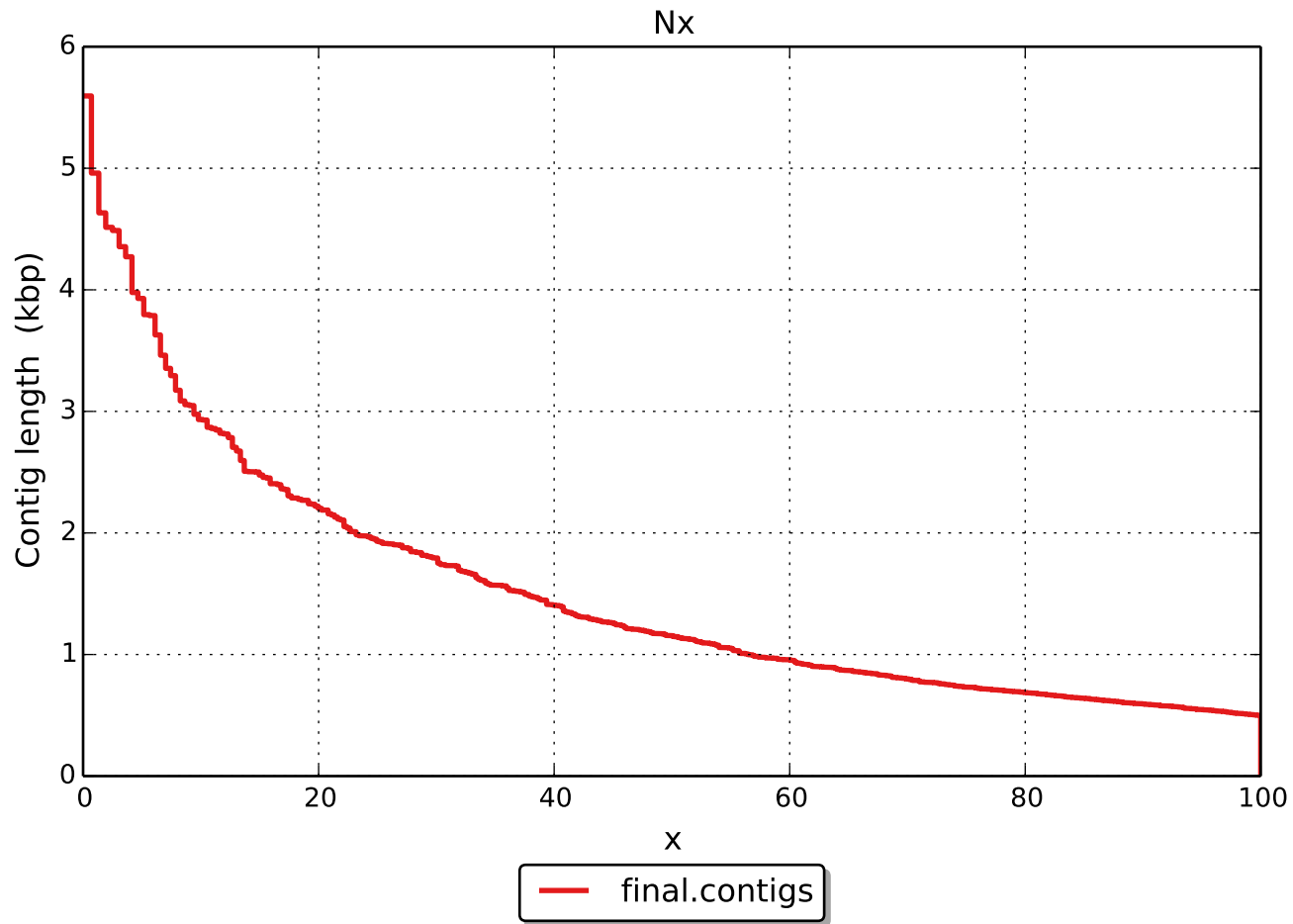
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

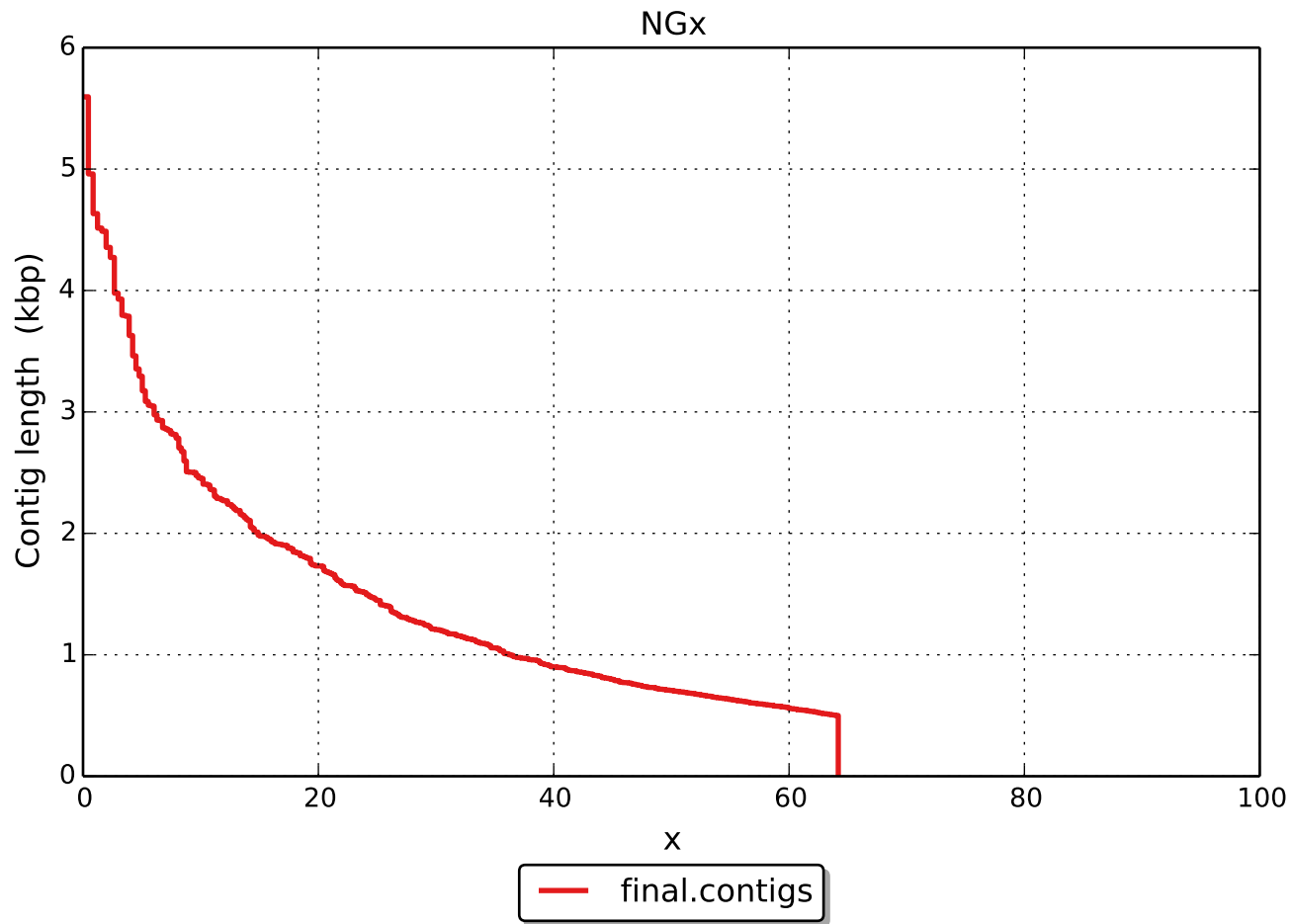
Cumulative length



GC content



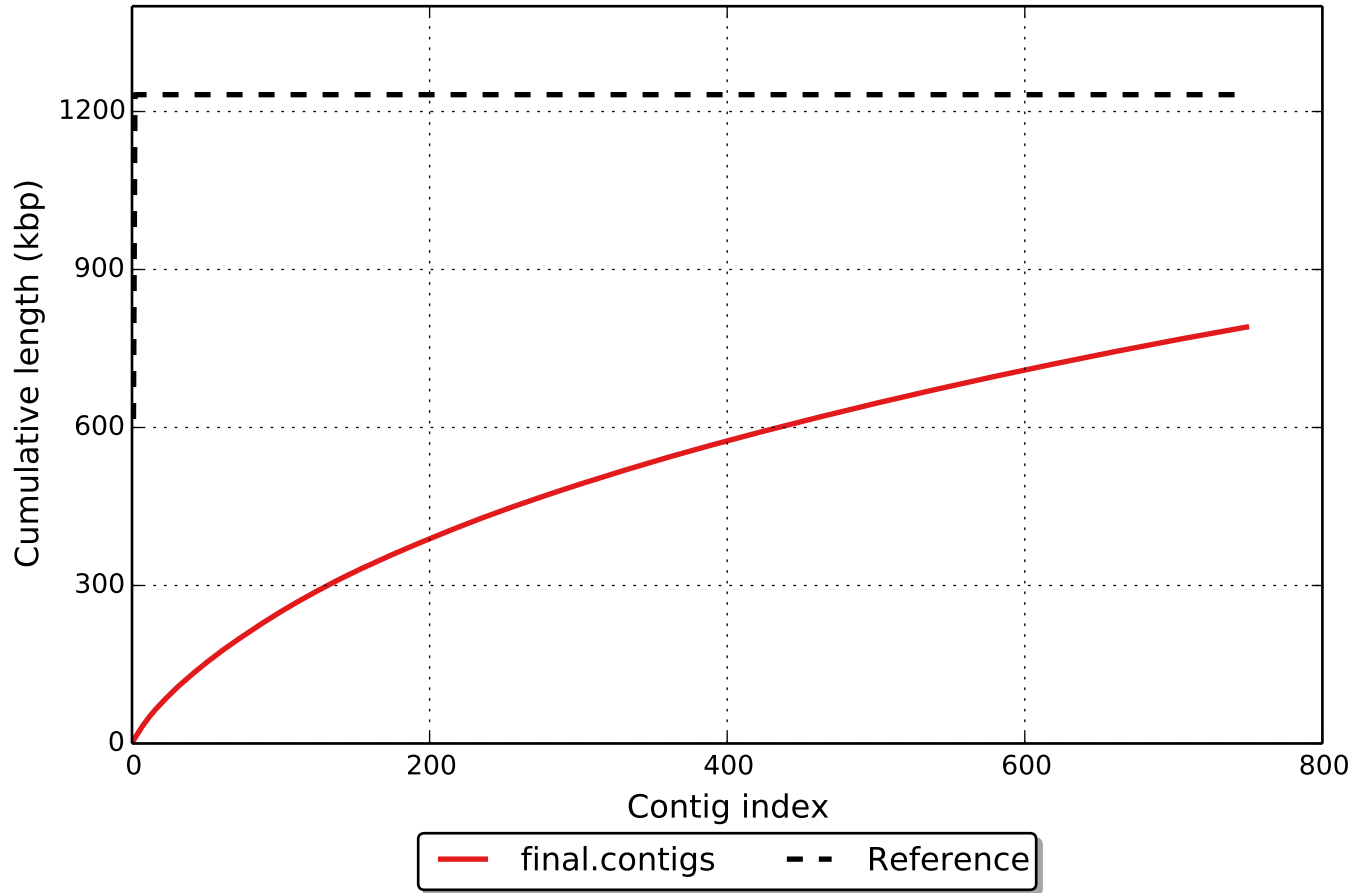


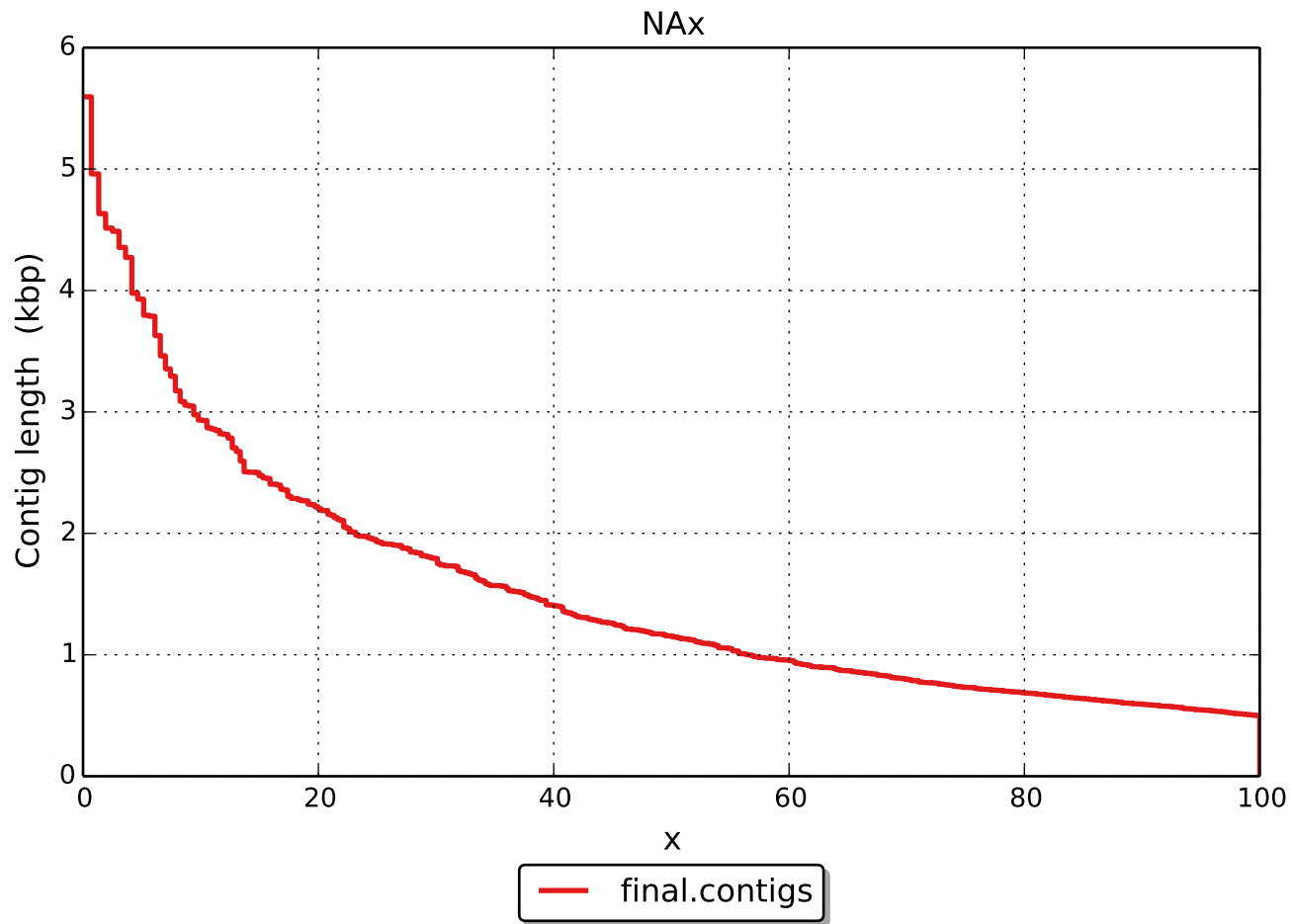


Misassemblies



Cumulative length (aligned contigs)





NGAx

