

Report

	final.contigs
# contigs (≥ 0 bp)	3065
# contigs (≥ 1000 bp)	1066
Total length (≥ 0 bp)	3176314
Total length (≥ 1000 bp)	1772753
# contigs	3065
Largest contig	5291
Total length	3176314
Reference length	1892775
GC (%)	32.26
Reference GC (%)	32.26
N50	1096
NG50	1671
N75	755
NG75	1199
L50	890
LG50	406
L75	1766
LG75	743
# misassemblies	30
# misassembled contigs	30
Misassembled contigs length	30021
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	246
Genome fraction (%)	86.611
Duplication ratio	1.937
# N's per 100 kbp	0.00
# mismatches per 100 kbp	997.47
# indels per 100 kbp	0.31
Largest alignment	5291
NA50	771
NGA50	1125
NGA75	851
LA50	1234
LGA50	540
LGA75	1026

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

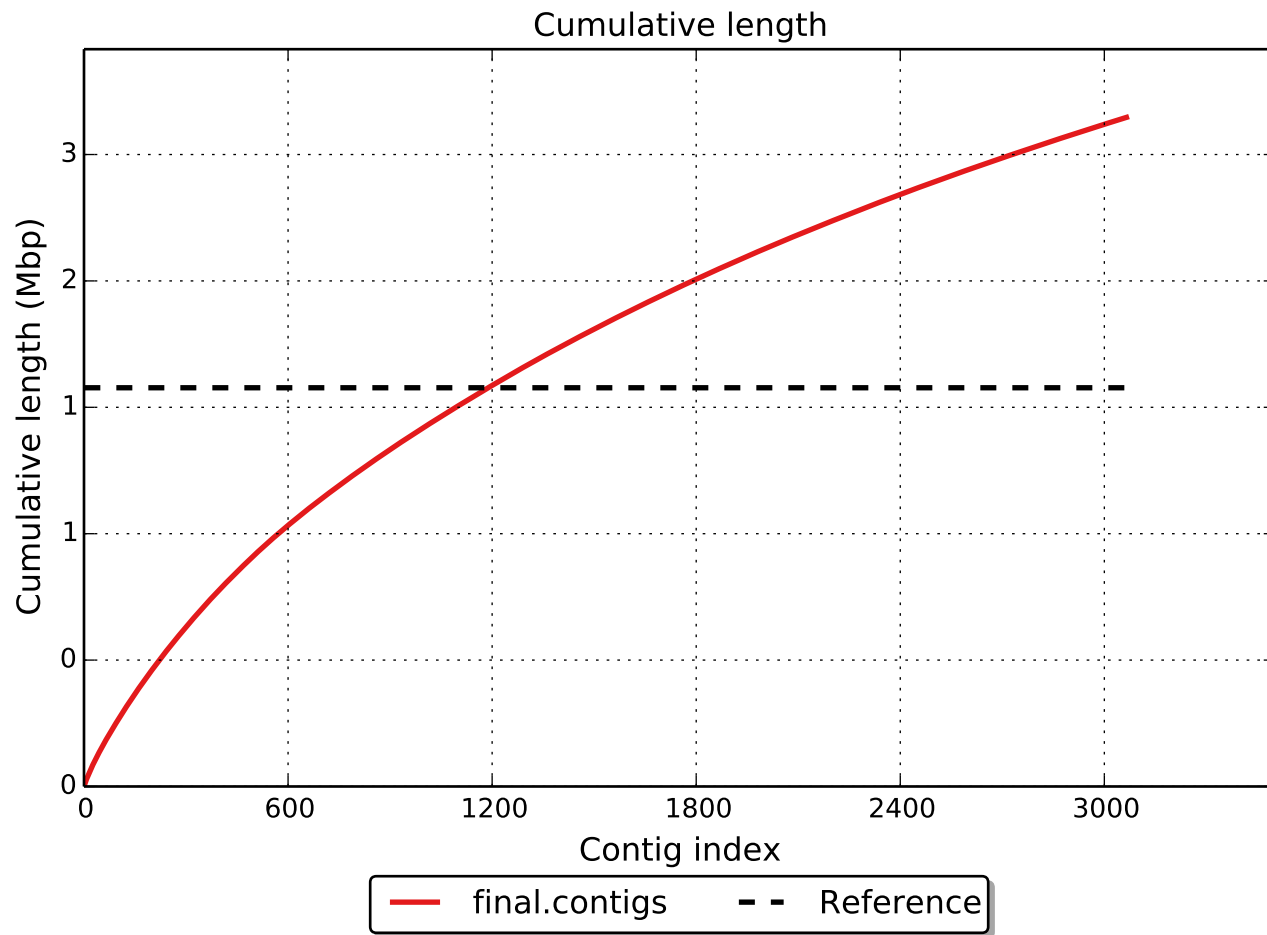
	final.contigs
# misassemblies	30
# relocations	28
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	30
Misassembled contigs length	30021
# local misassemblies	0
# mismatches	16352
# indels	5
# short indels	4
# long indels	1
Indels length	22

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).

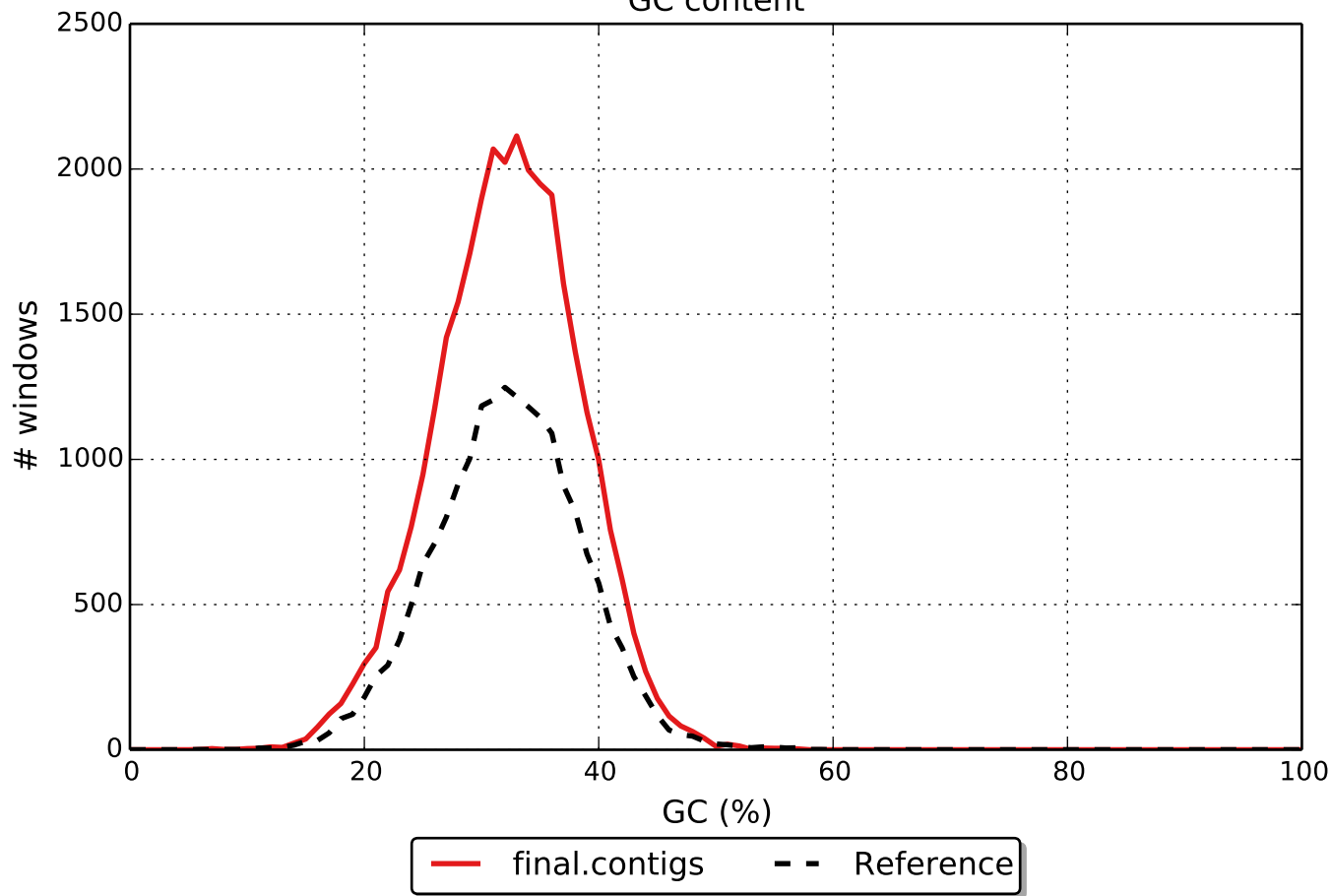
Unaligned report

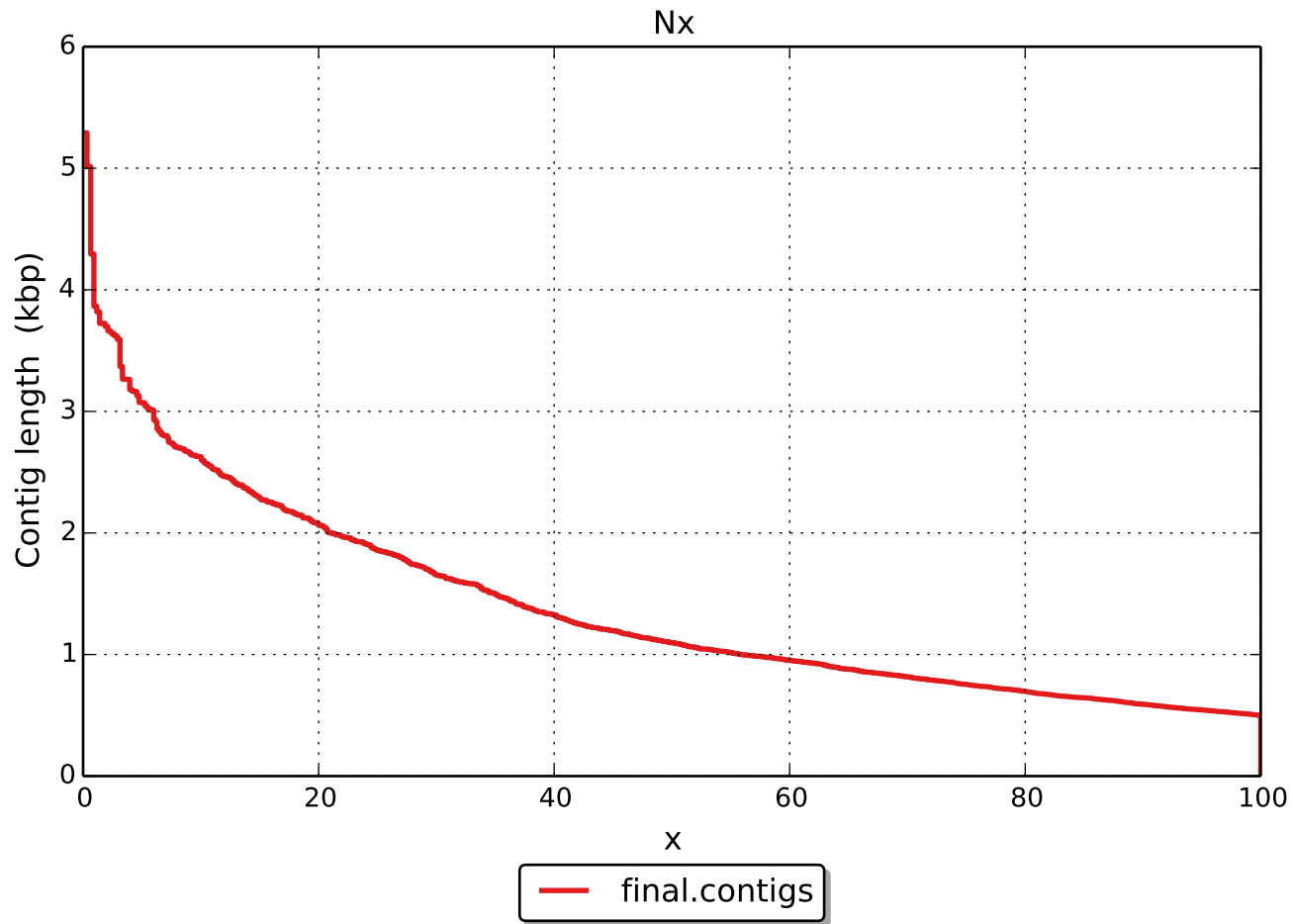
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	246
# N's	0

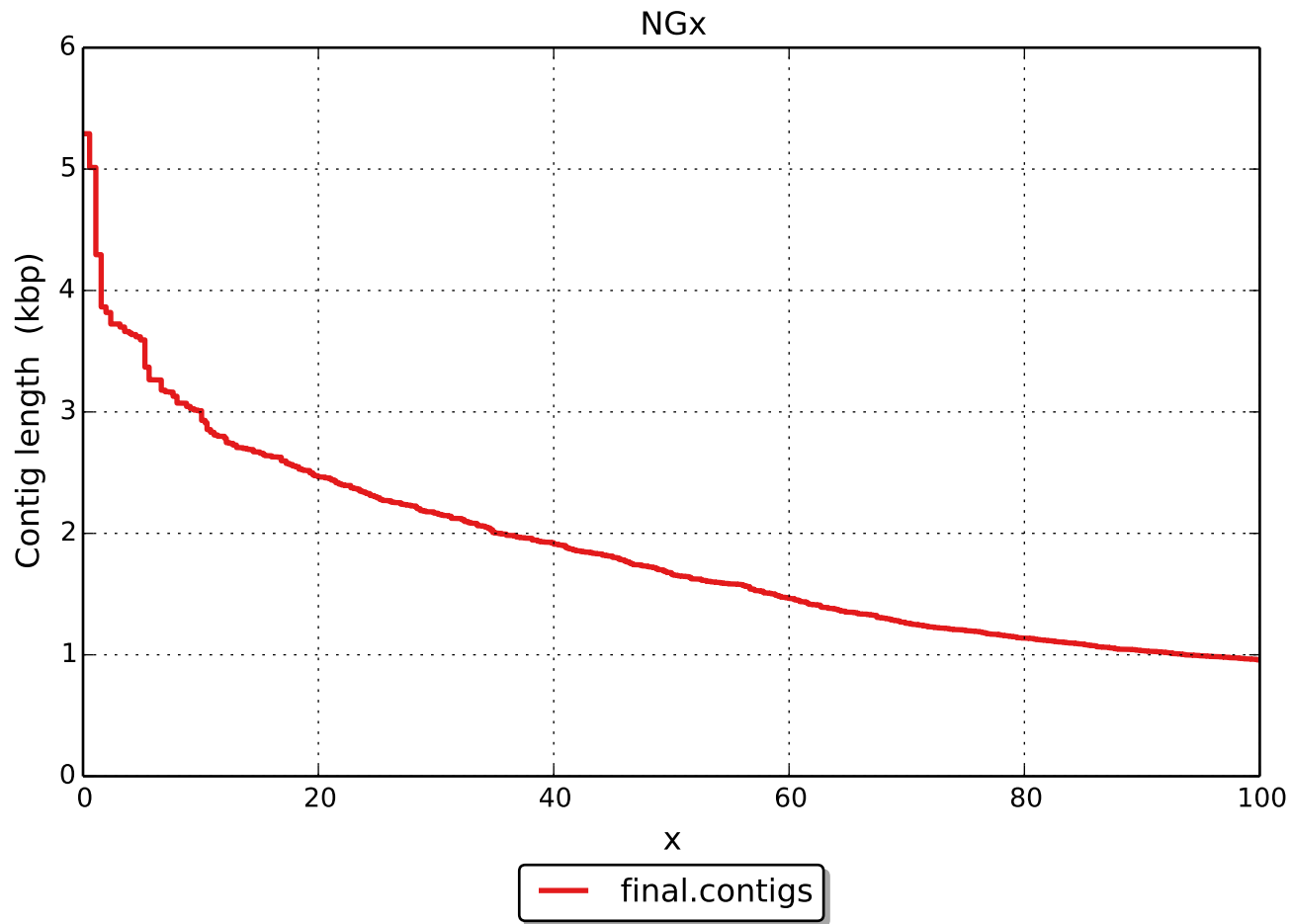
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



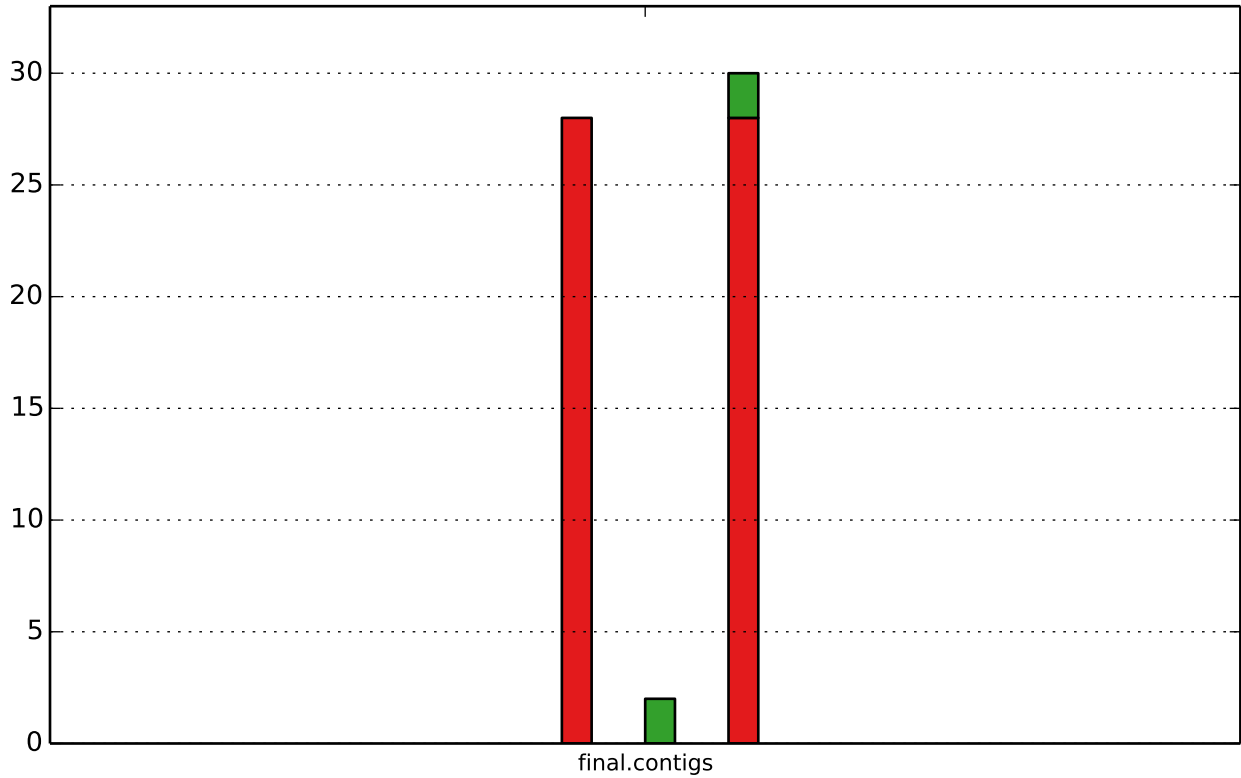
GC content



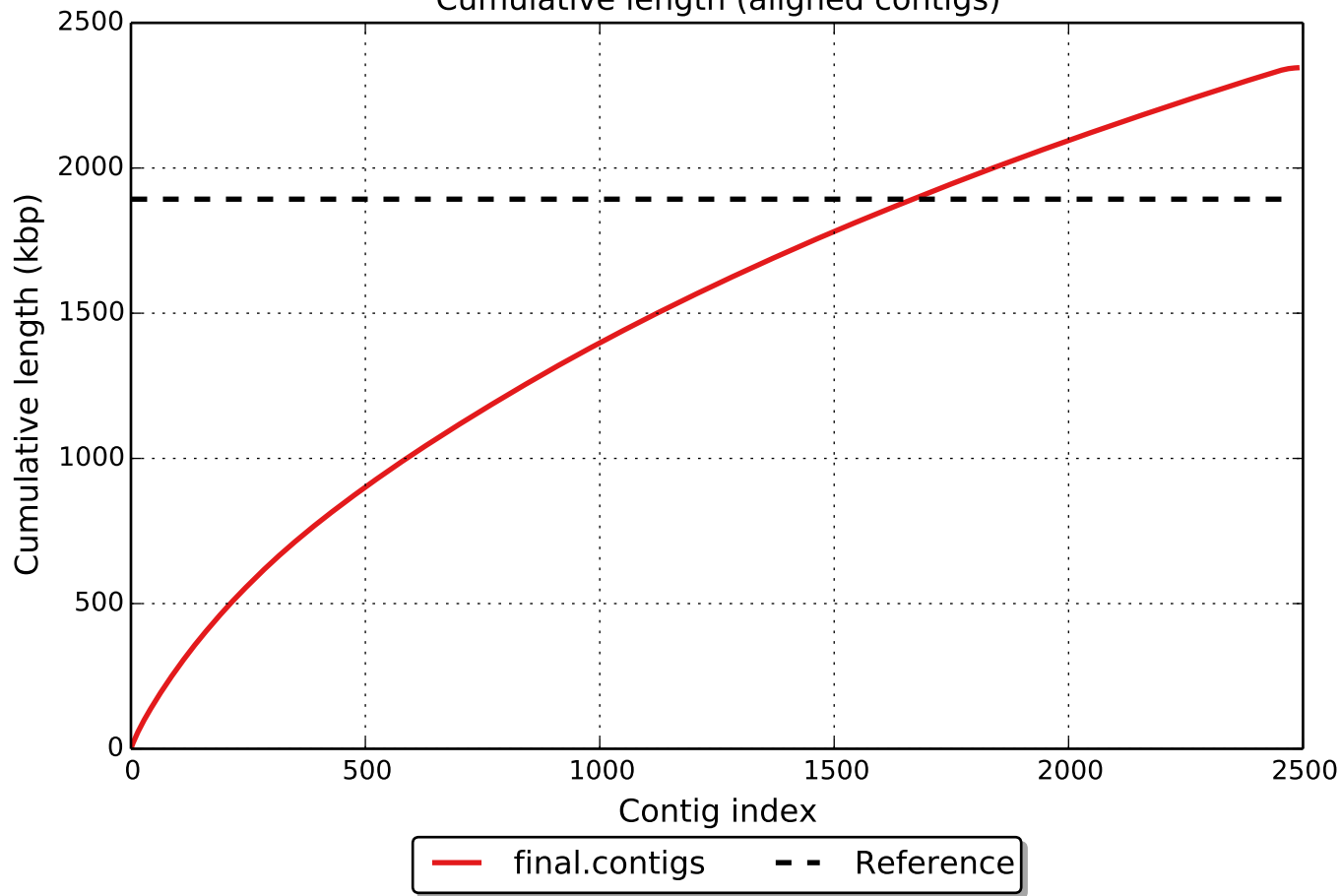


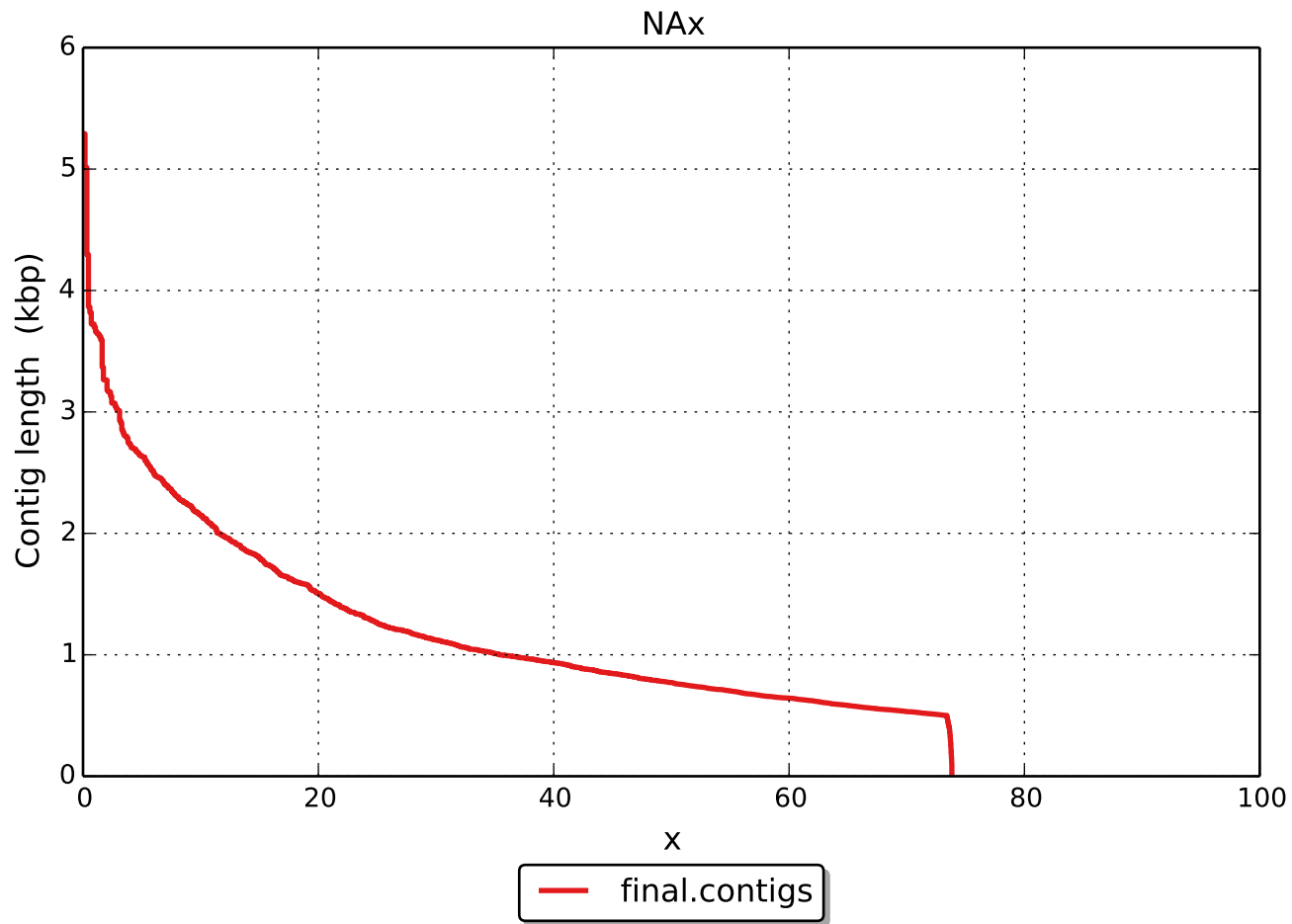


Misassemblies



Cumulative length (aligned contigs)





NGAx

