

Report

	final.contigs
# contigs (≥ 0 bp)	1630
# contigs (≥ 1000 bp)	349
Total length (≥ 0 bp)	1197605
Total length (≥ 1000 bp)	478013
# contigs	1087
Largest contig	3516
Total length	1000855
Reference length	1231960
GC (%)	25.37
Reference GC (%)	25.35
N50	972
NG50	842
N75	727
NG75	566
L50	372
LG50	500
L75	672
LG75	944
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	77.293
Duplication ratio	1.051
# N's per 100 kbp	0.00
# mismatches per 100 kbp	108.17
# indels per 100 kbp	0.00
Largest alignment	3516
NA50	972
NGA50	842
NA75	727
NGA75	566
LA50	372
LGA50	500
LA75	672
LGA75	944

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	1030
# indels	0
# short indels	0
# long indels	0
Indels length	0

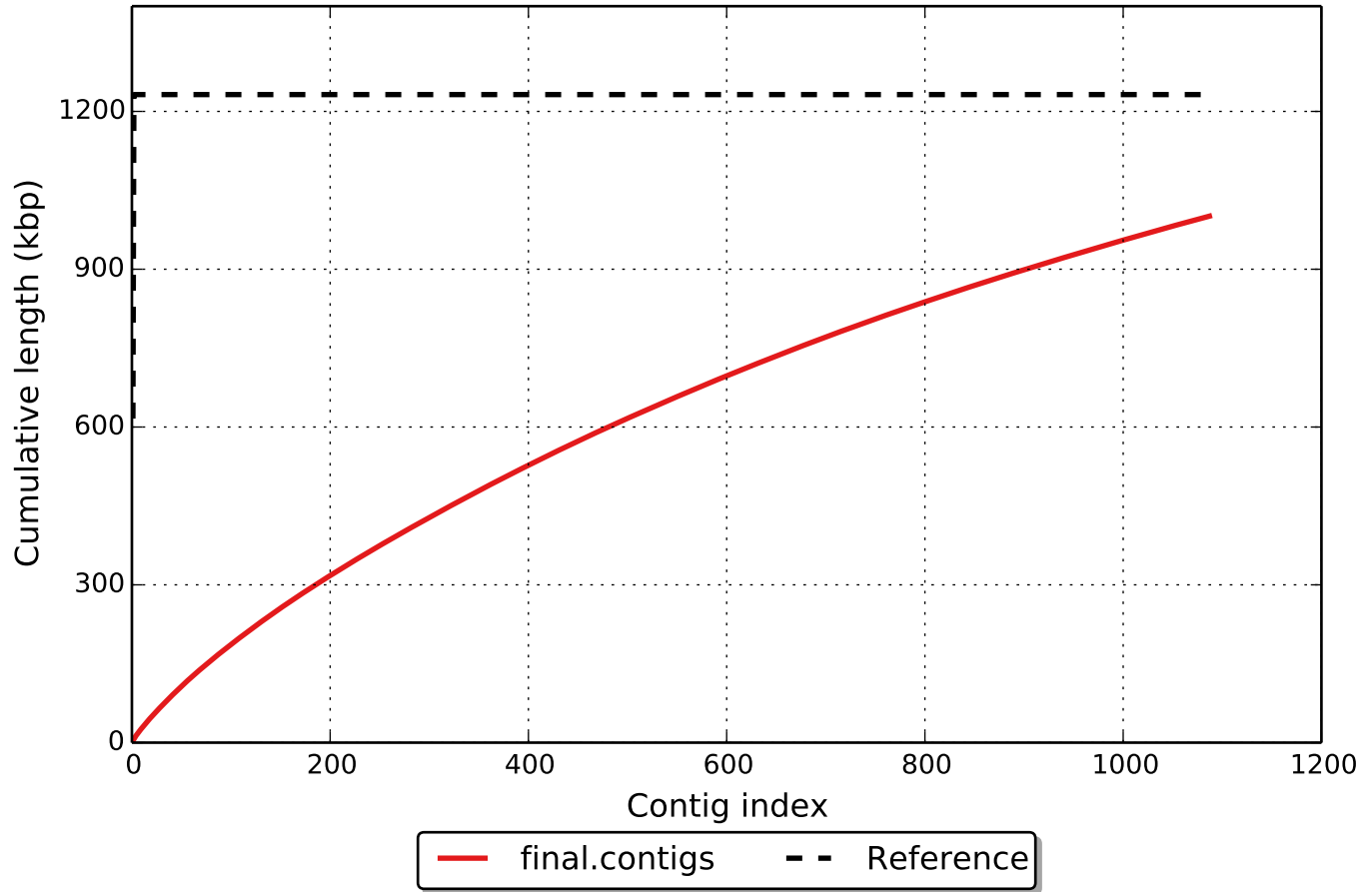
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

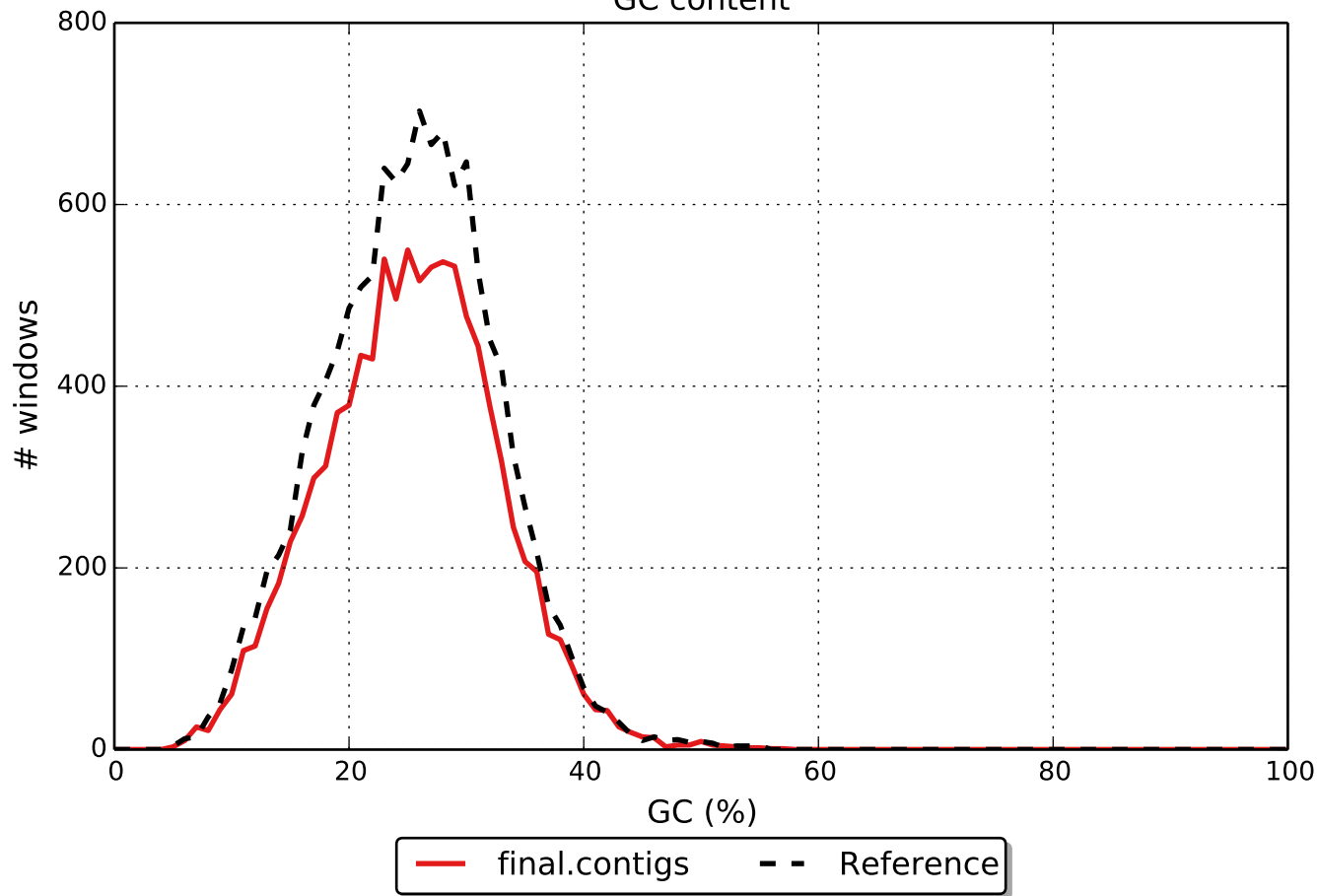
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

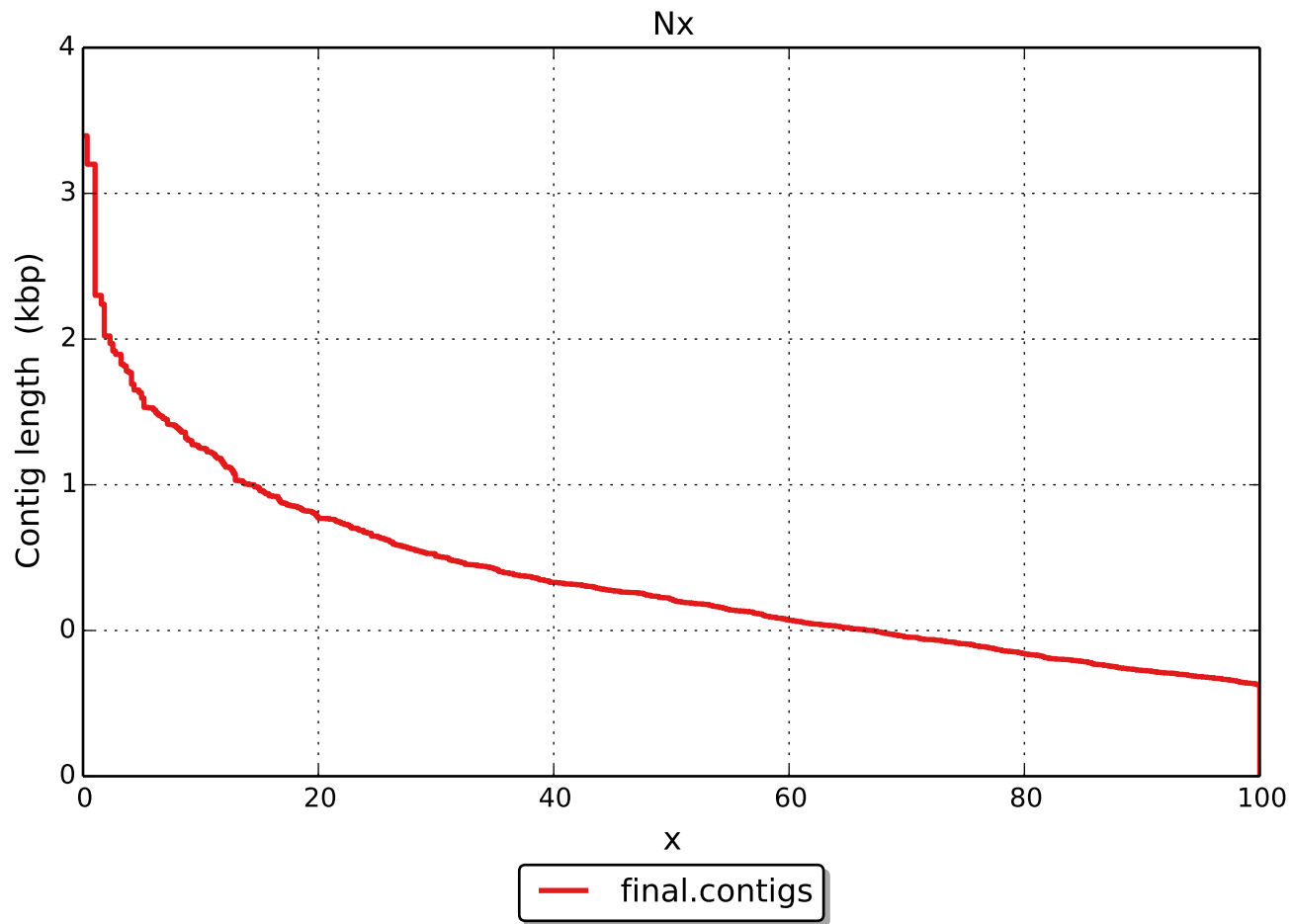
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

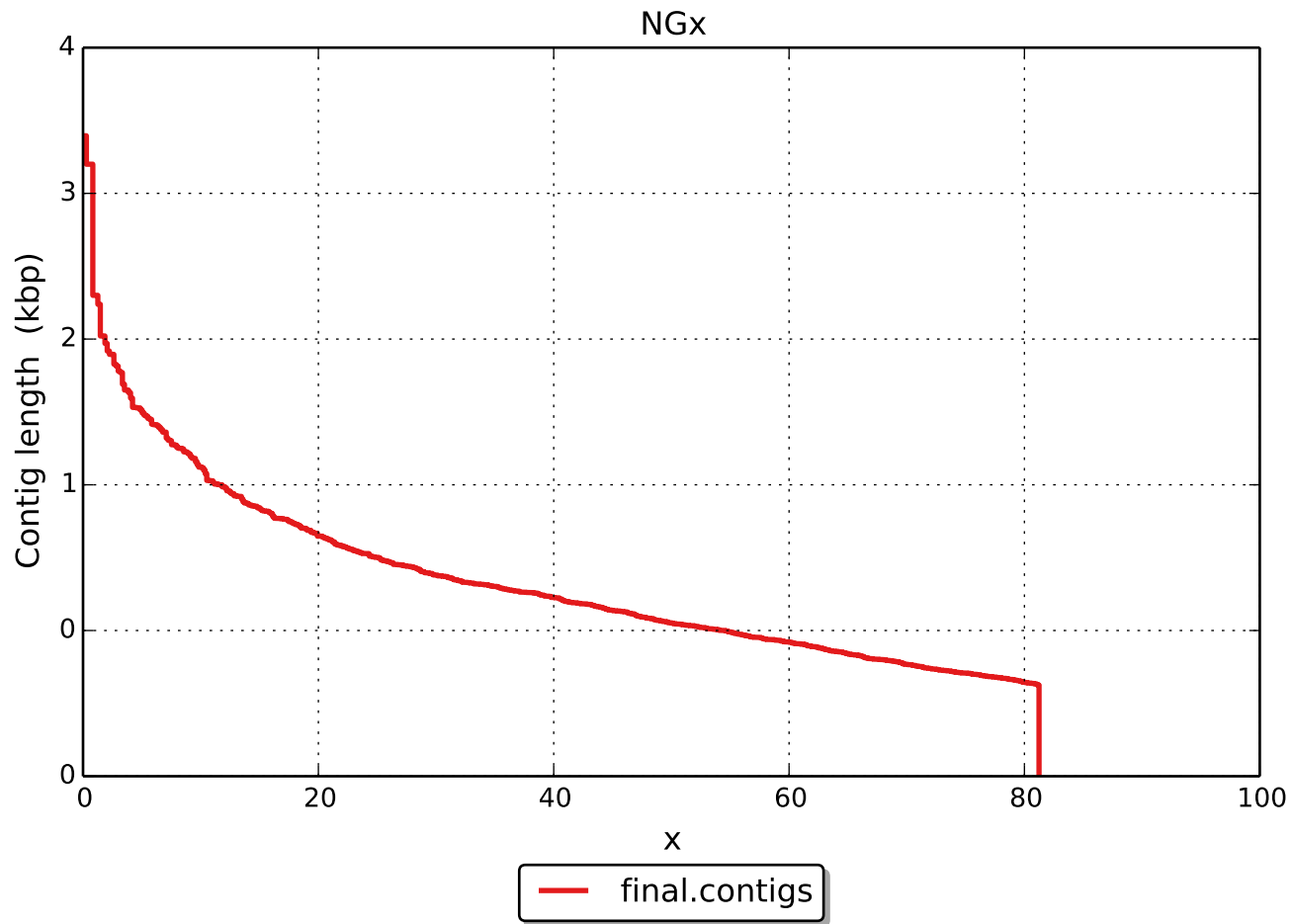
Cumulative length



GC content



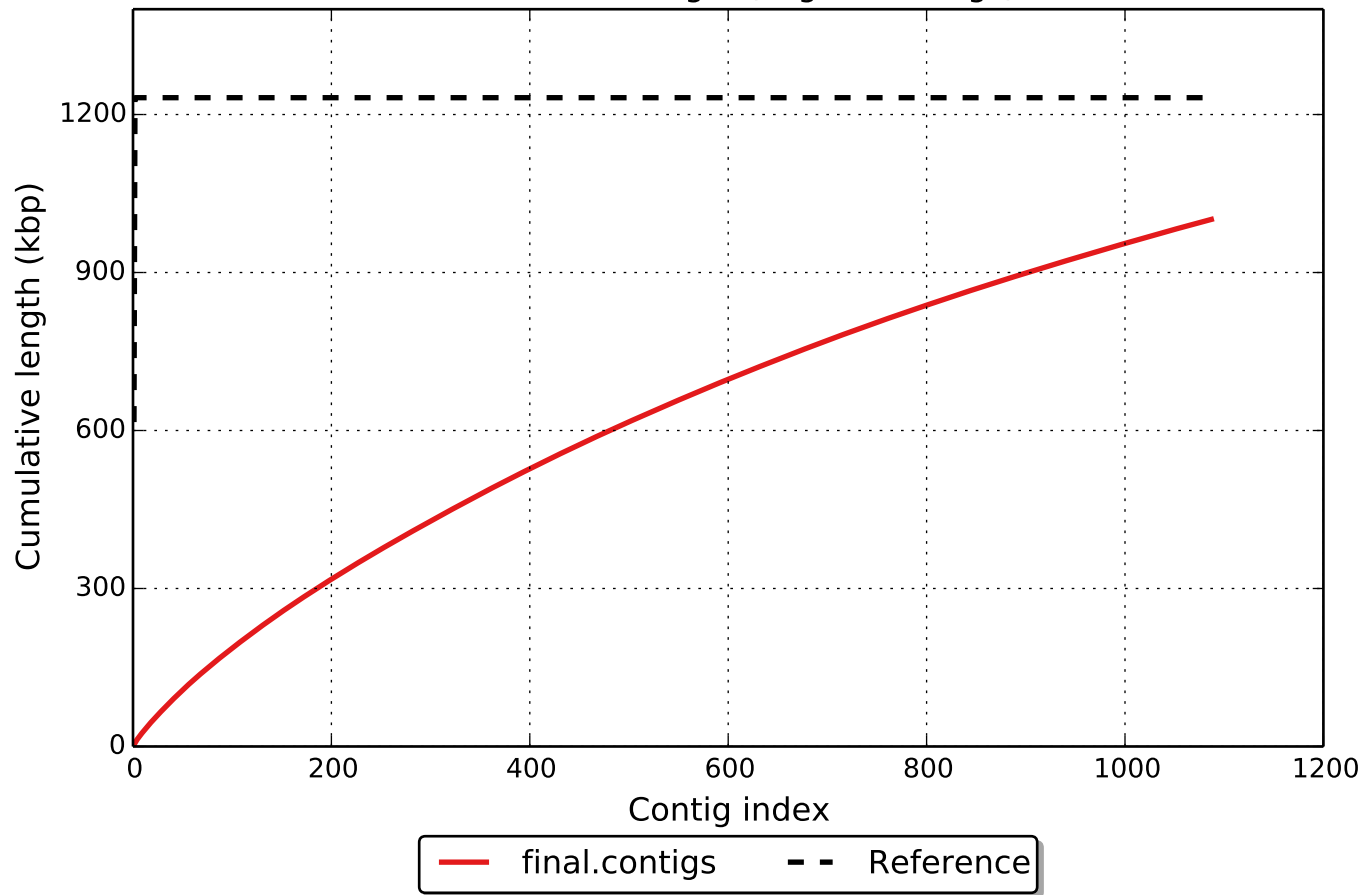


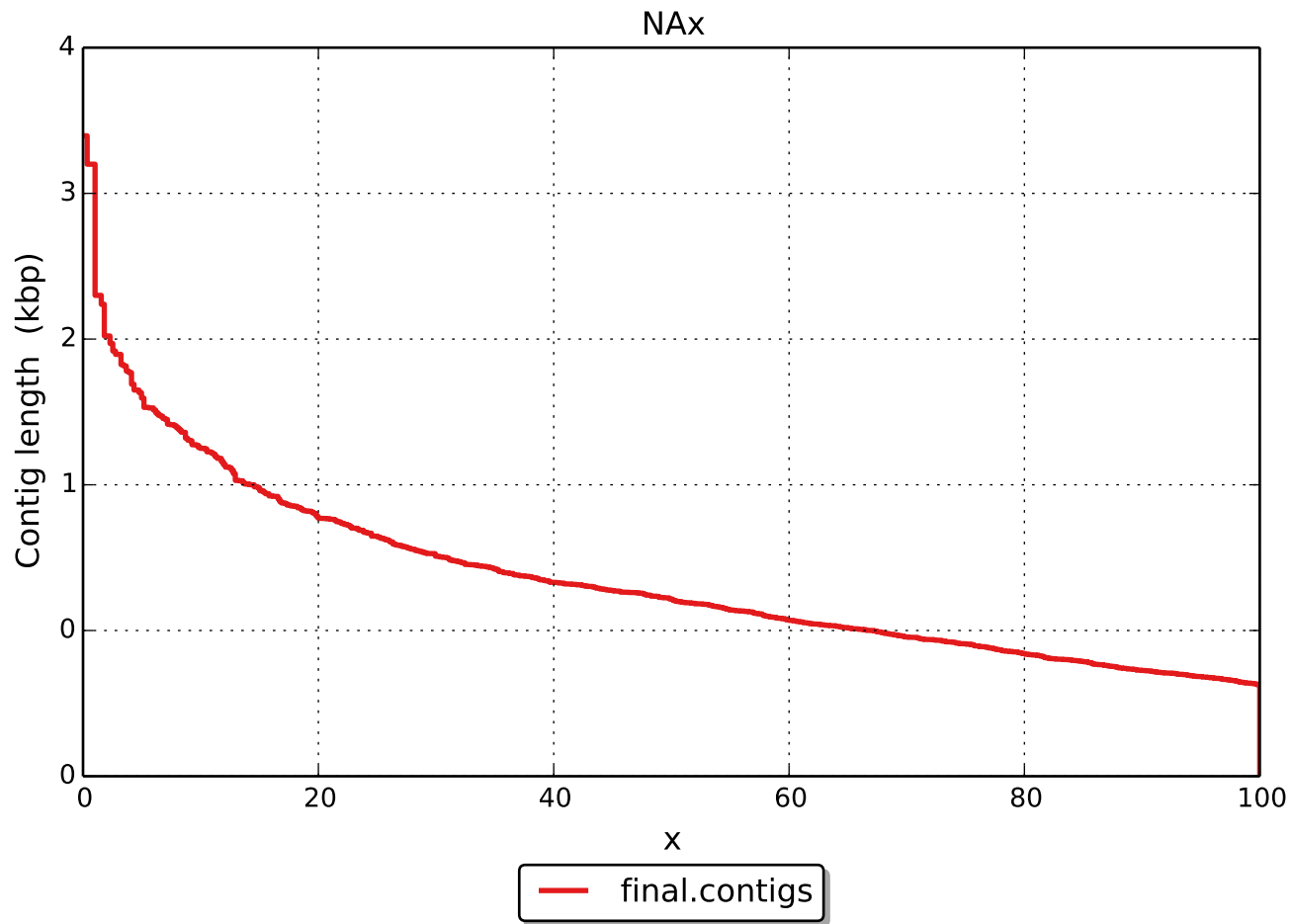


Misassemblies



Cumulative length (aligned contigs)





NGAx

