

Report

	final.contigs
# contigs (≥ 0 bp)	4622
# contigs (≥ 1000 bp)	2042
Total length (≥ 0 bp)	5179795
Total length (≥ 1000 bp)	3326922
# contigs	4622
Largest contig	5549
Total length	5179795
Reference length	5547323
GC (%)	50.46
Reference GC (%)	50.49
N50	1243
NG50	1177
N75	843
NG75	768
L50	1381
LG50	1533
L75	2650
LG75	2992
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	135
Genome fraction (%)	88.662
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	81.12
# indels per 100 kbp	0.00
Largest alignment	5549
NA50	1243
NGA50	1177
NA75	843
NGA75	768
LA50	1381
LGA50	1533
LA75	2650
LGA75	2992

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

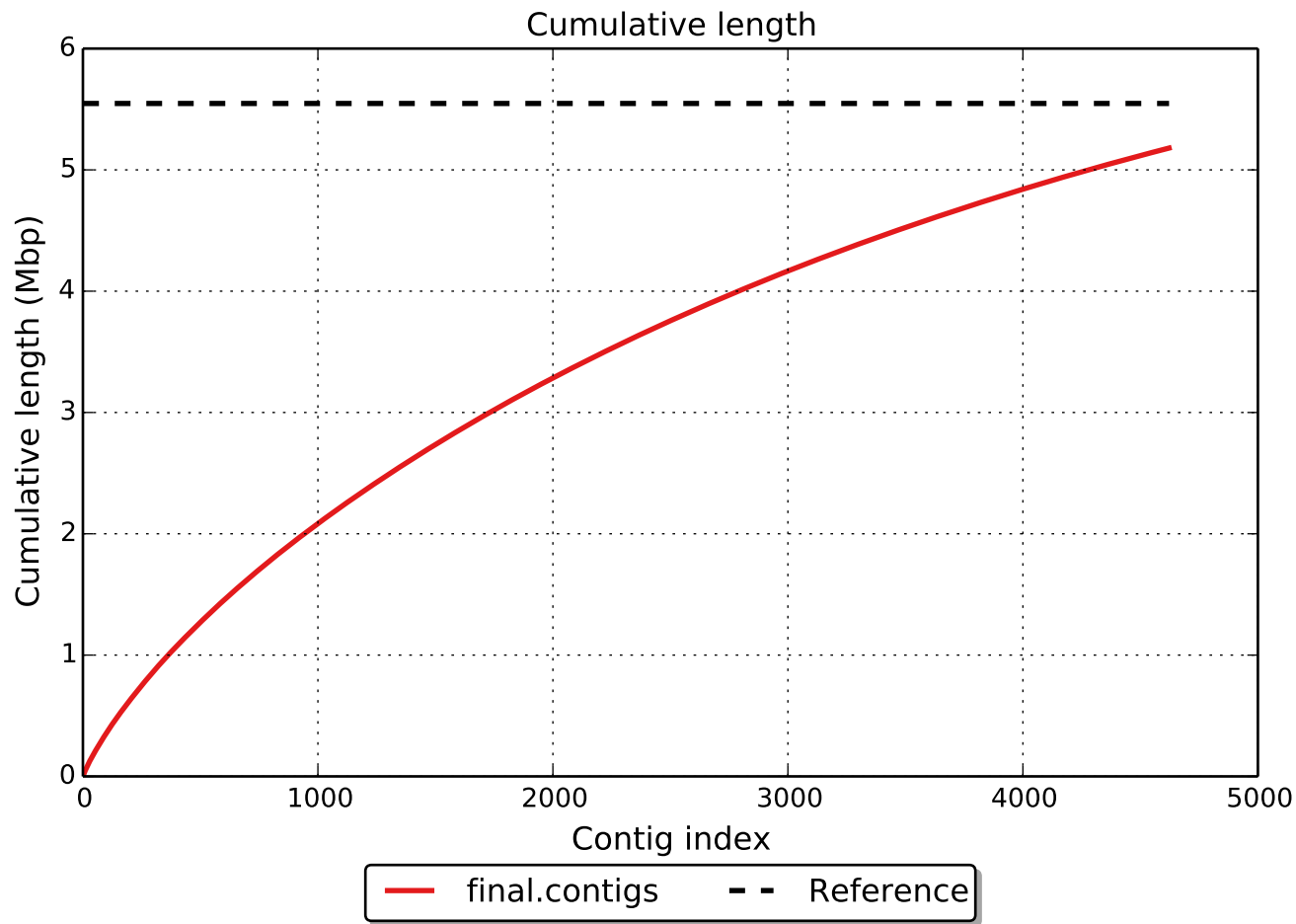
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3990
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

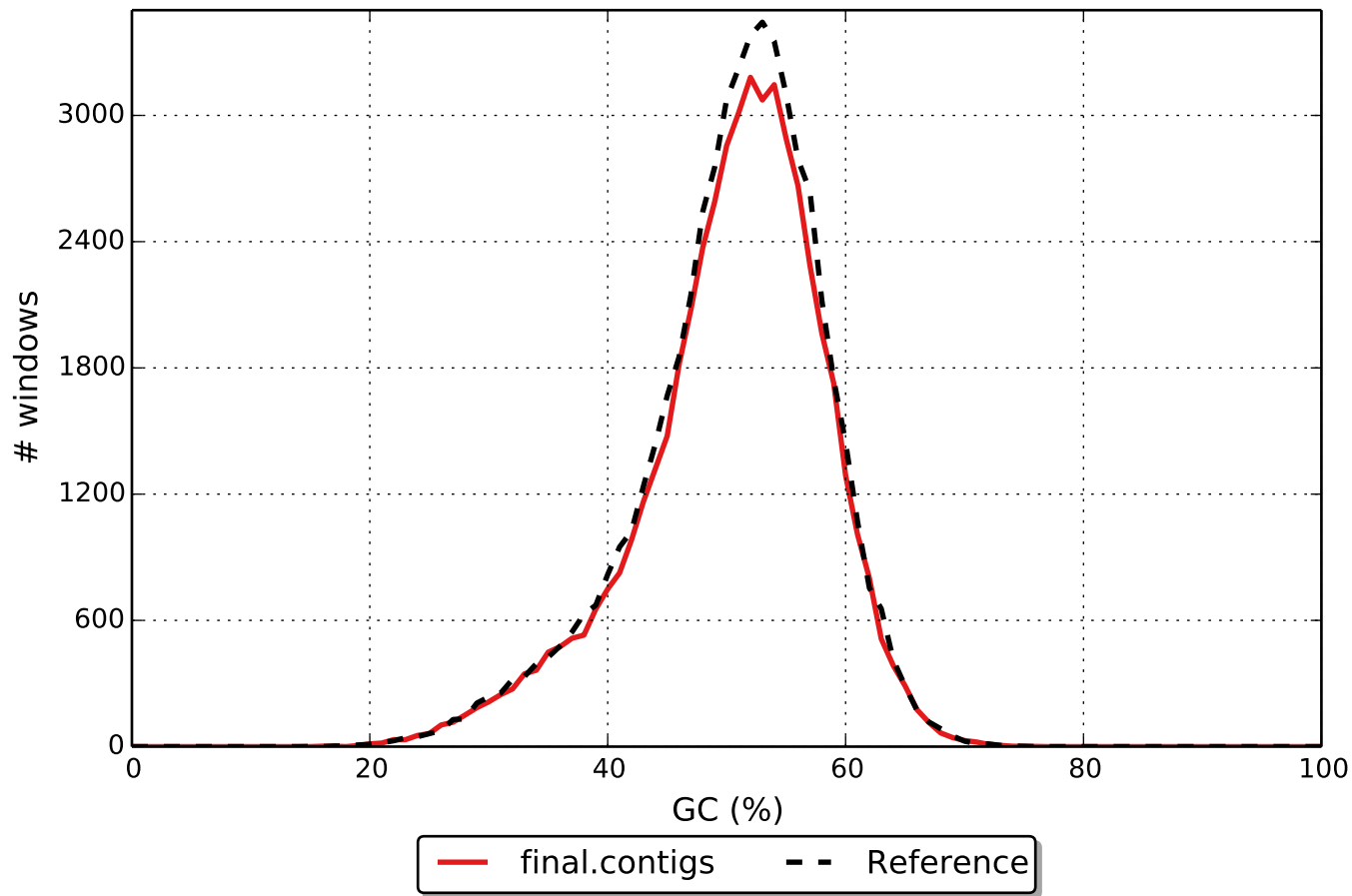
Unaligned report

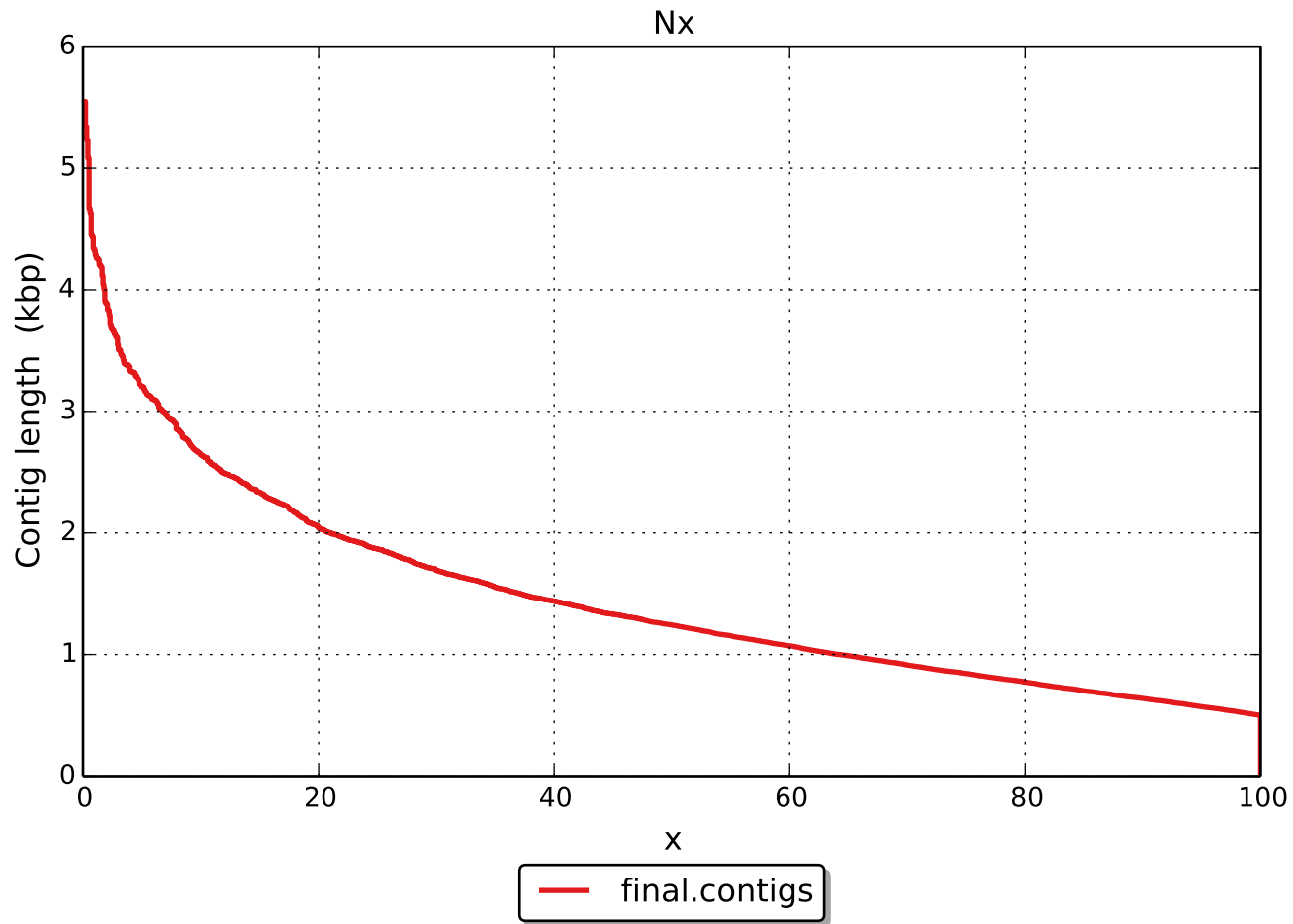
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	135
# N's	0

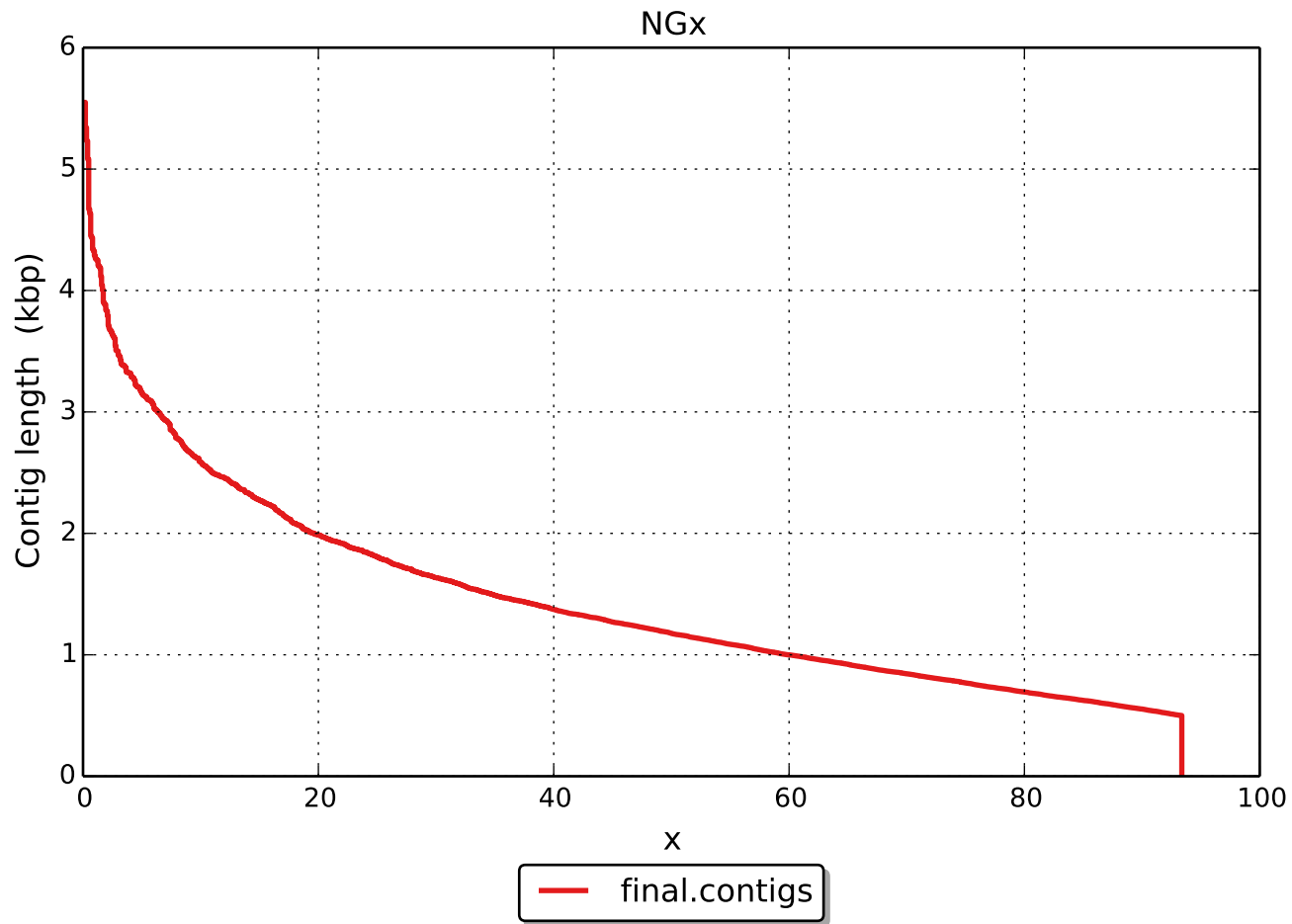
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

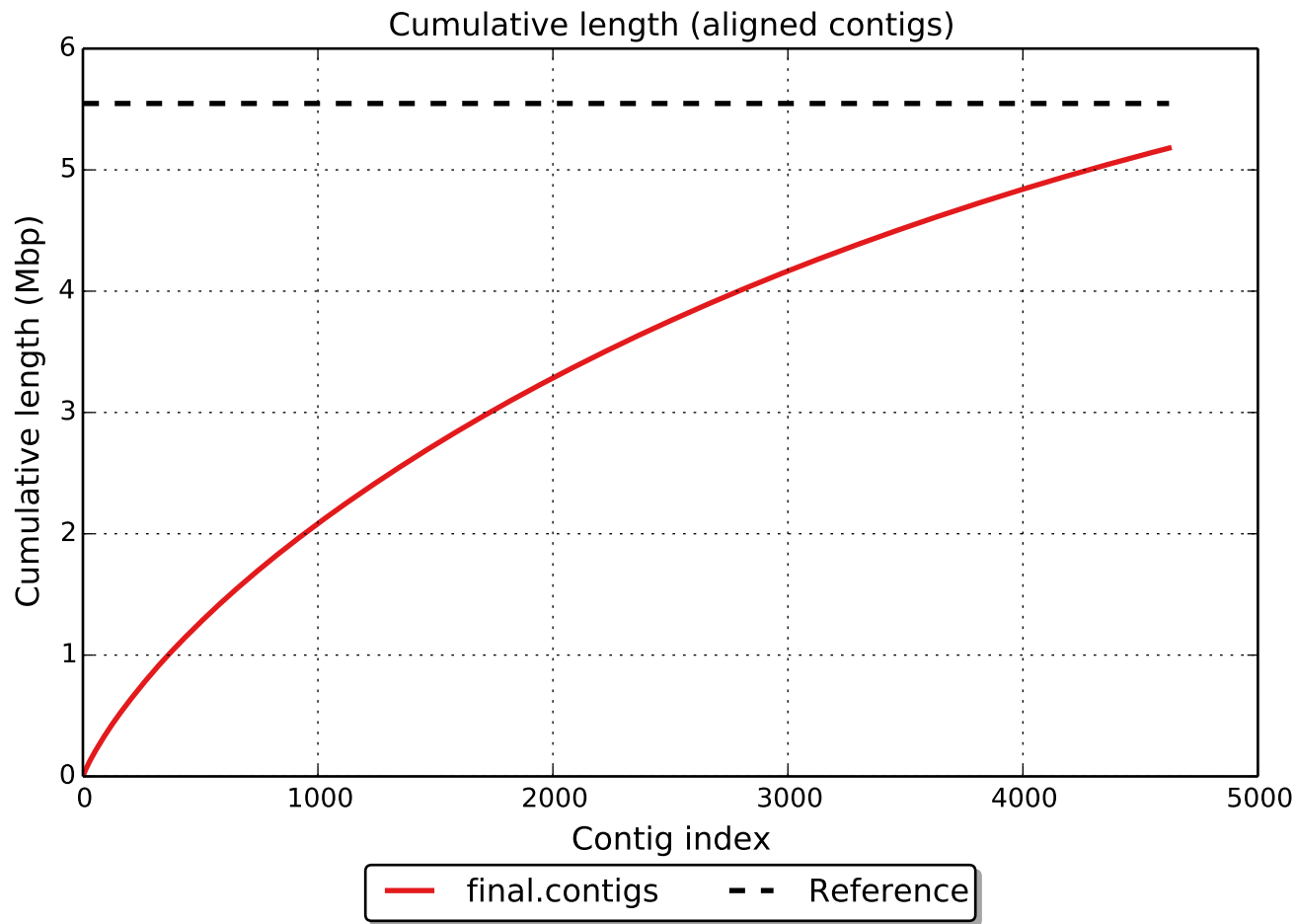


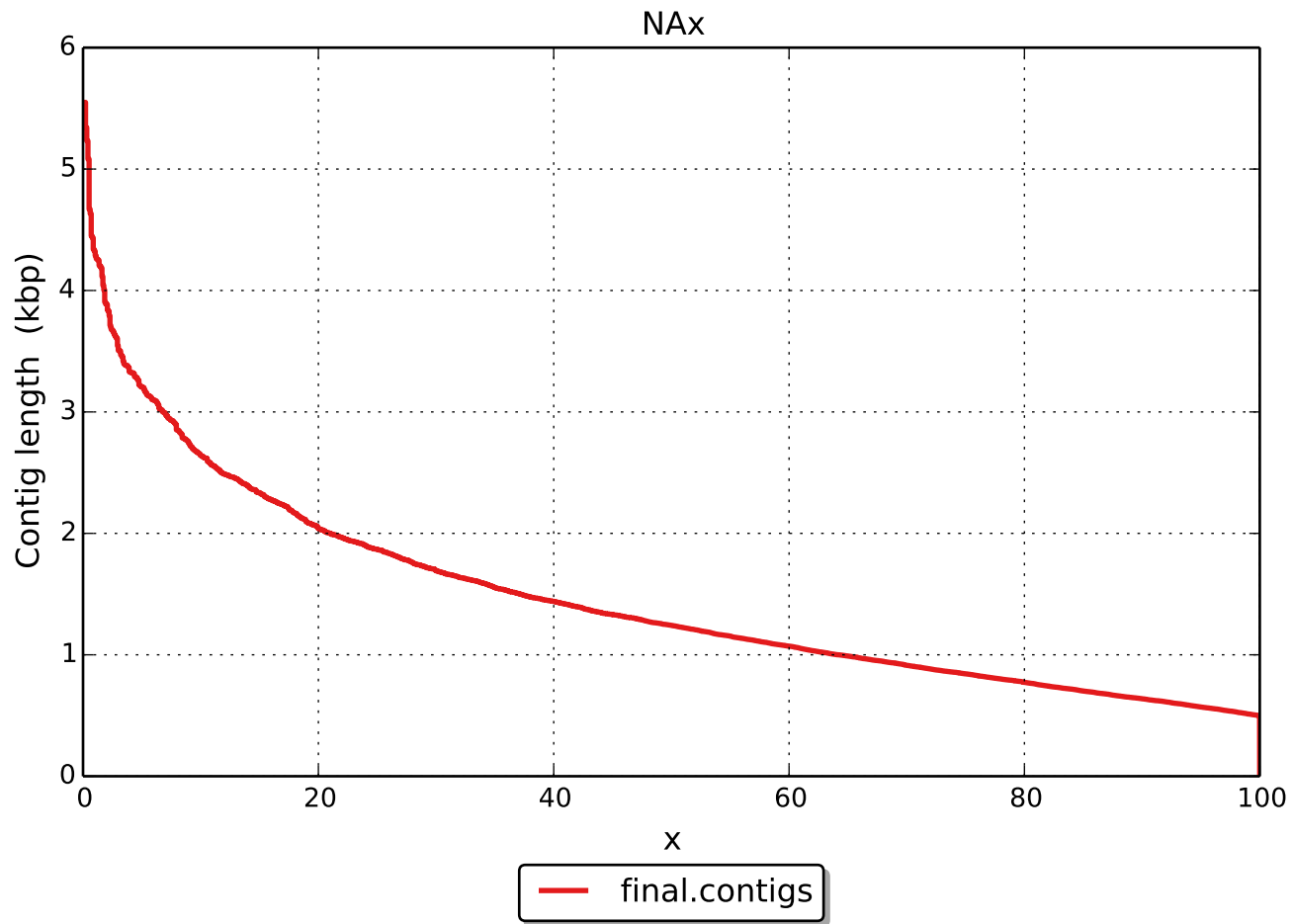




Misassemblies







NGAx

