

Report

	final.contigs
# contigs (≥ 0 bp)	4036
# contigs (≥ 1000 bp)	1100
Total length (≥ 0 bp)	3675438
Total length (≥ 1000 bp)	1641053
# contigs	4036
Largest contig	4517
Total length	3675438
Reference length	5547323
GC (%)	50.45
Reference GC (%)	50.48
N50	936
NG50	677
N75	681
L50	1303
LG50	2488
L75	2463
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 1 part
Unaligned length	40
Genome fraction (%)	63.329
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	213.40
# indels per 100 kbp	0.06
Largest alignment	4517
NA50	936
NGA50	677
NA75	681
LA50	1303
LGA50	2488
LA75	2463

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

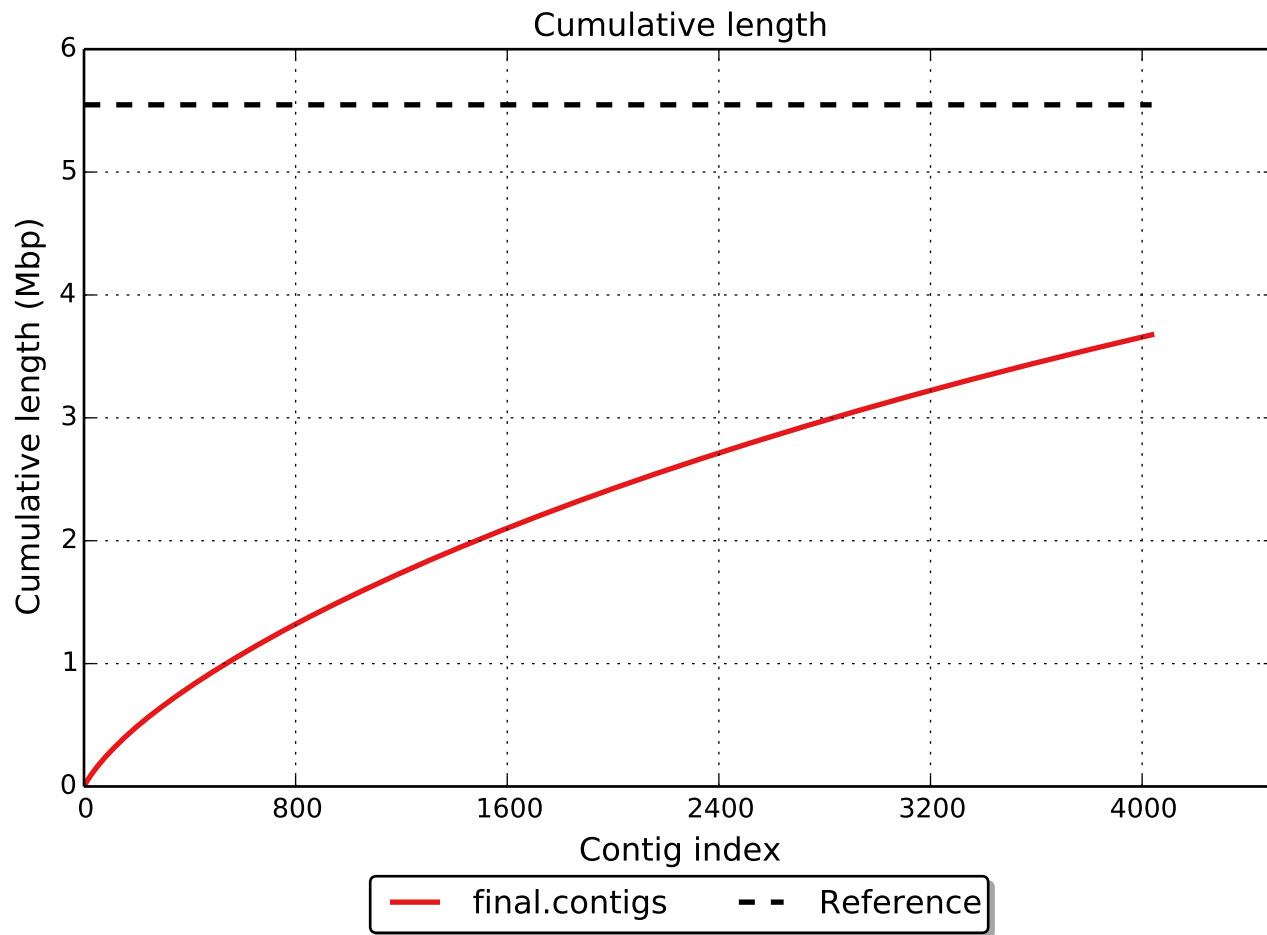
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	7497
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

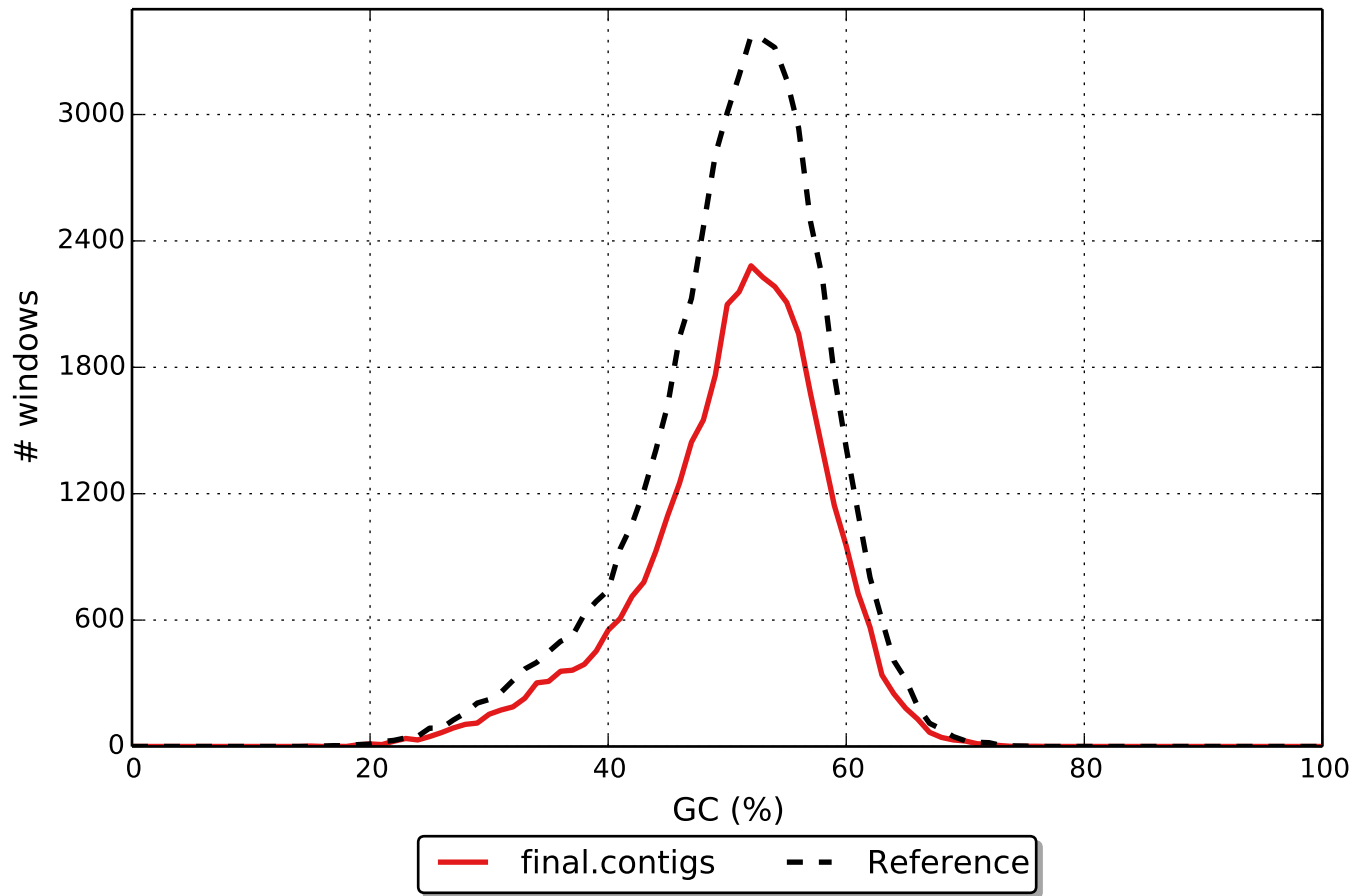
Unaligned report

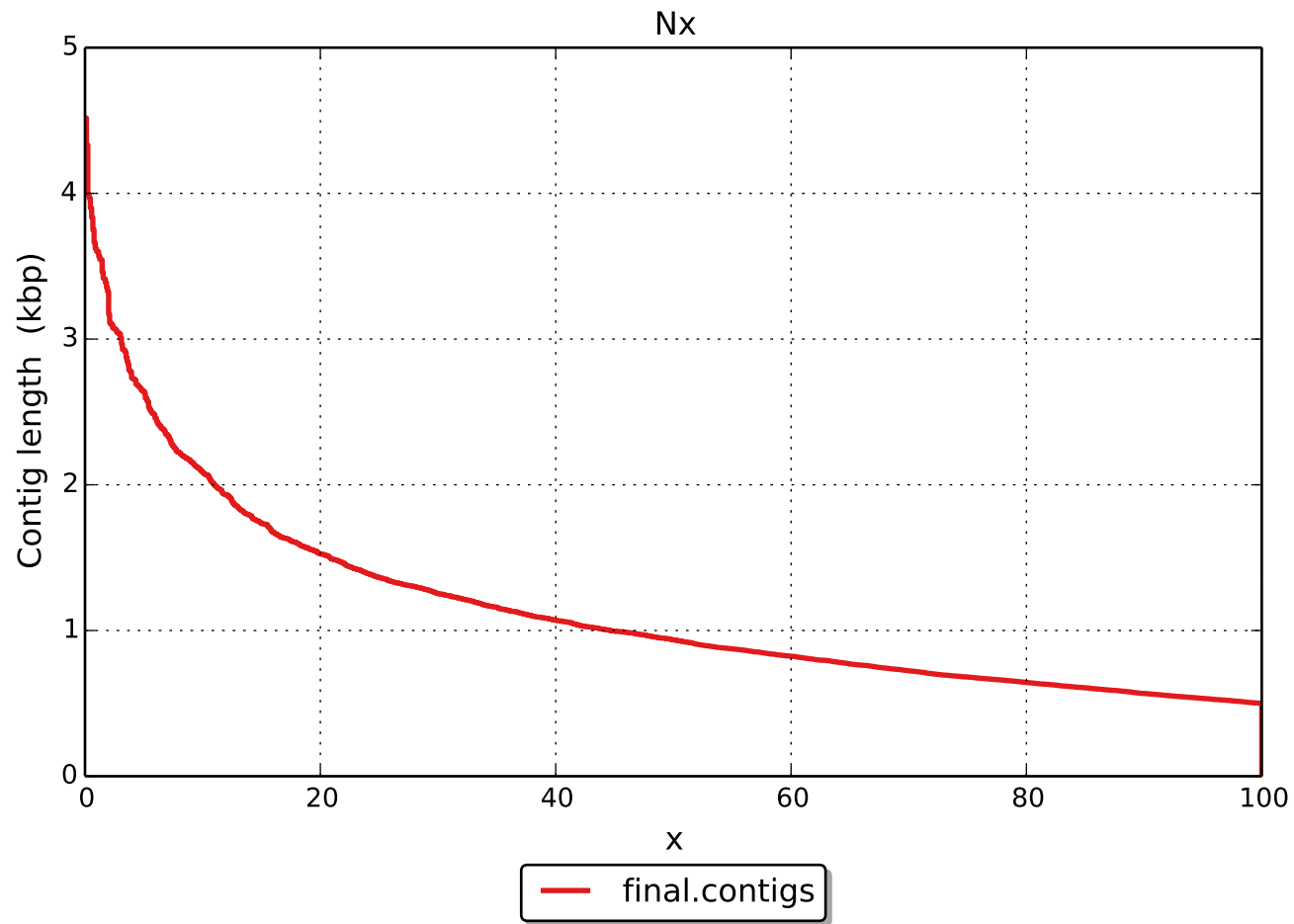
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	40
# N's	0

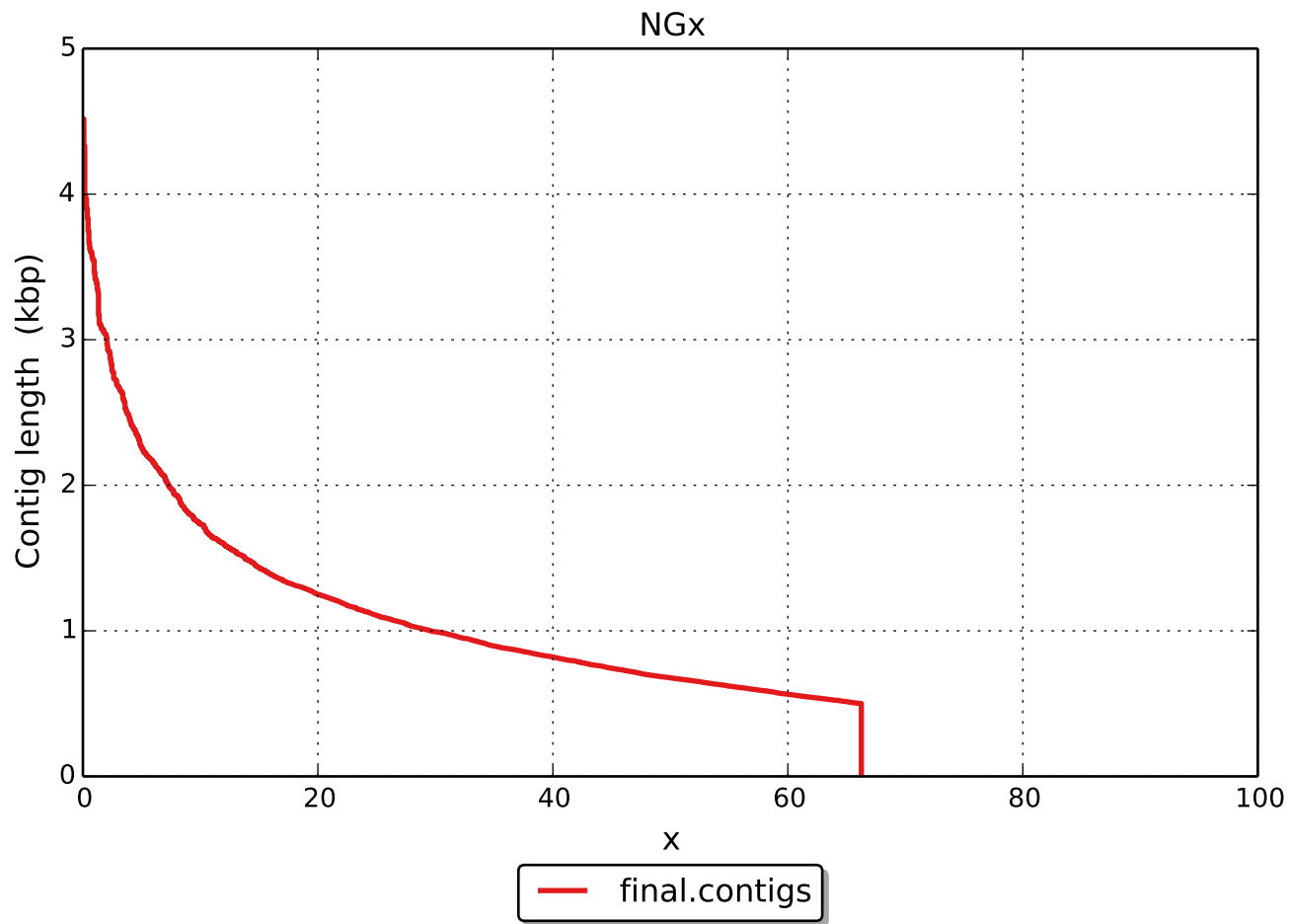
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

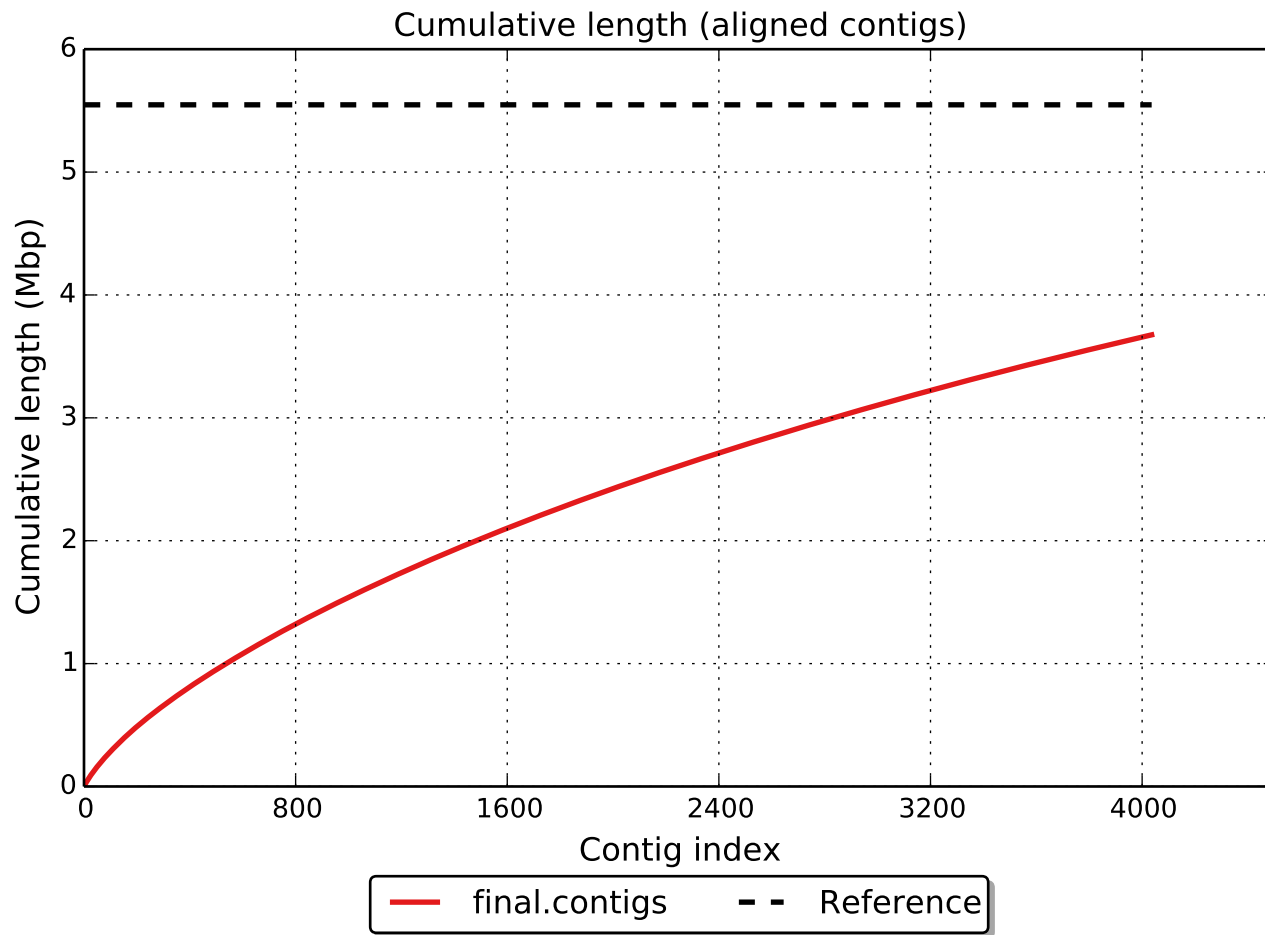


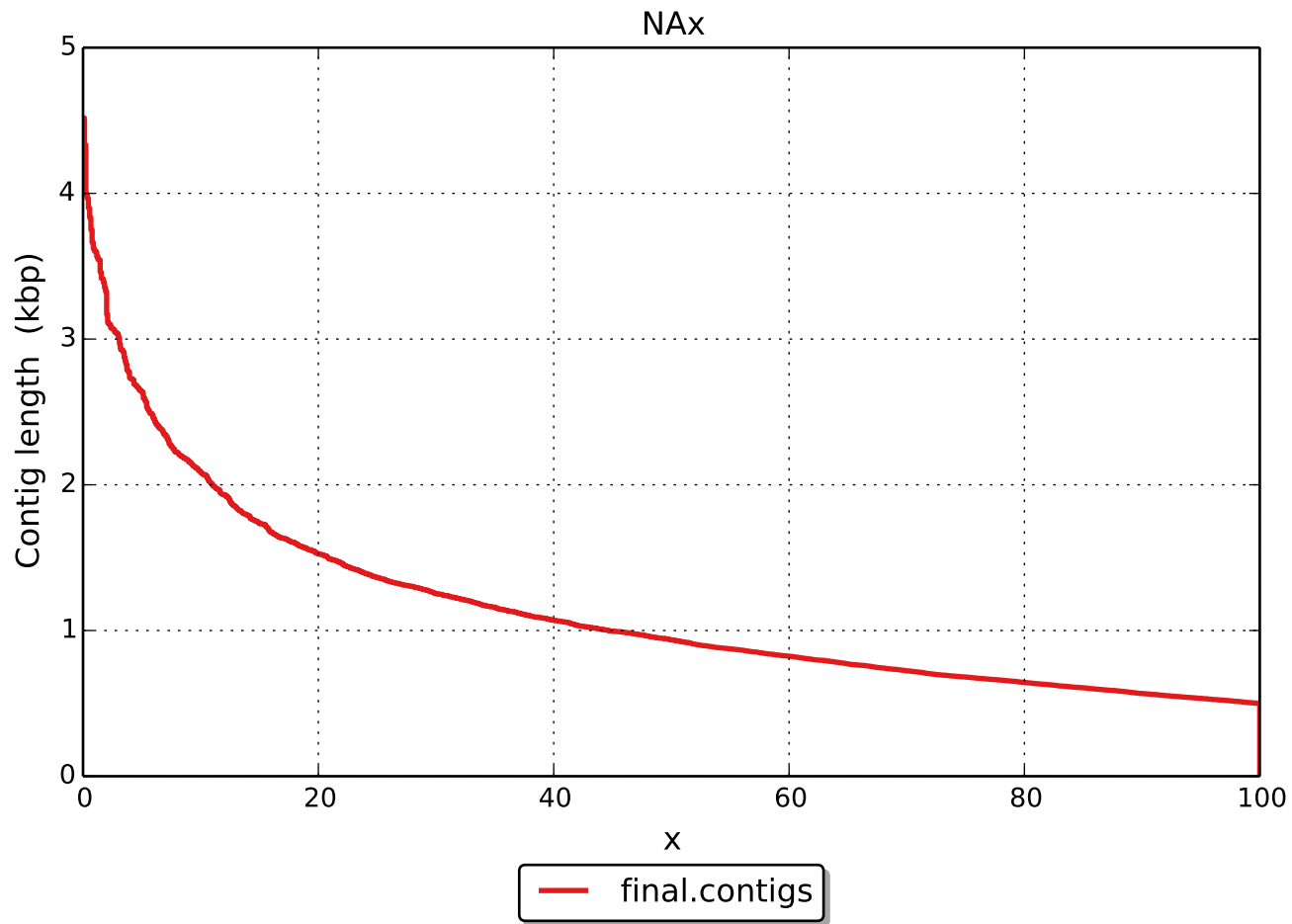




Misassemblies







NGAx

