

Report

	final.contigs
# contigs (≥ 0 bp)	5017
# contigs (≥ 1000 bp)	1775
Total length (≥ 0 bp)	4902815
Total length (≥ 1000 bp)	2611164
# contigs	5017
Largest contig	4277
Total length	4902815
Reference length	5478683
GC (%)	50.50
Reference GC (%)	50.50
N50	1040
NG50	965
N75	742
NG75	658
L50	1619
LG50	1906
L75	3018
LG75	3636
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.561
Duplication ratio	1.058
# N's per 100 kbp	0.00
# mismatches per 100 kbp	131.50
# indels per 100 kbp	0.11
Largest alignment	4277
NA50	1039
NGA50	965
NA75	742
NGA75	658
LA50	1619
LGA50	1906
LA75	3018
LGA75	3637

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

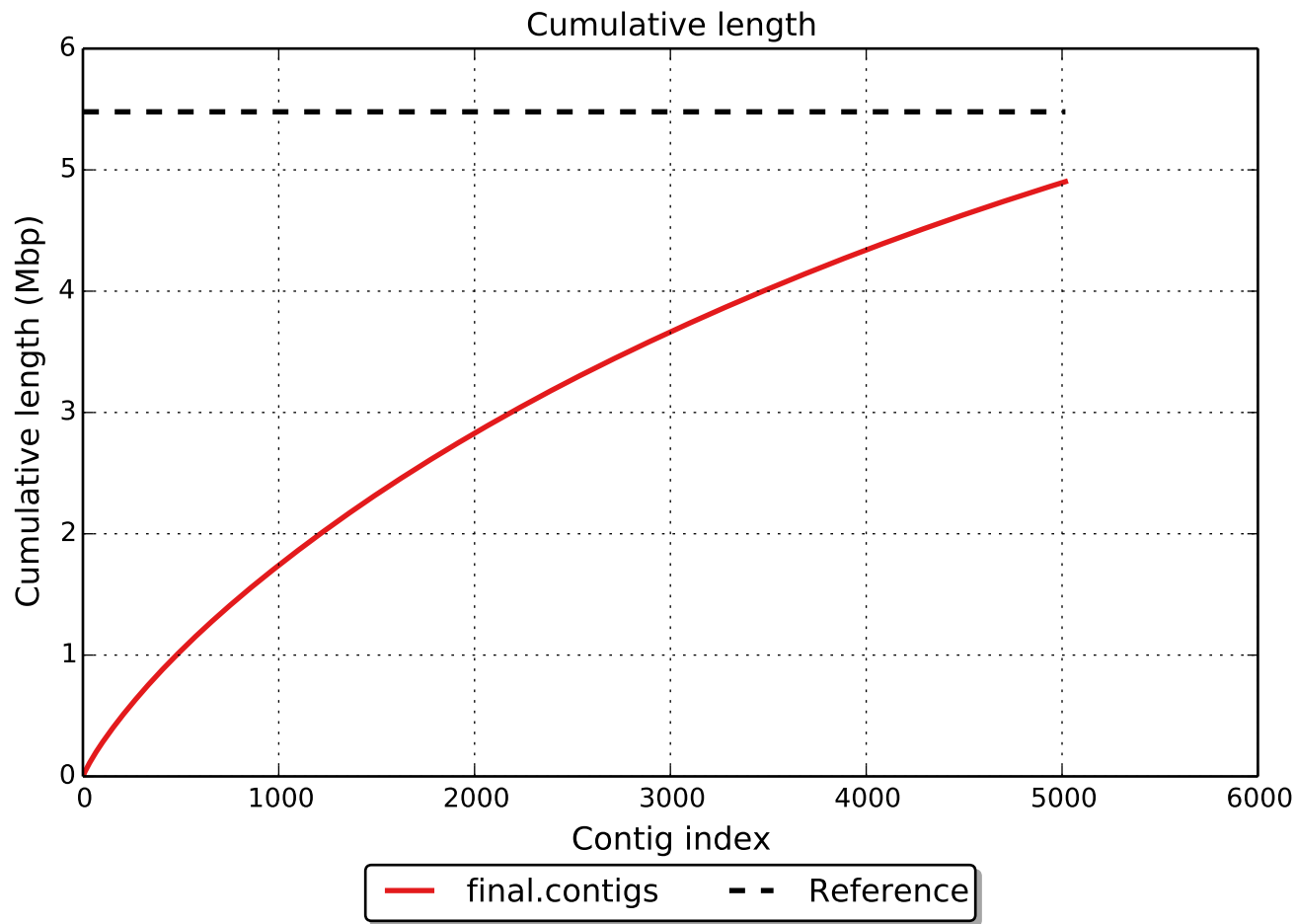
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# mismatches	6092
# indels	5
# short indels	2
# long indels	3
Indels length	47

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).

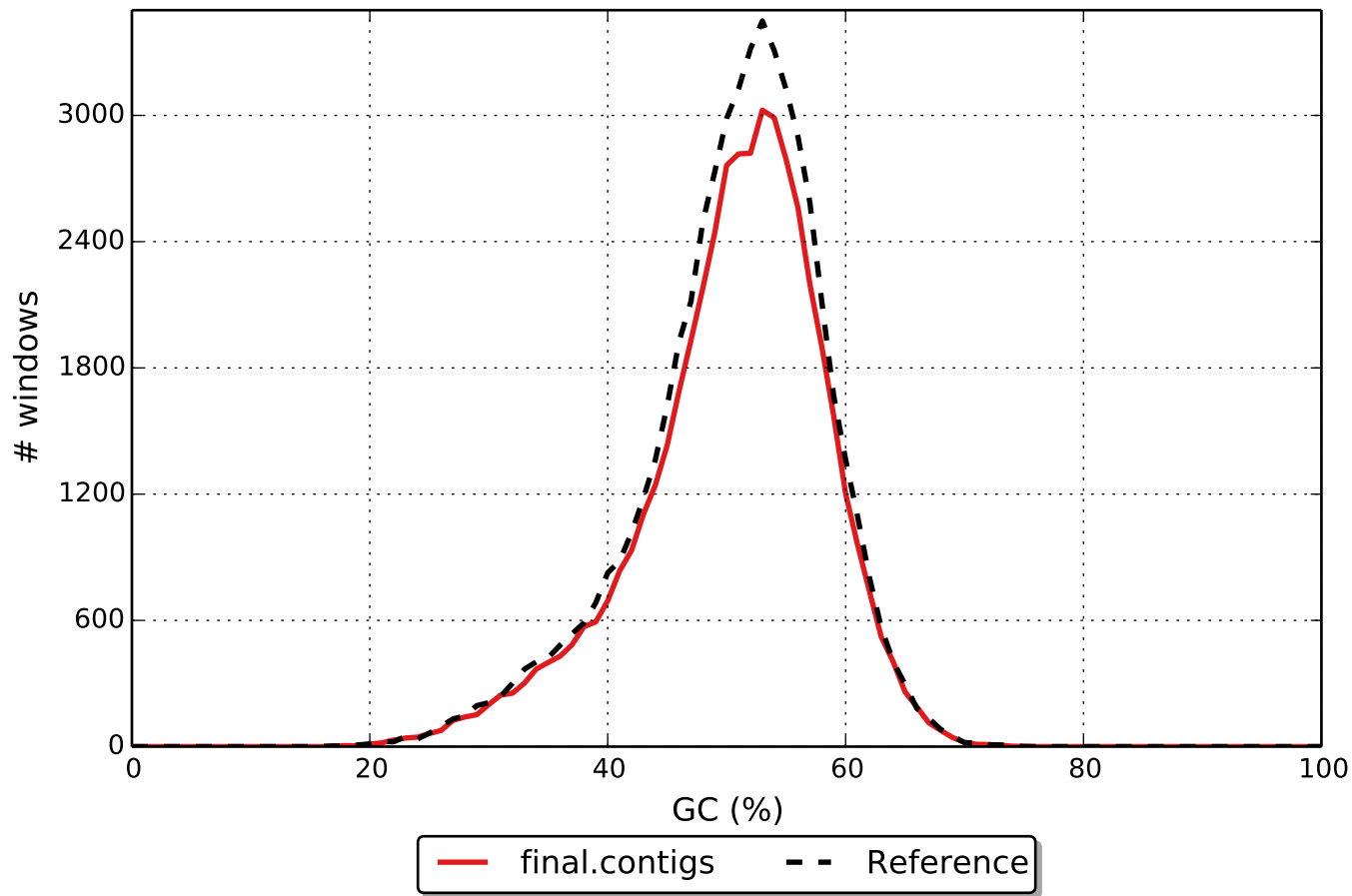
Unaligned report

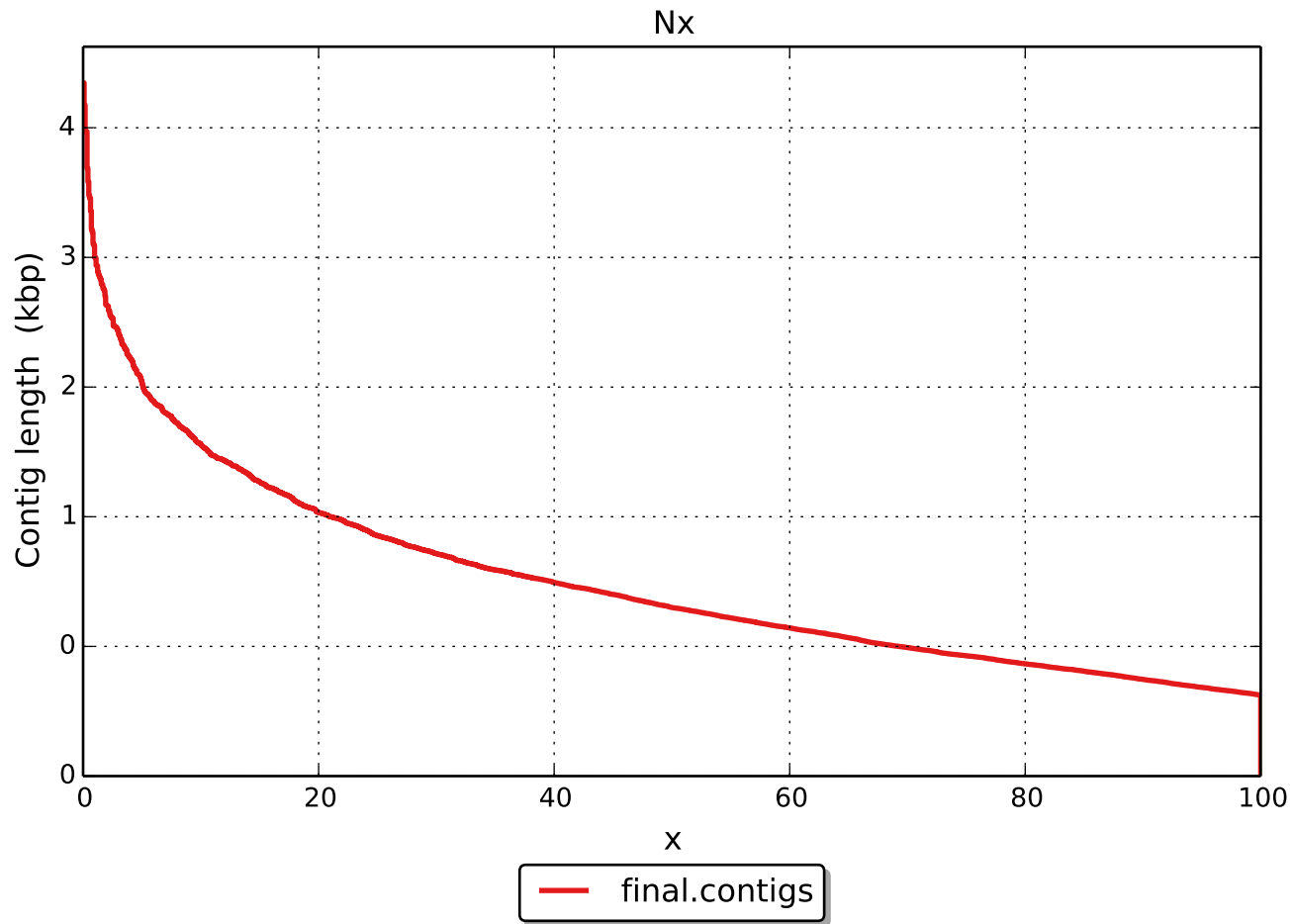
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

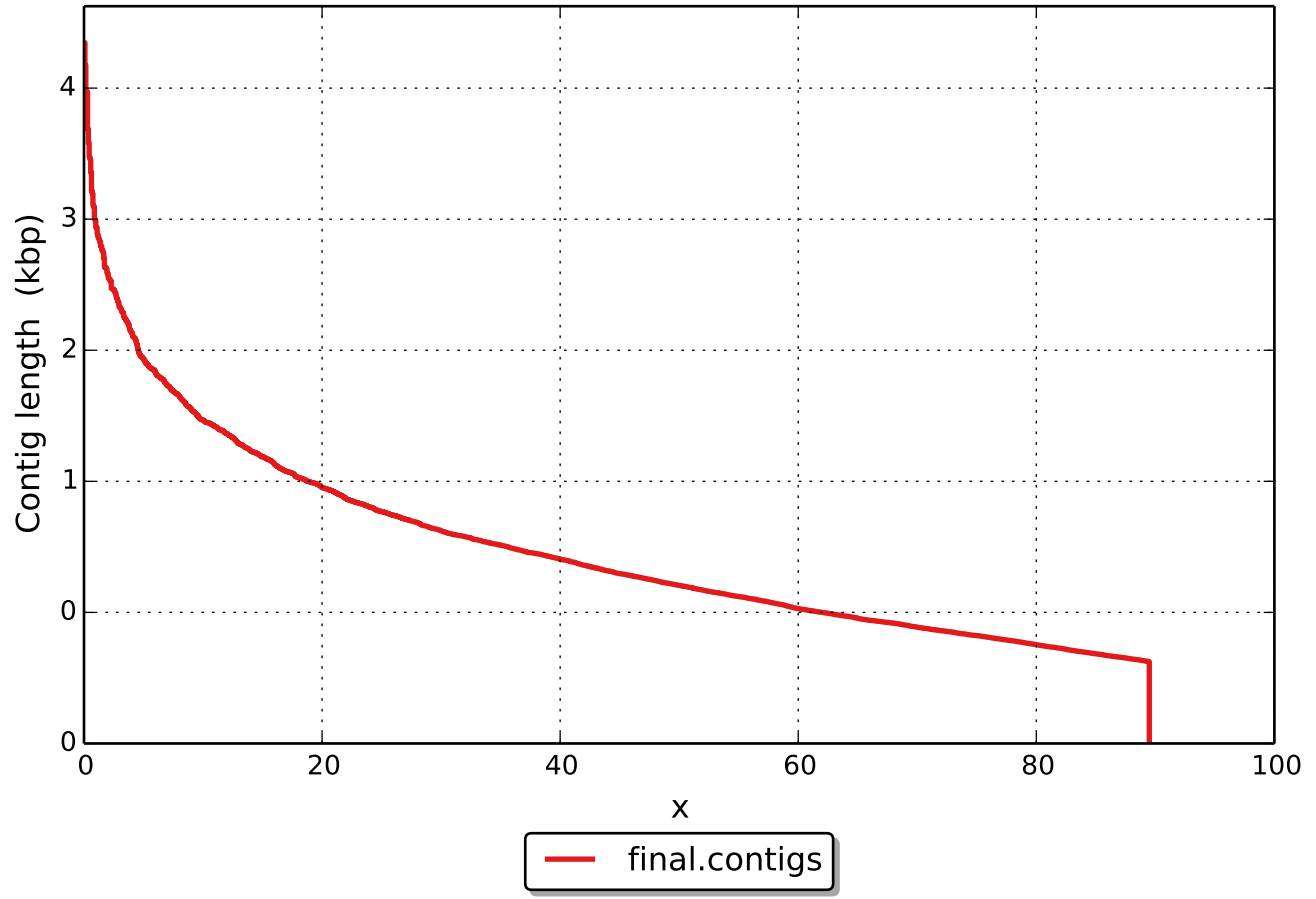


GC content

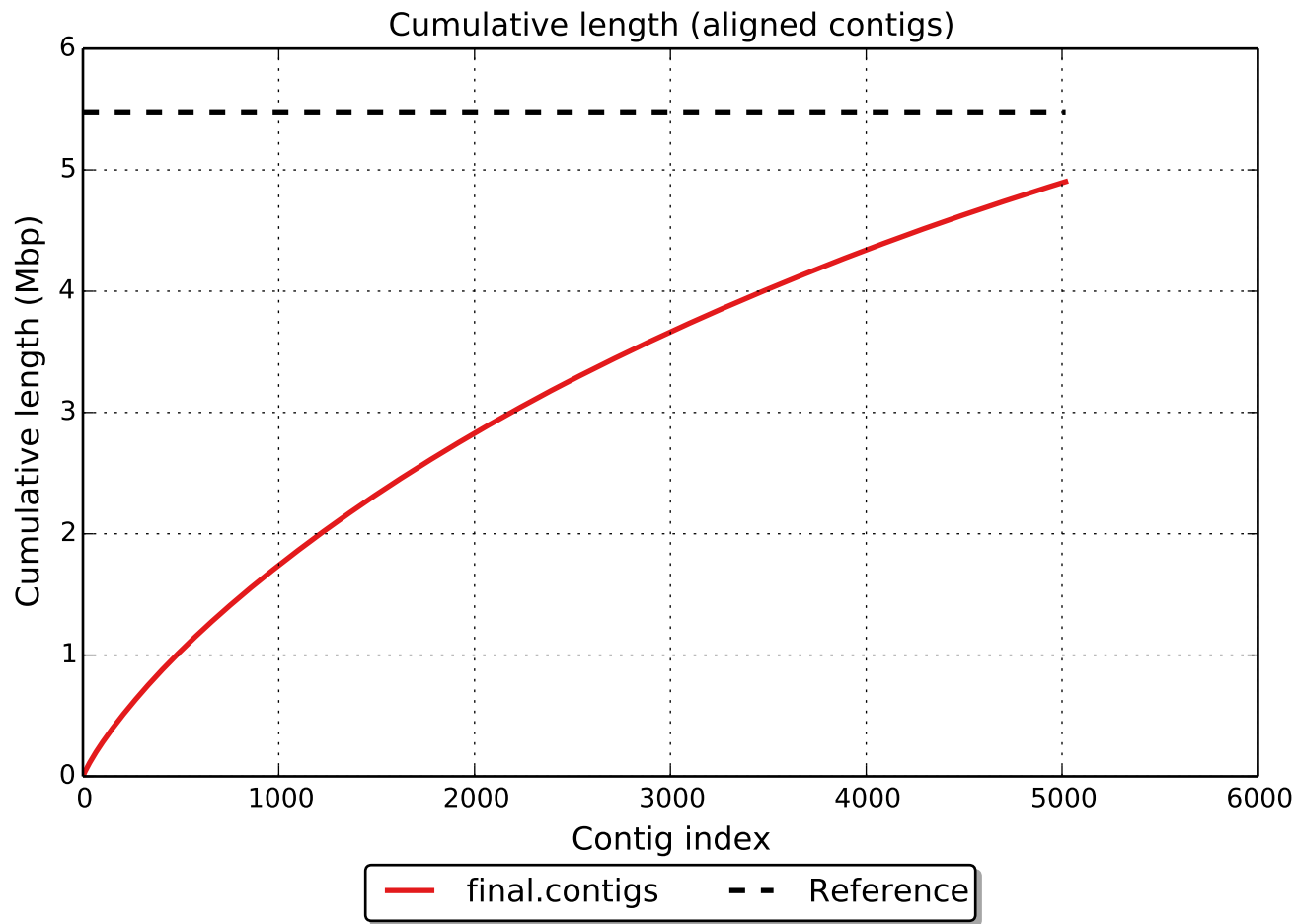




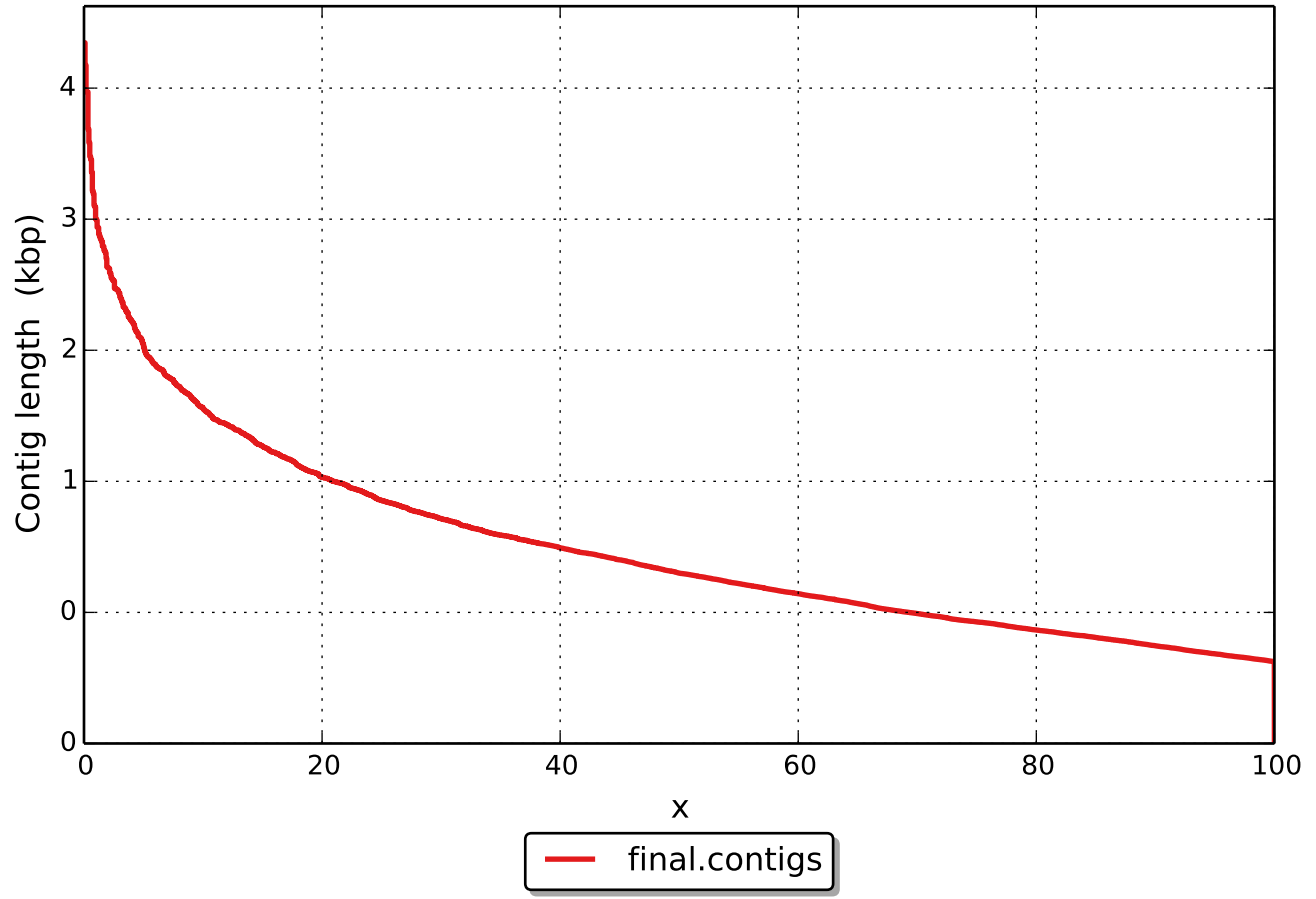
NGx







NAx



NGAx

