

Report

	final.contigs
# contigs (>= 0 bp)	524
# contigs (>= 1000 bp)	224
Total length (>= 0 bp)	710395
Total length (>= 1000 bp)	506273
# contigs	524
Largest contig	13980
Total length	710395
Reference length	615980
GC (%)	25.24
Reference GC (%)	25.35
N50	1718
NG50	1987
N75	900
NG75	1217
L50	110
LG50	84
L75	252
LG75	184
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	6959
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	95.314
Duplication ratio	1.210
# N's per 100 kbp	0.00
# mismatches per 100 kbp	826.93
# indels per 100 kbp	0.00
Largest alignment	13980
NA50	1718
NGA50	1987
NA75	885
NGA75	1217
LA50	110
LGA50	84
LA75	253
LGA75	184

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

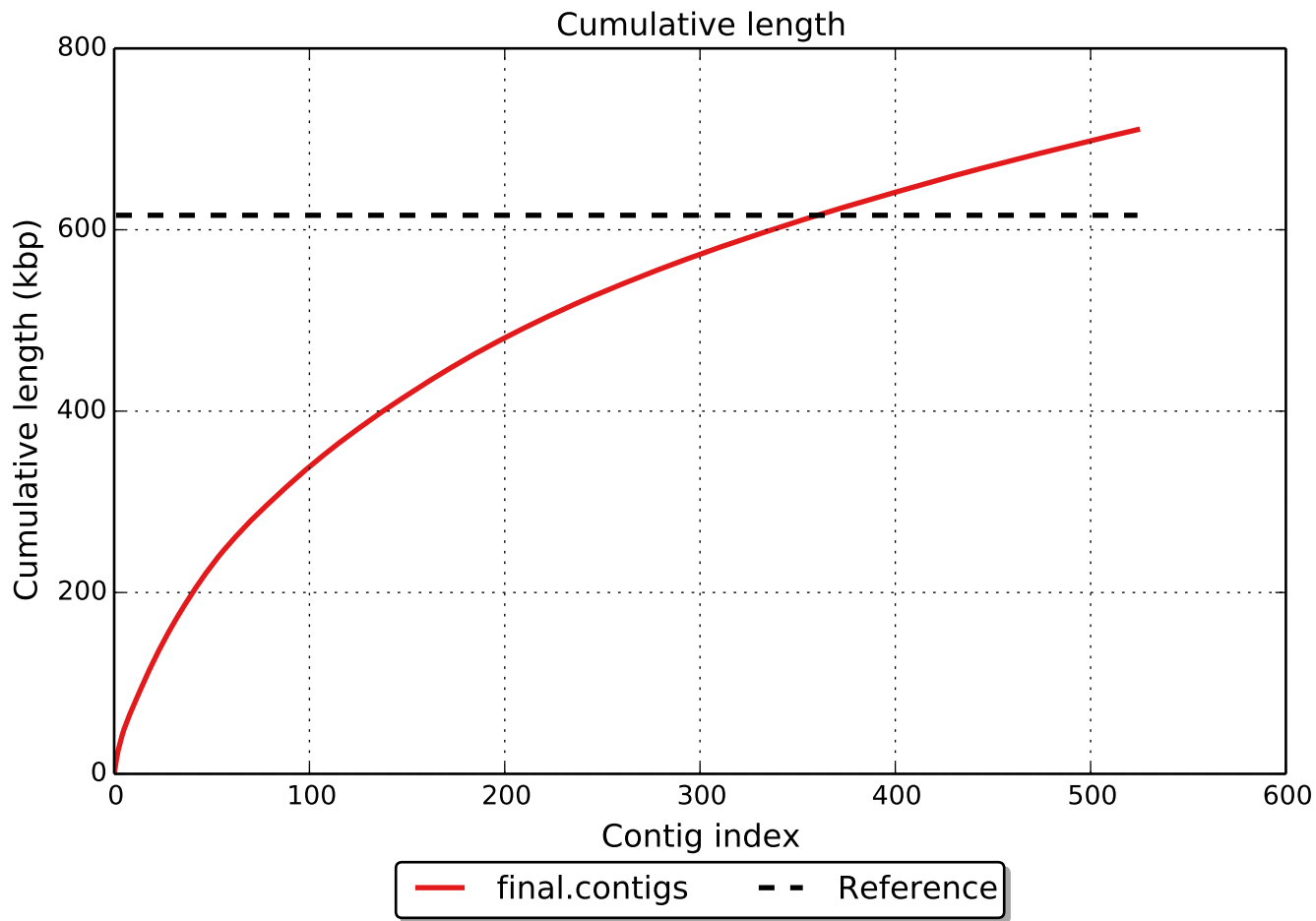
	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	6959
# local misassemblies	0
# mismatches	4855
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

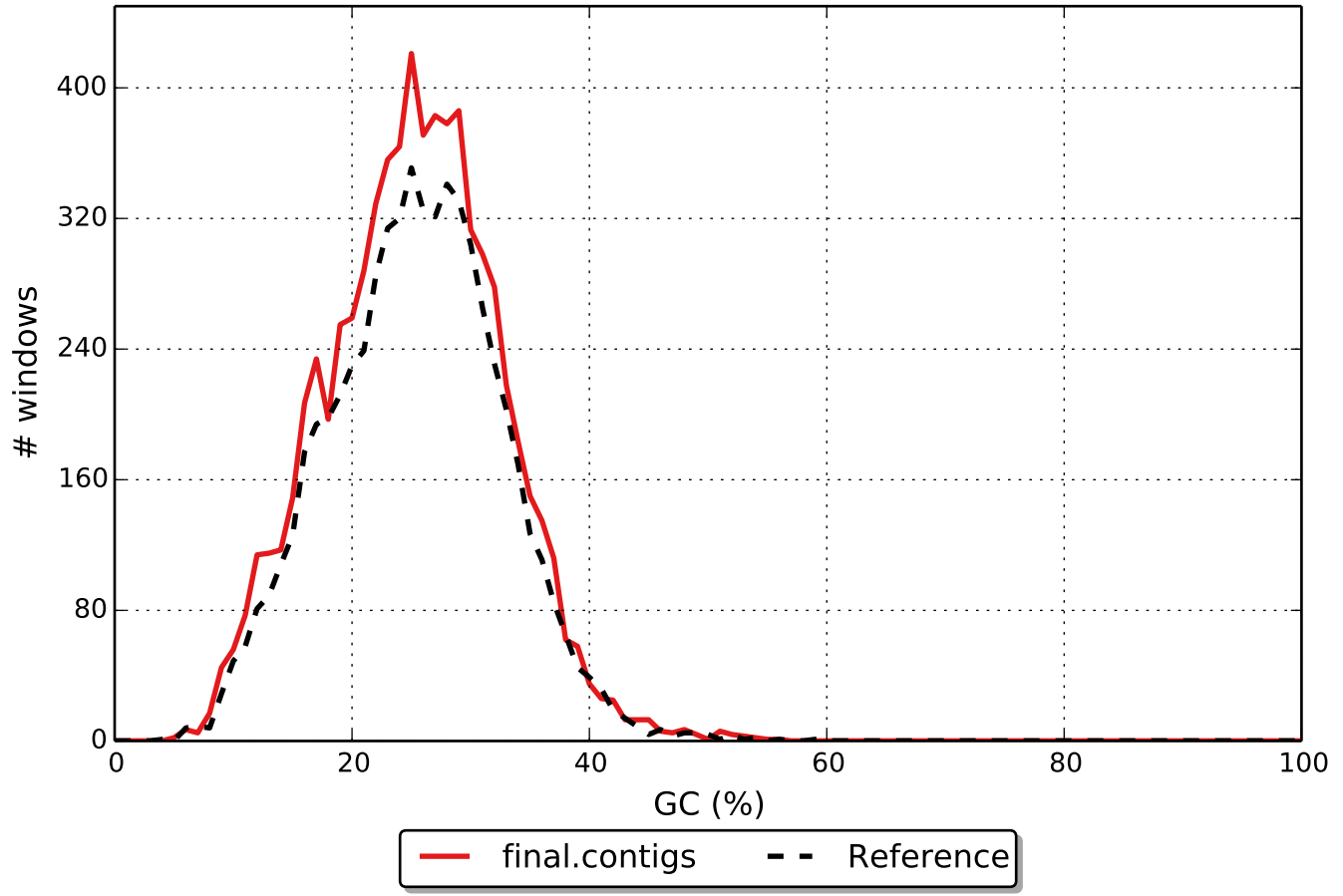
Unaligned report

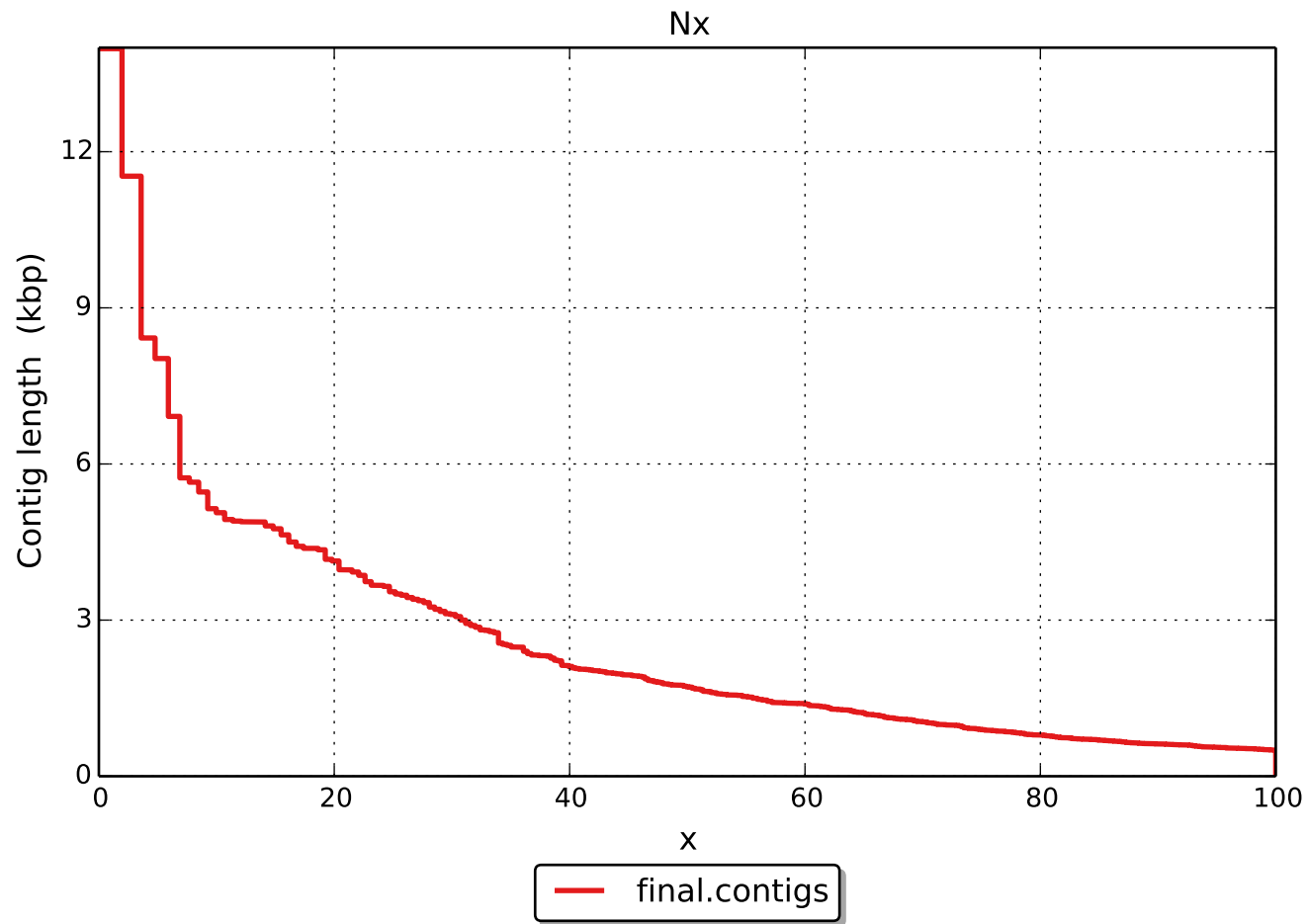
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

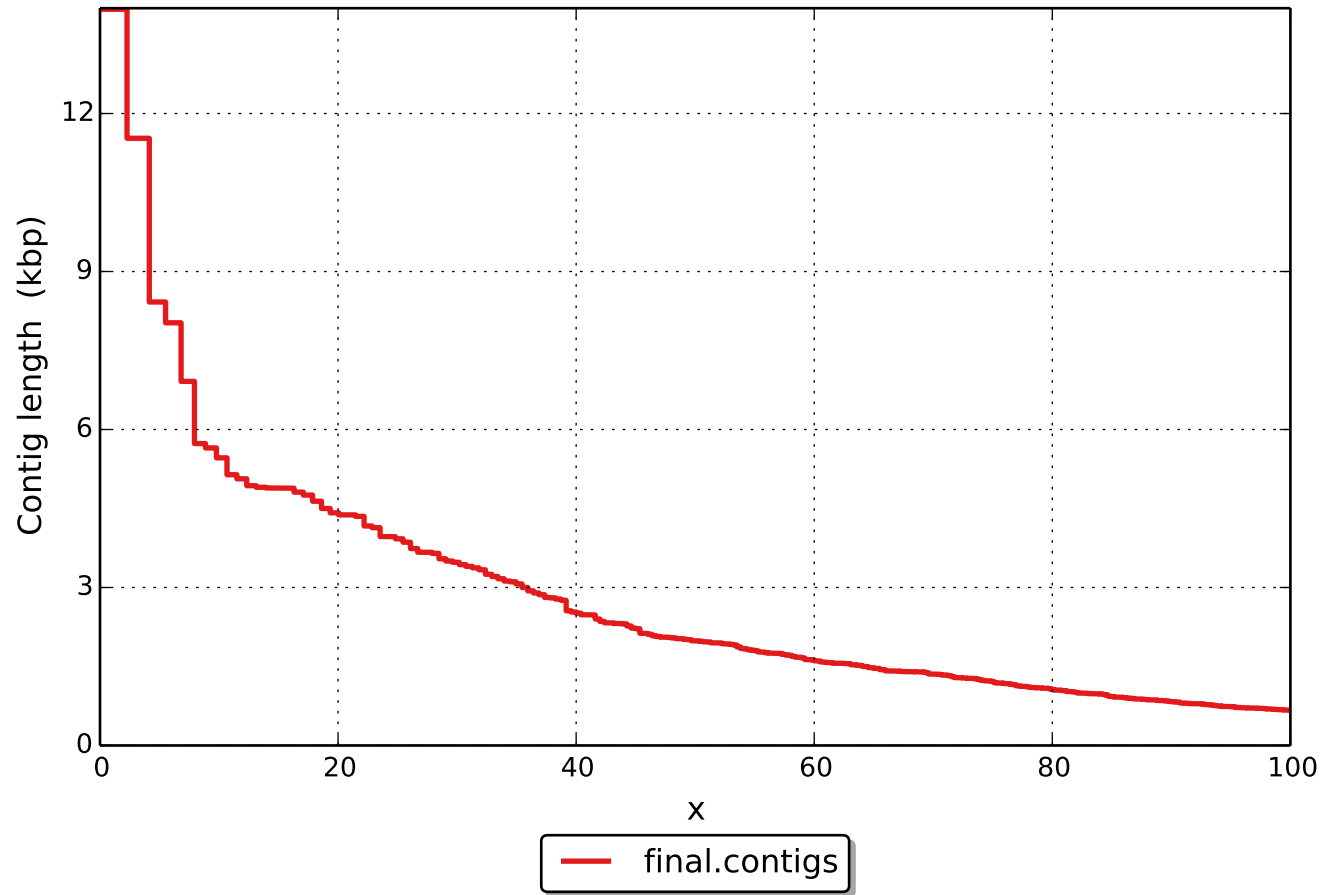


GC content

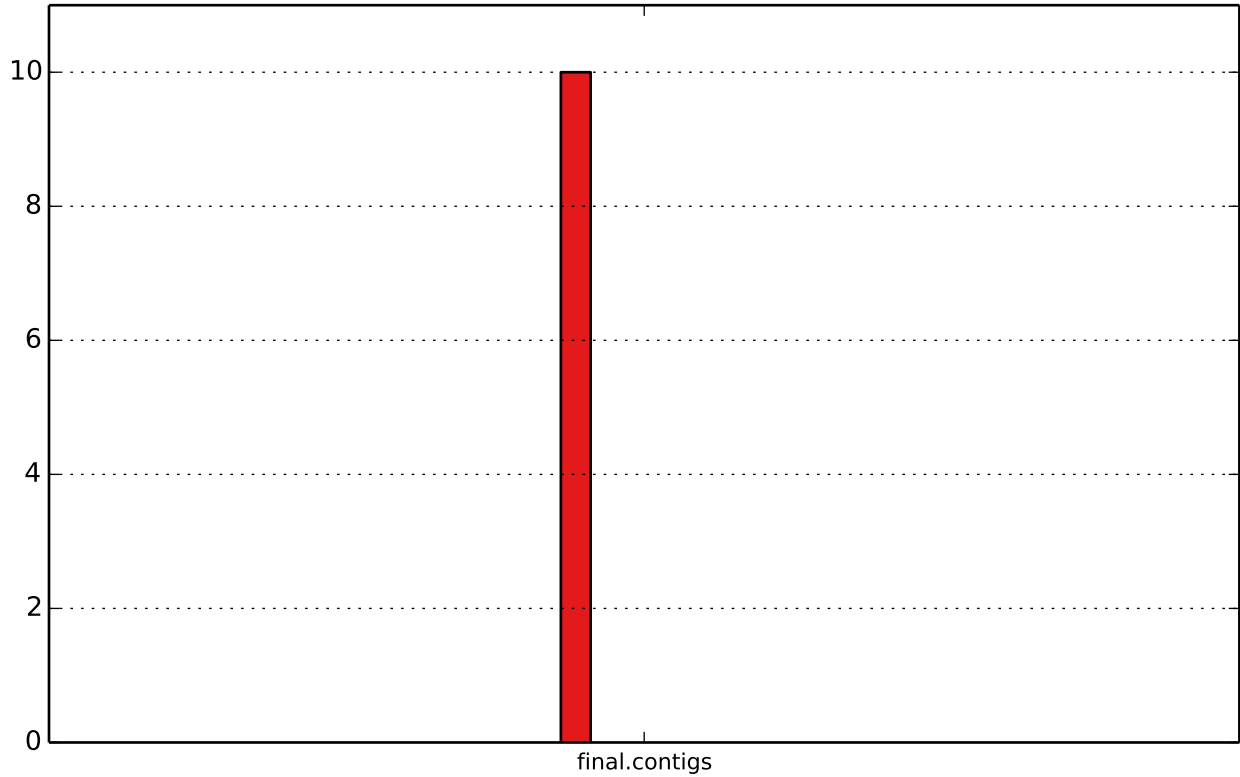


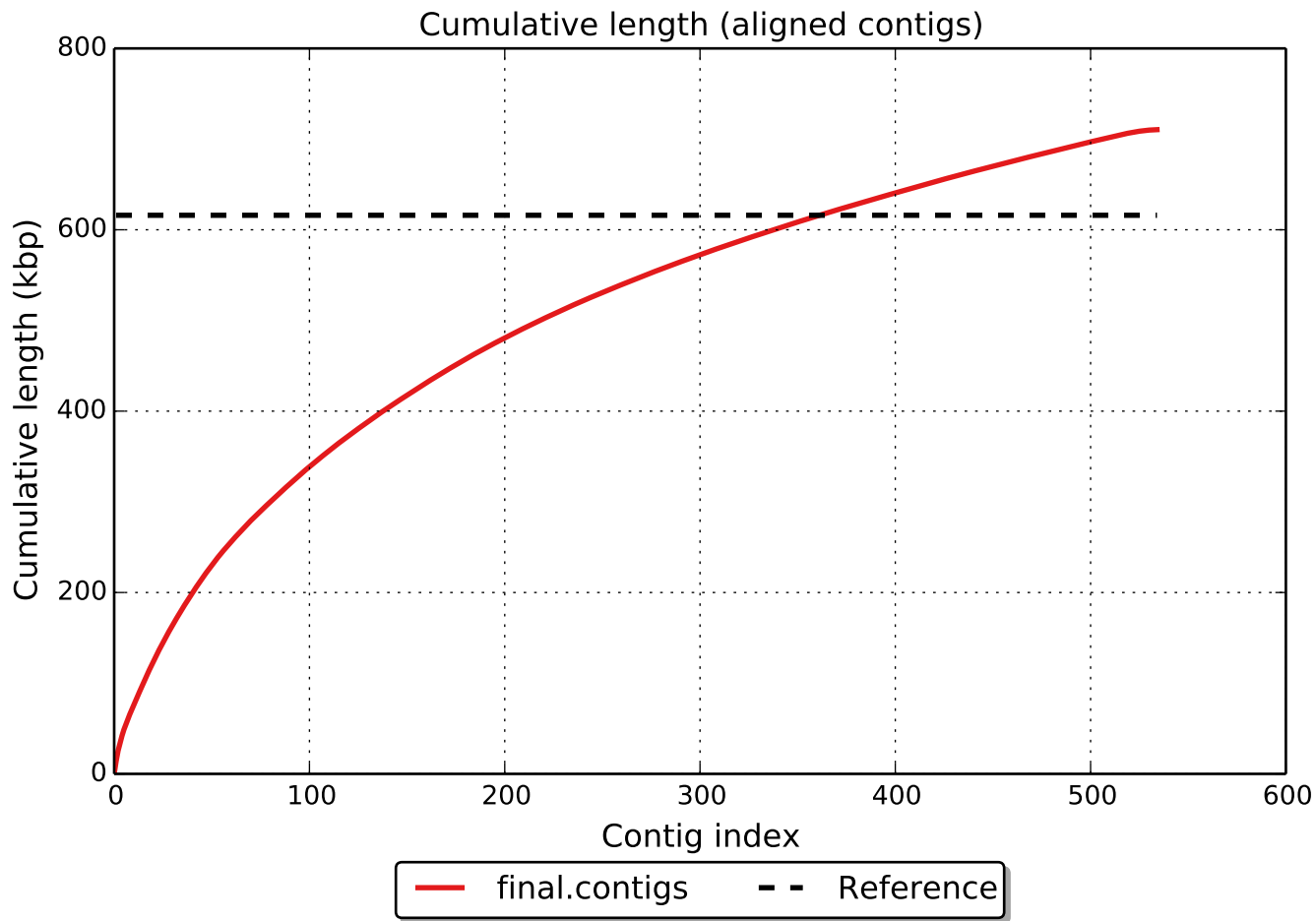


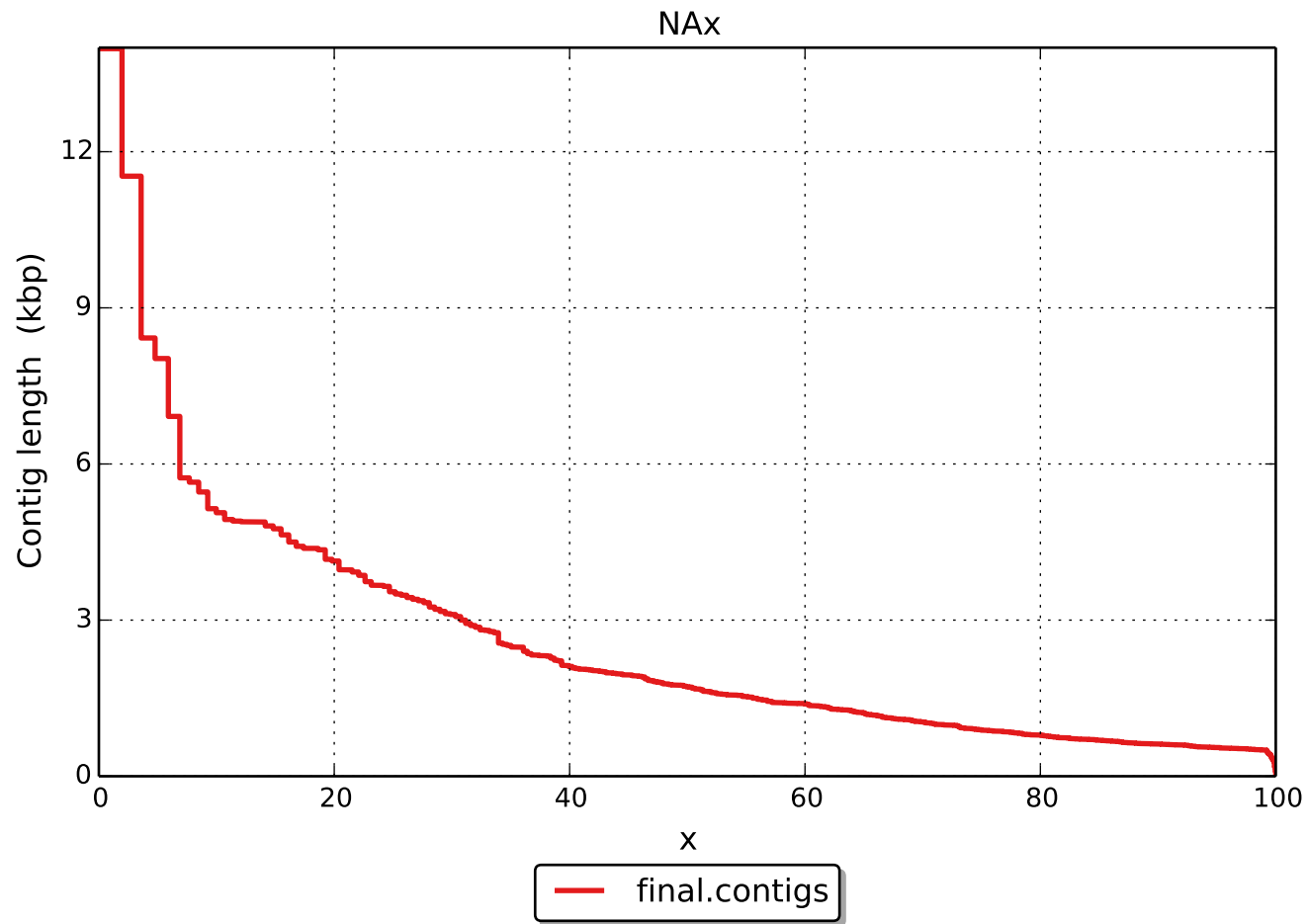
NGx



Misassemblies







NGAx

