

Report

	final.contigs
# contigs (≥ 0 bp)	754
# contigs (≥ 1000 bp)	407
Total length (≥ 0 bp)	1181123
Total length (≥ 1000 bp)	942173
# contigs	754
Largest contig	13980
Total length	1181123
Reference length	615980
GC (%)	25.36
Reference GC (%)	25.35
N50	1987
NG50	3739
N75	1173
NG75	2757
L50	163
LG50	58
L75	356
LG75	105
# 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	2.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	829.65
# indels per 100 kbp	0.00
Largest alignment	13980
NA50	718
NGA50	1987
NGA75	1217
LA50	325
LGA50	84
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	4871
# indels	0
# short indels	0
# long indels	0
Indels length	0

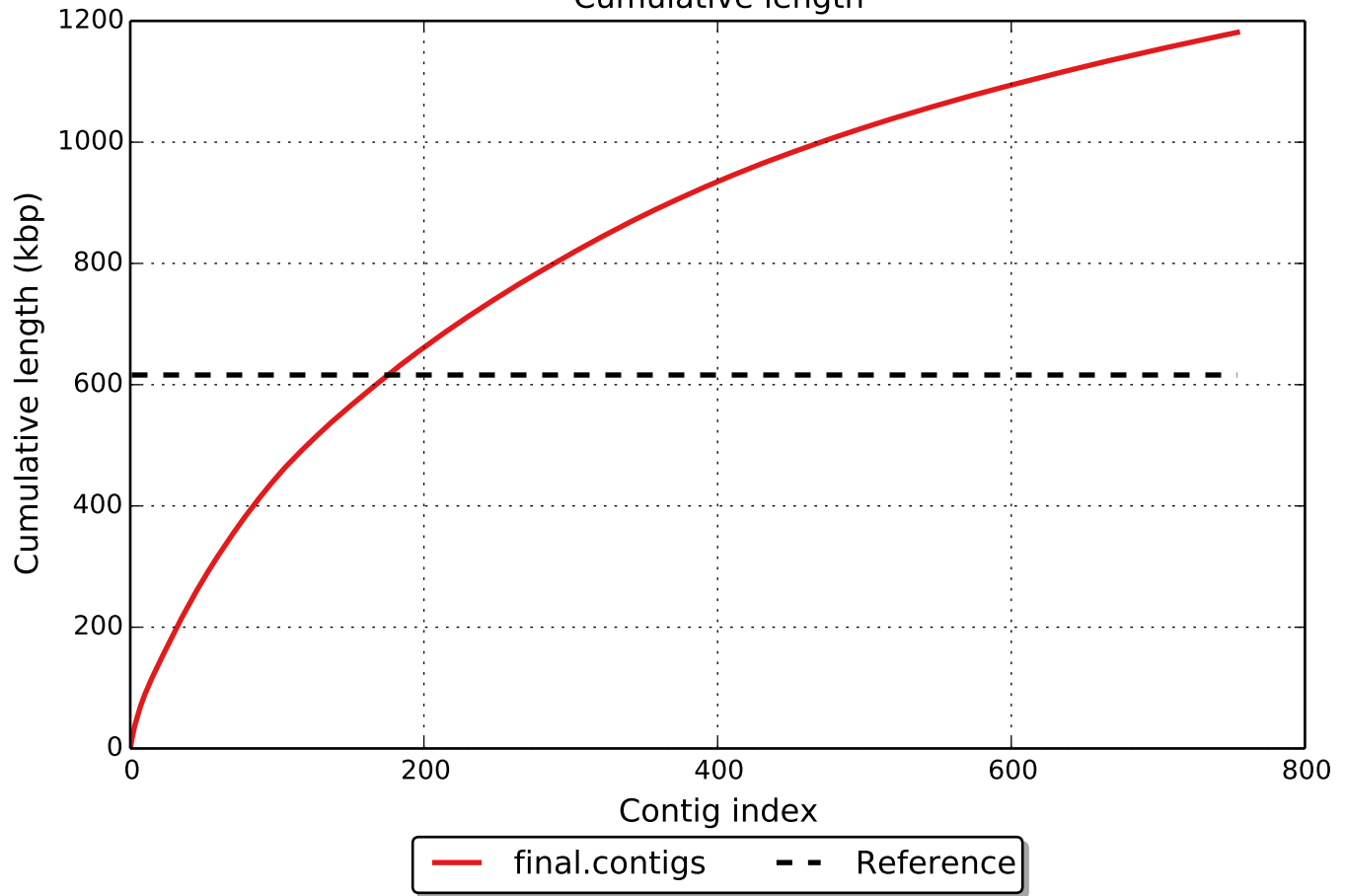
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

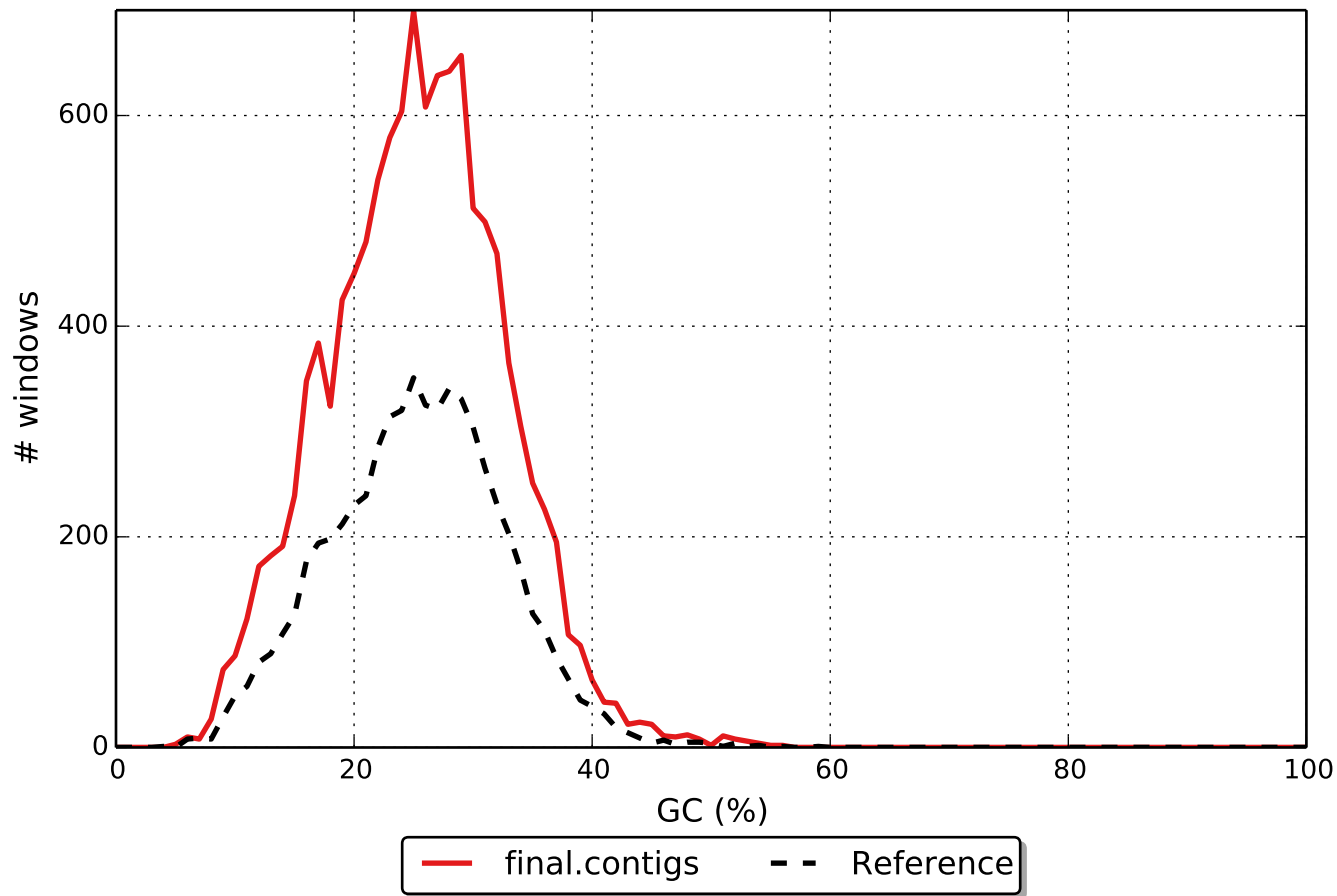
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

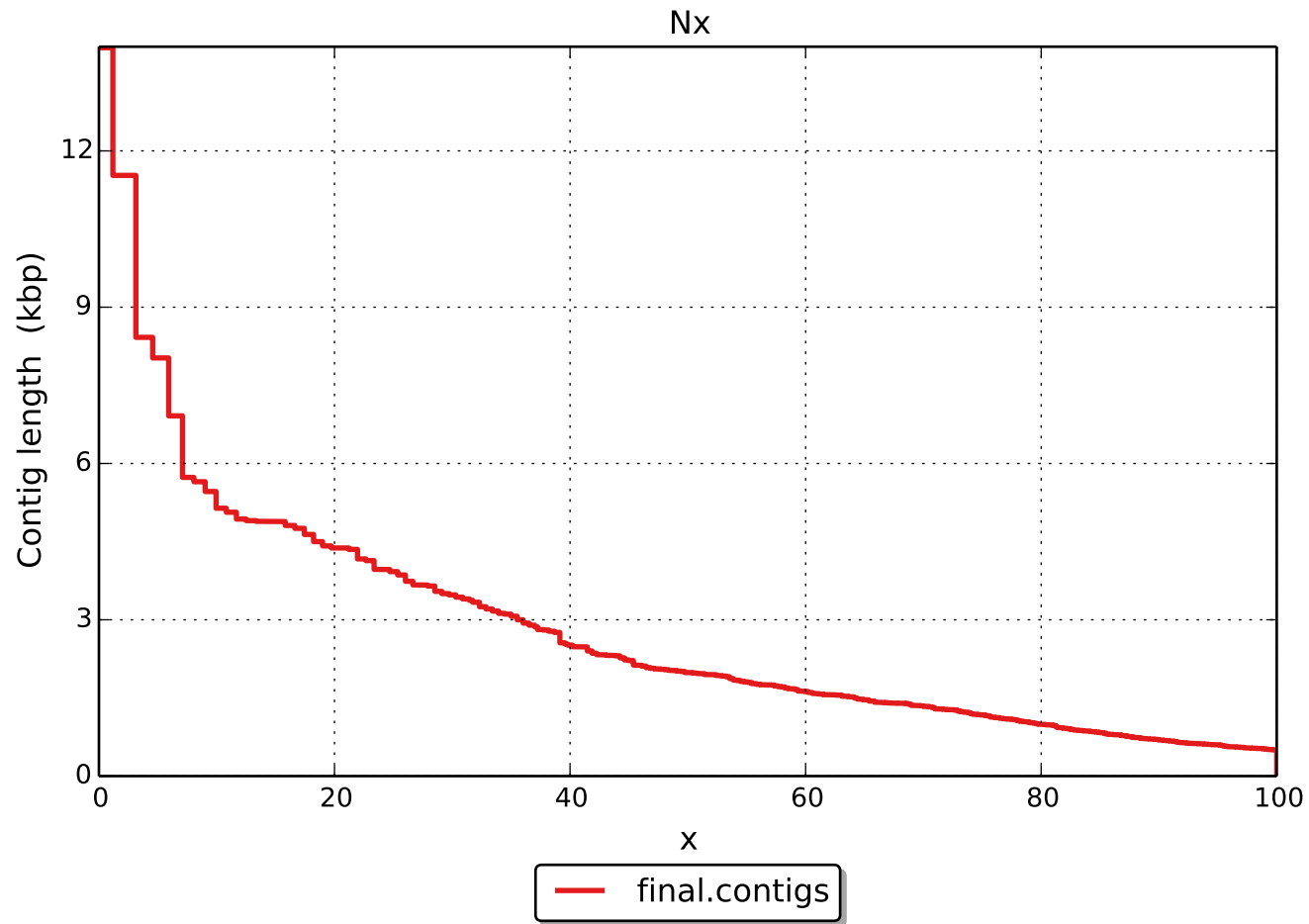
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

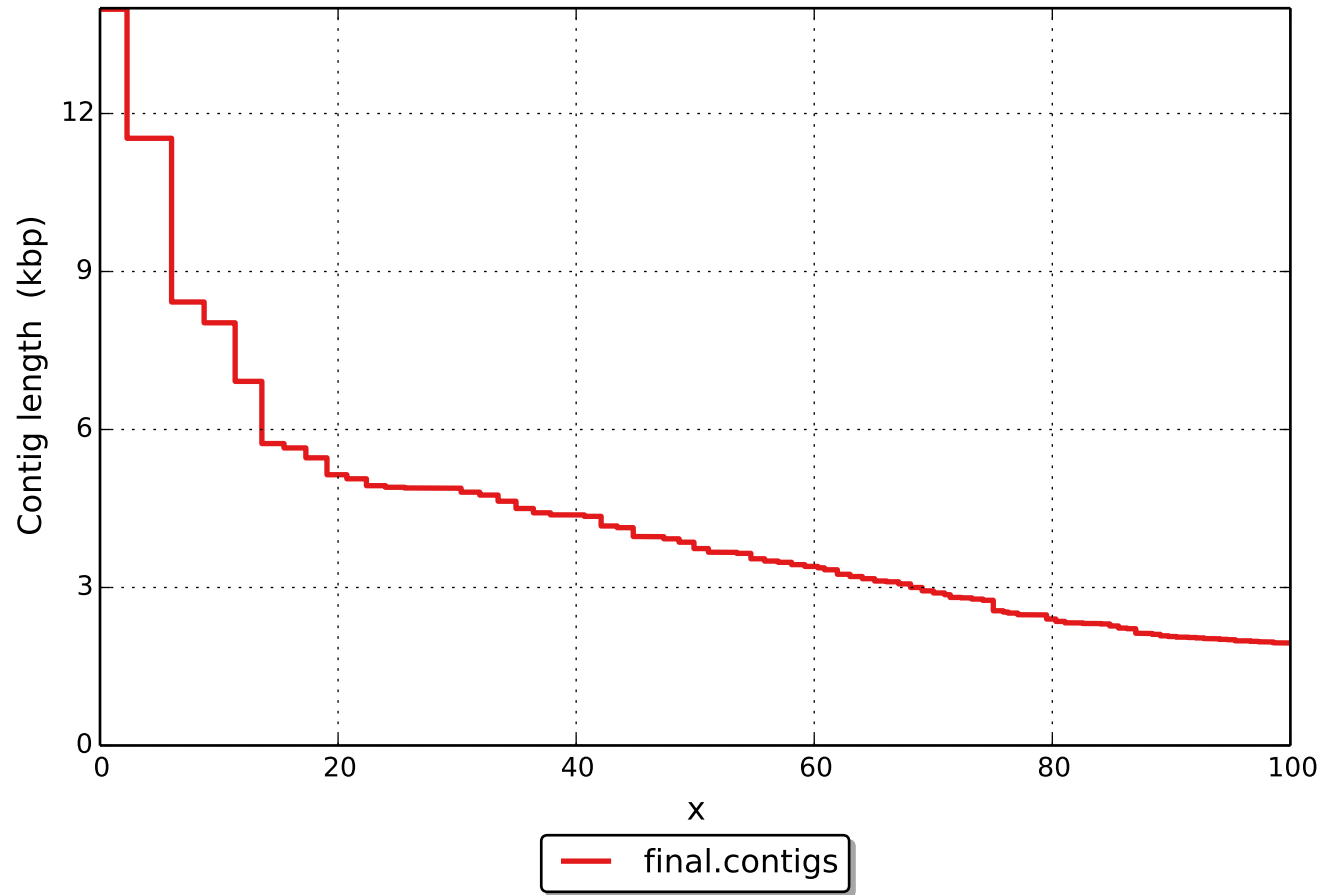


GC content

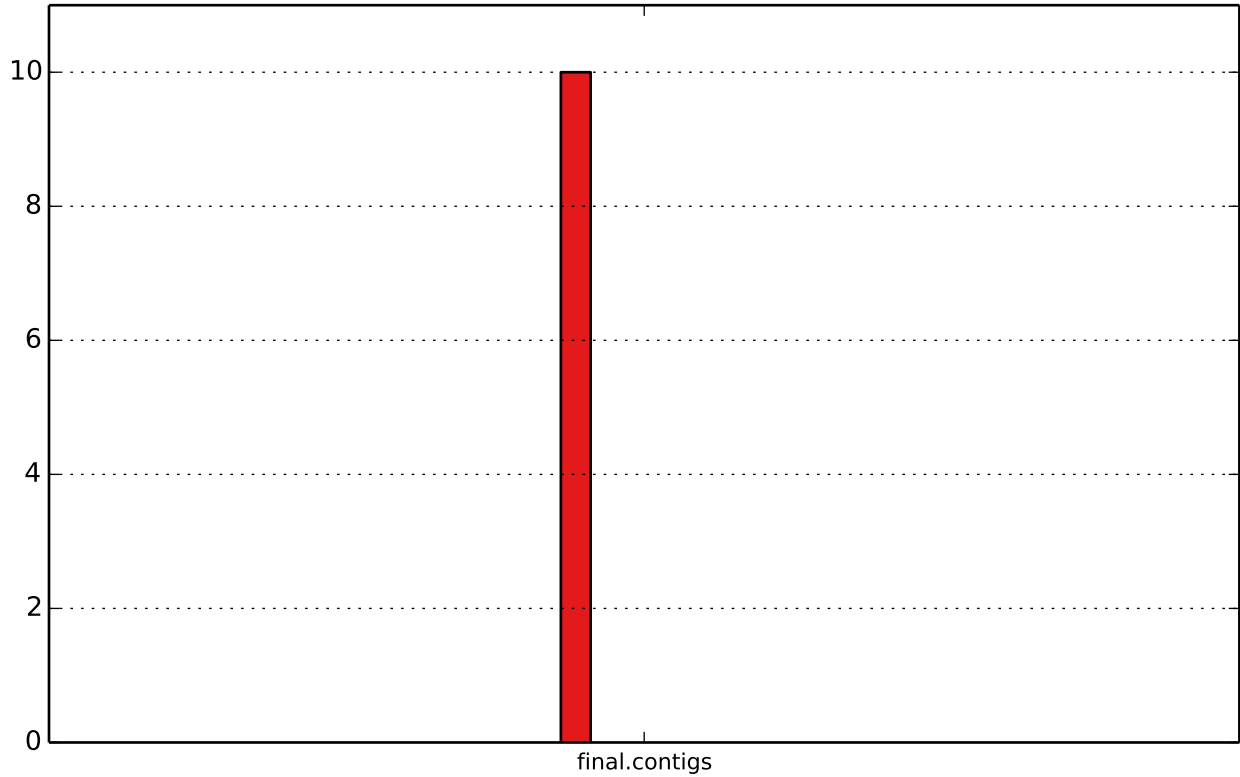


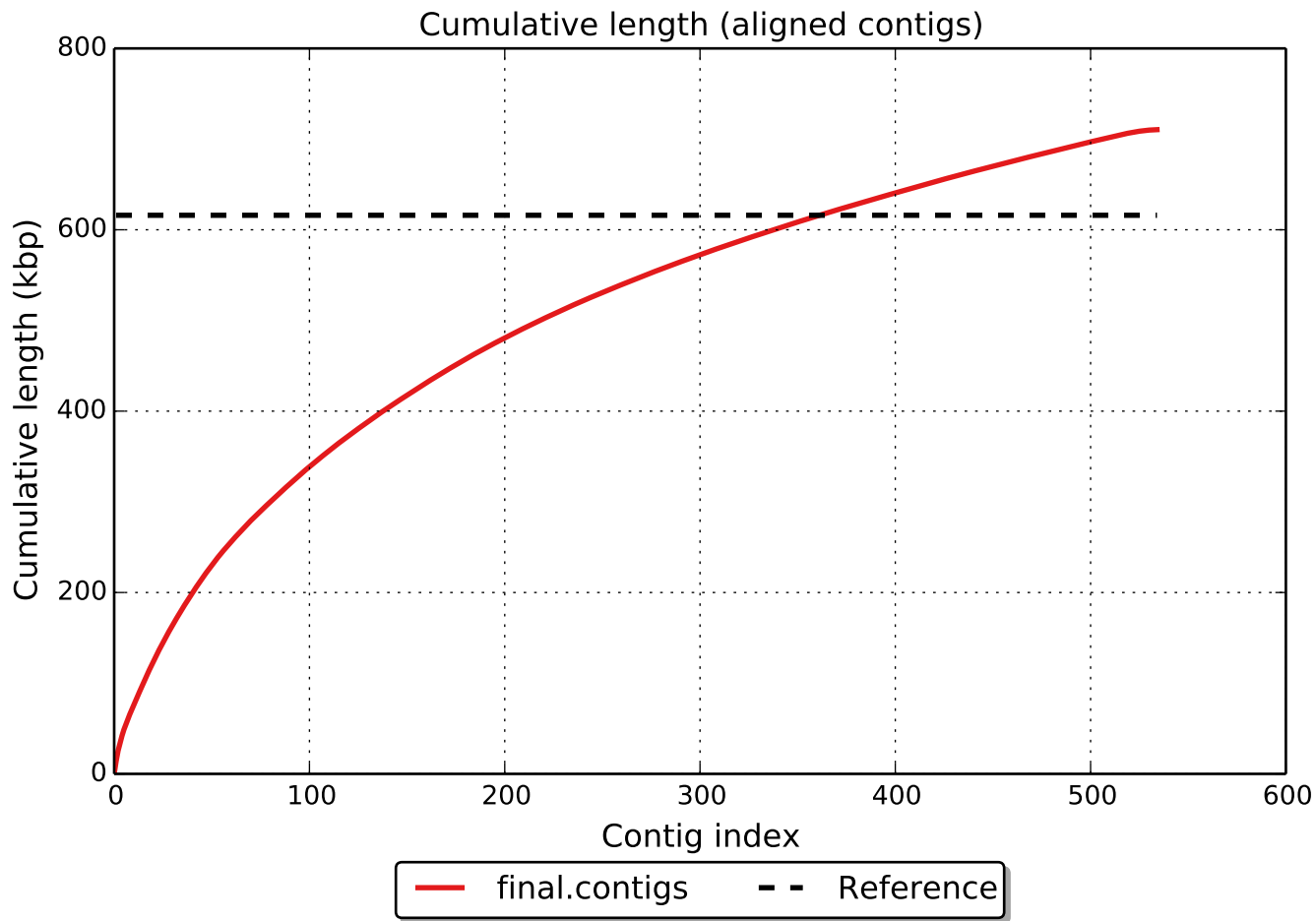


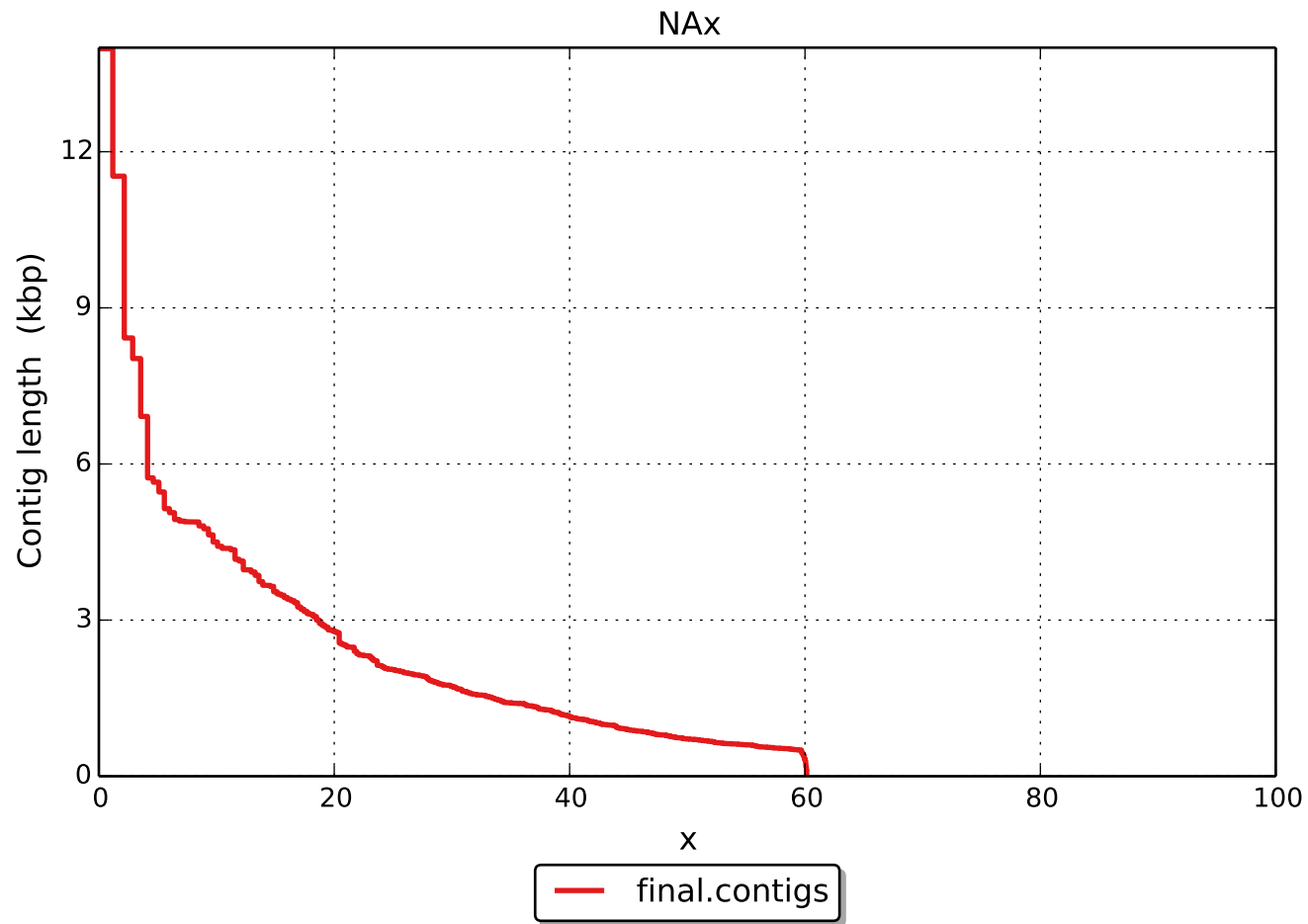
NGx



Misassemblies







NGAx

