

Report

	final.contigs
# contigs (≥ 0 bp)	185
# contigs (≥ 1000 bp)	161
Total length (≥ 0 bp)	1226179
Total length (≥ 1000 bp)	1211339
# contigs	185
Largest contig	36312
Total length	1226179
Reference length	615980
GC (%)	25.35
Reference GC (%)	25.35
N50	11581
NG50	15730
N75	7210
NG75	12526
L50	38
LG50	14
L75	71
LG75	26
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1131
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.828
Duplication ratio	2.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	498.72
# indels per 100 kbp	0.00
Largest alignment	36312
NA50	645
NGA50	11348
NGA75	7210
LA50	91
LGA50	20
LGA75	36

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	1131
# local misassemblies	0
# mismatches	3036
# indels	0
# short indels	0
# long indels	0
Indels length	0

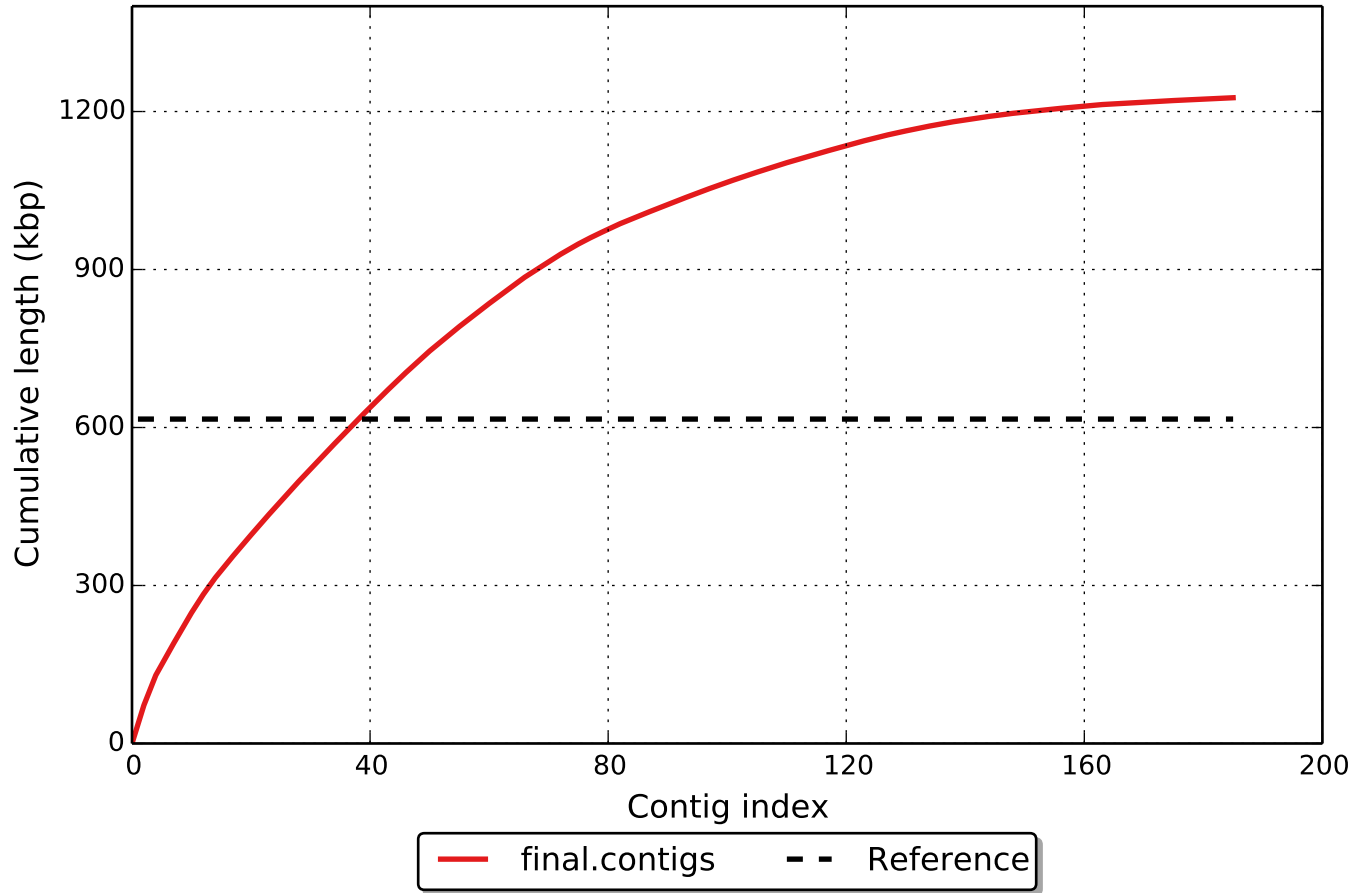
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

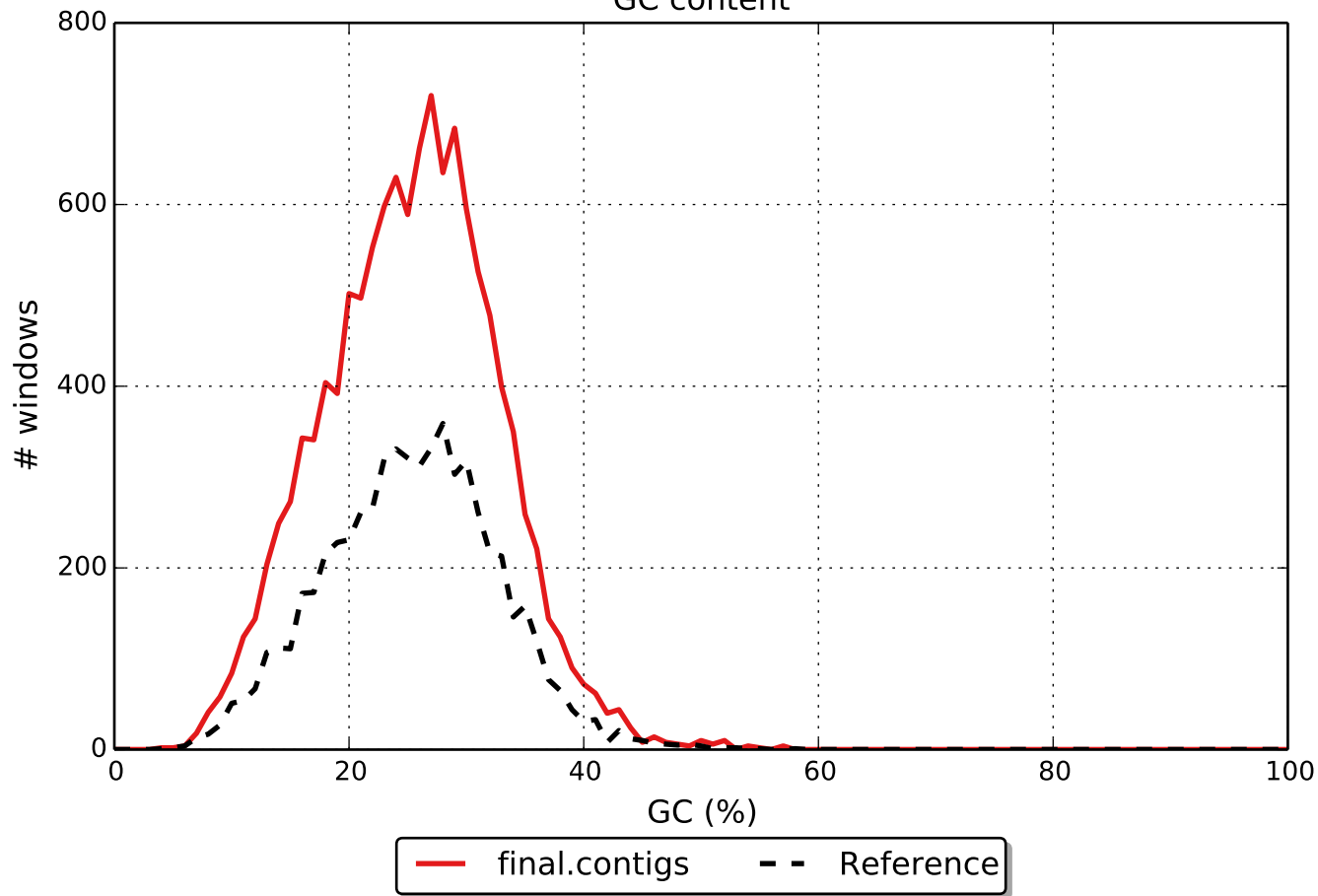
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

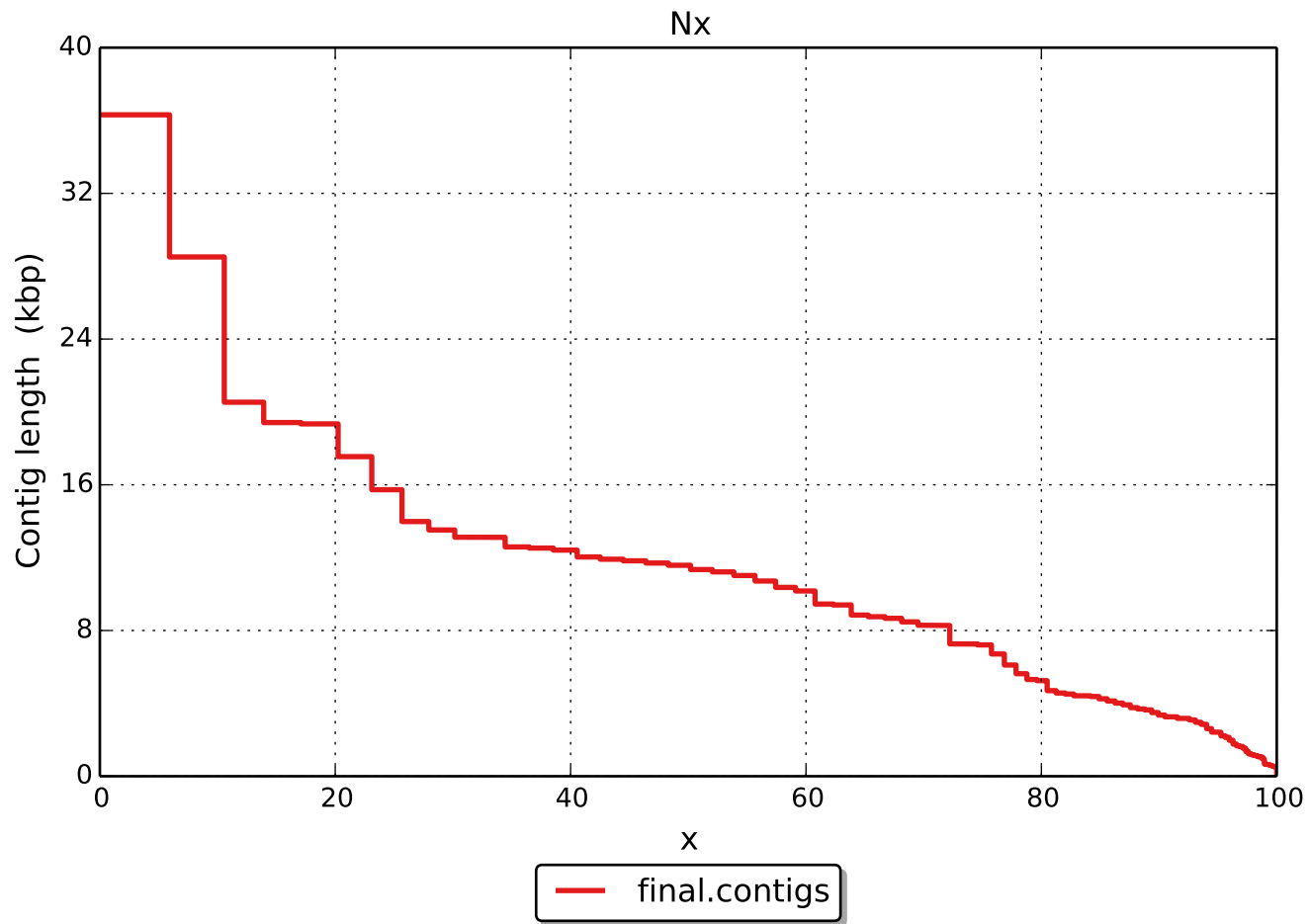
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

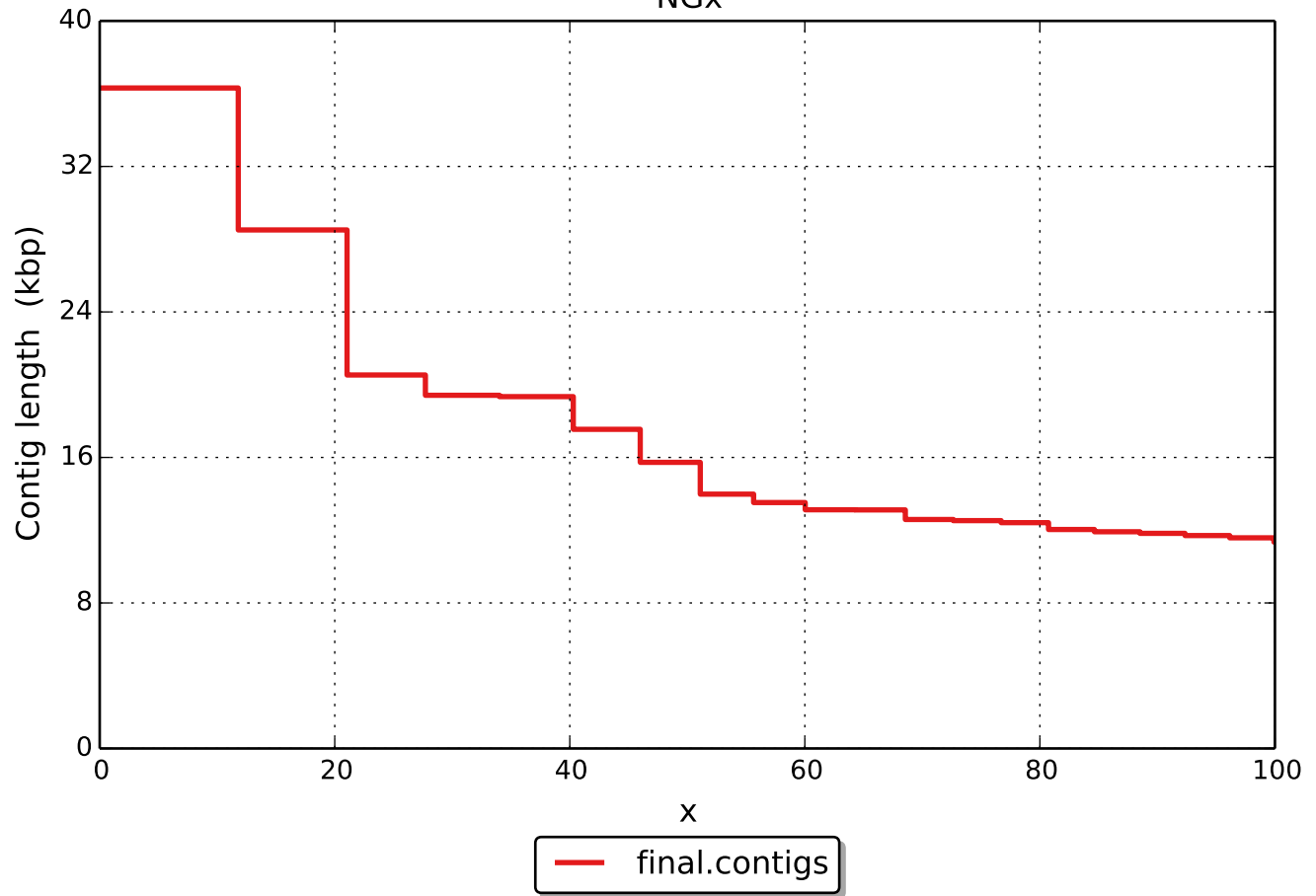


GC content



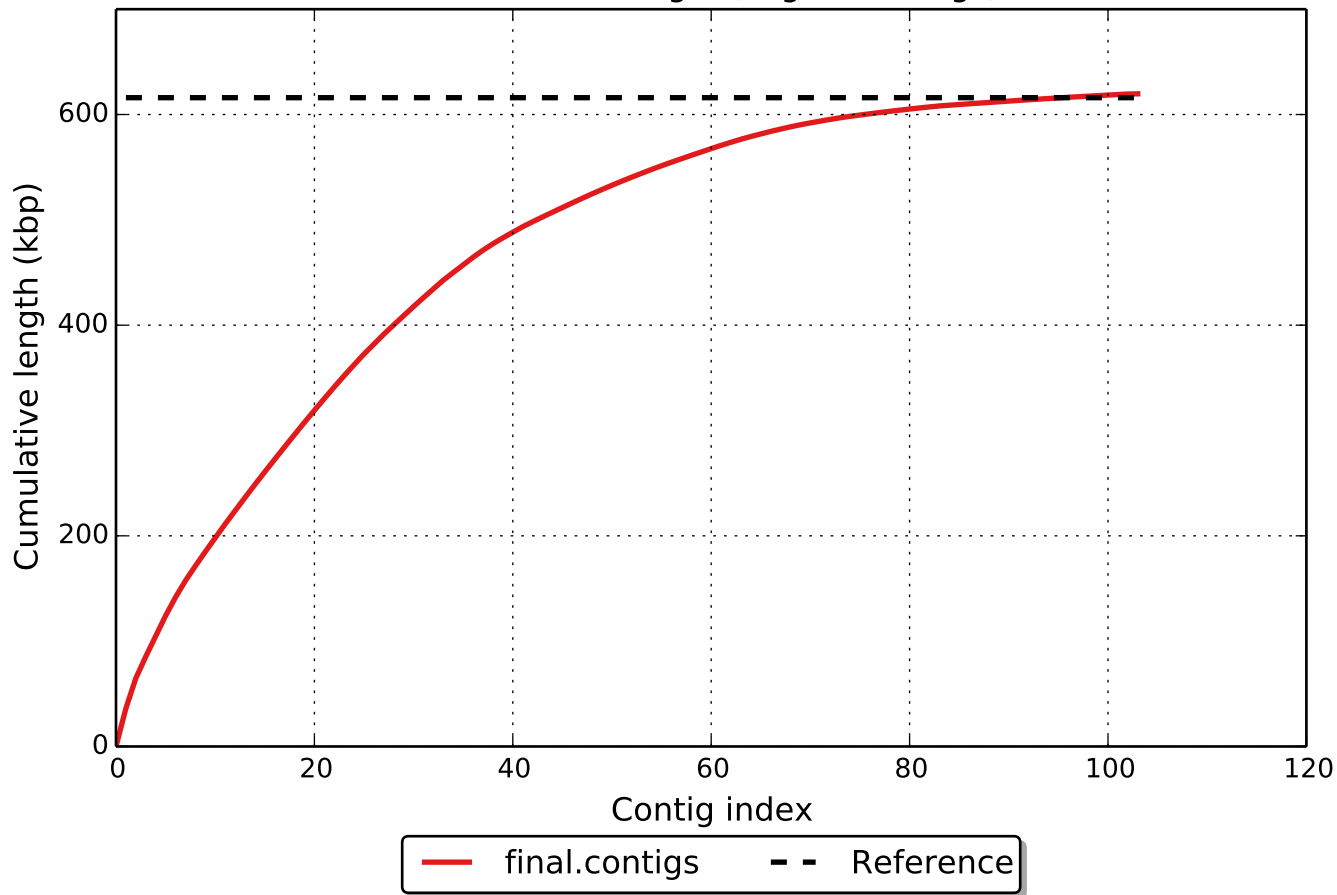


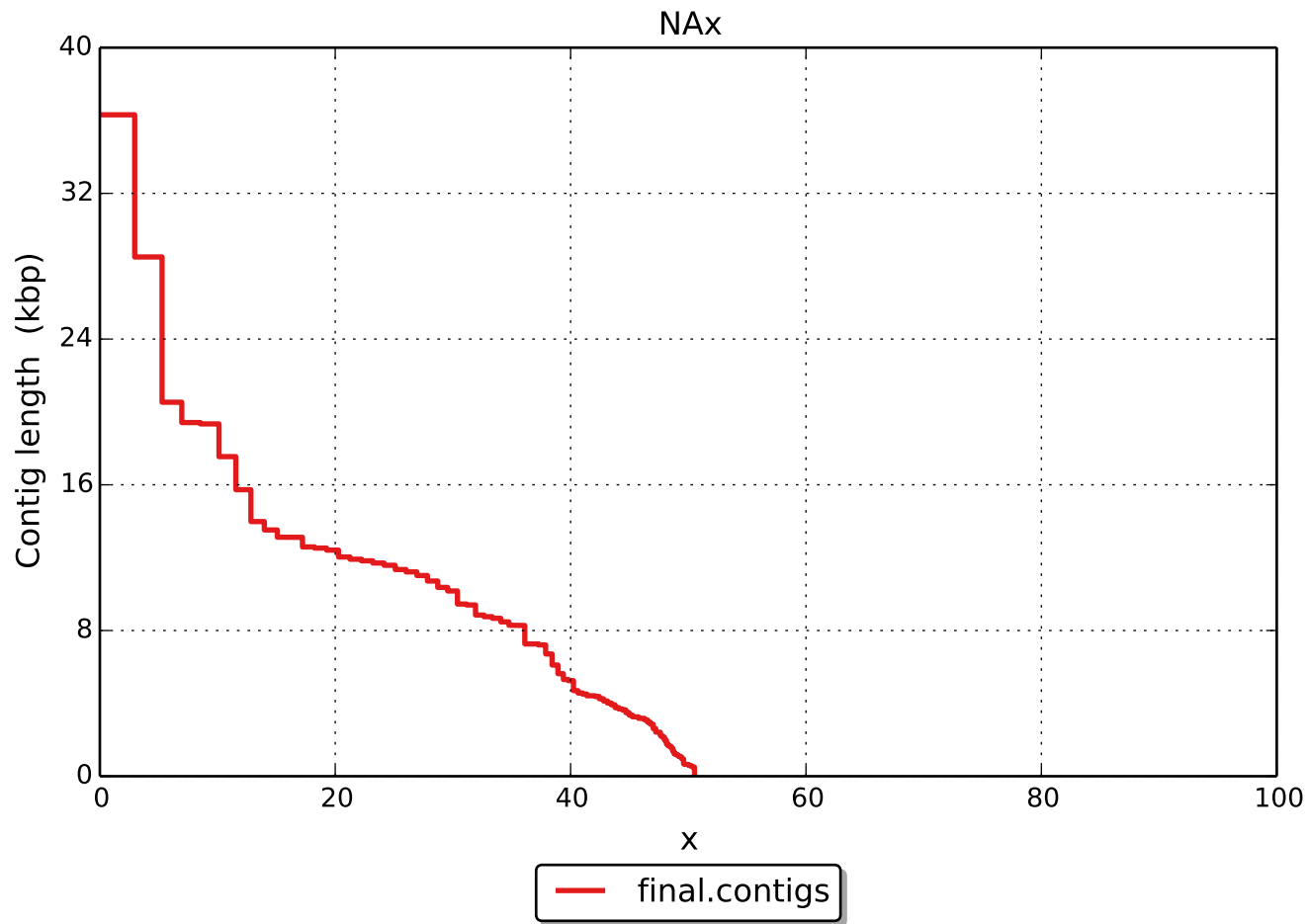
NGx





Cumulative length (aligned contigs)





NGAx

