

Report

	final.contigs
# contigs (>= 0 bp)	300
# contigs (>= 1000 bp)	277
Total length (>= 0 bp)	3709797
Total length (>= 1000 bp)	3692267
# contigs	300
Largest contig	75385
Total length	3709797
Reference length	1892775
GC (%)	32.26
Reference GC (%)	32.27
N50	19328
NG50	31029
N75	12313
NG75	24541
L50	60
LG50	23
L75	120
LG75	40
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	123 + 58 part
Unaligned length	1785966
Genome fraction (%)	99.949
Duplication ratio	1.017
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.95
# indels per 100 kbp	0.11
Largest alignment	75385
NA50	5287
NGA50	28635
NGA75	14649
LA50	95
LGA50	24
LGA75	48

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

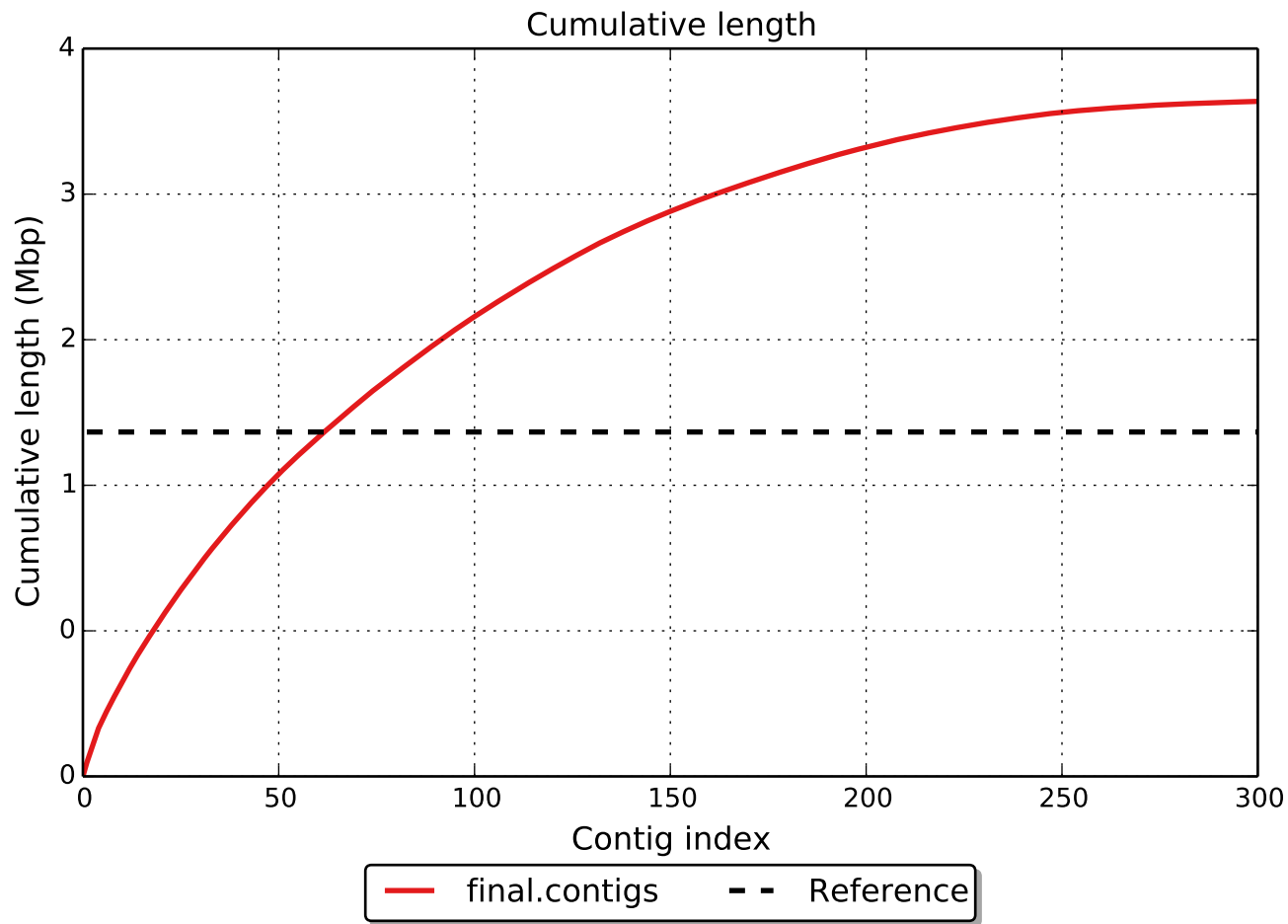
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	264
# indels	2
# short indels	2
# long indels	0
Indels length	2

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).

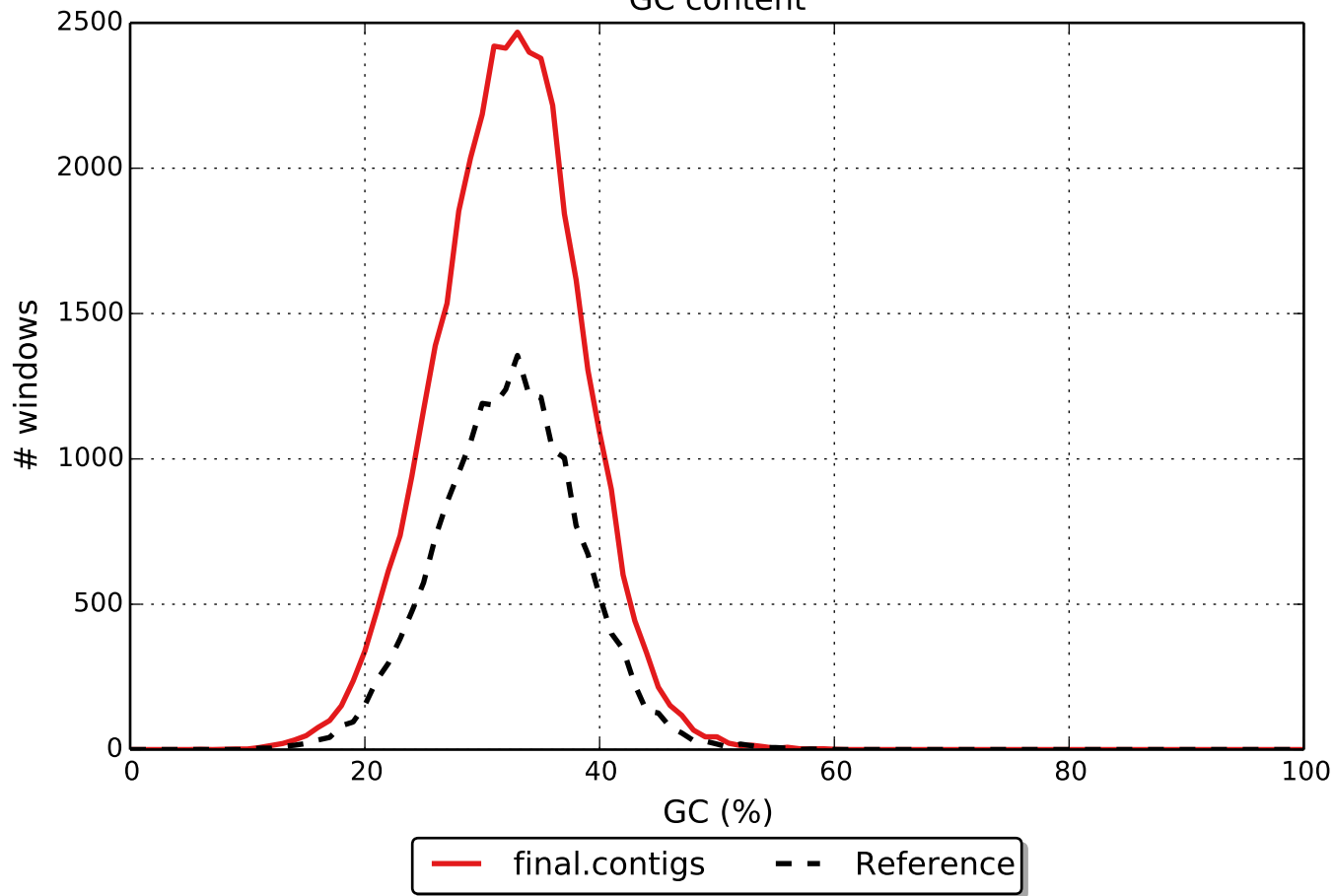
Unaligned report

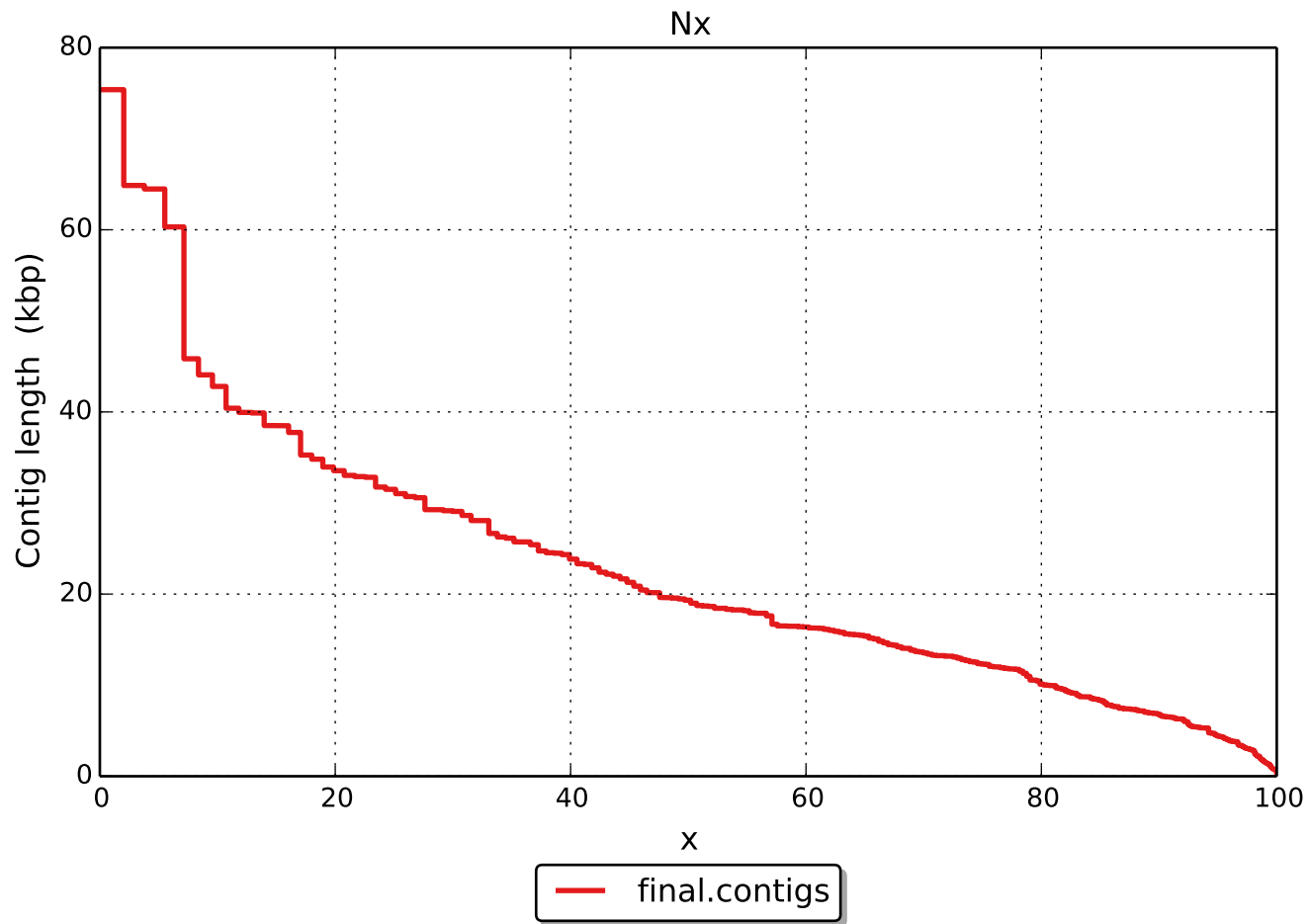
	final.contigs
# fully unaligned contigs	123
Fully unaligned length	1150697
# partially unaligned contigs	58
# with misassembly	10
# both parts are significant	3
Partially unaligned length	635269
# N's	0

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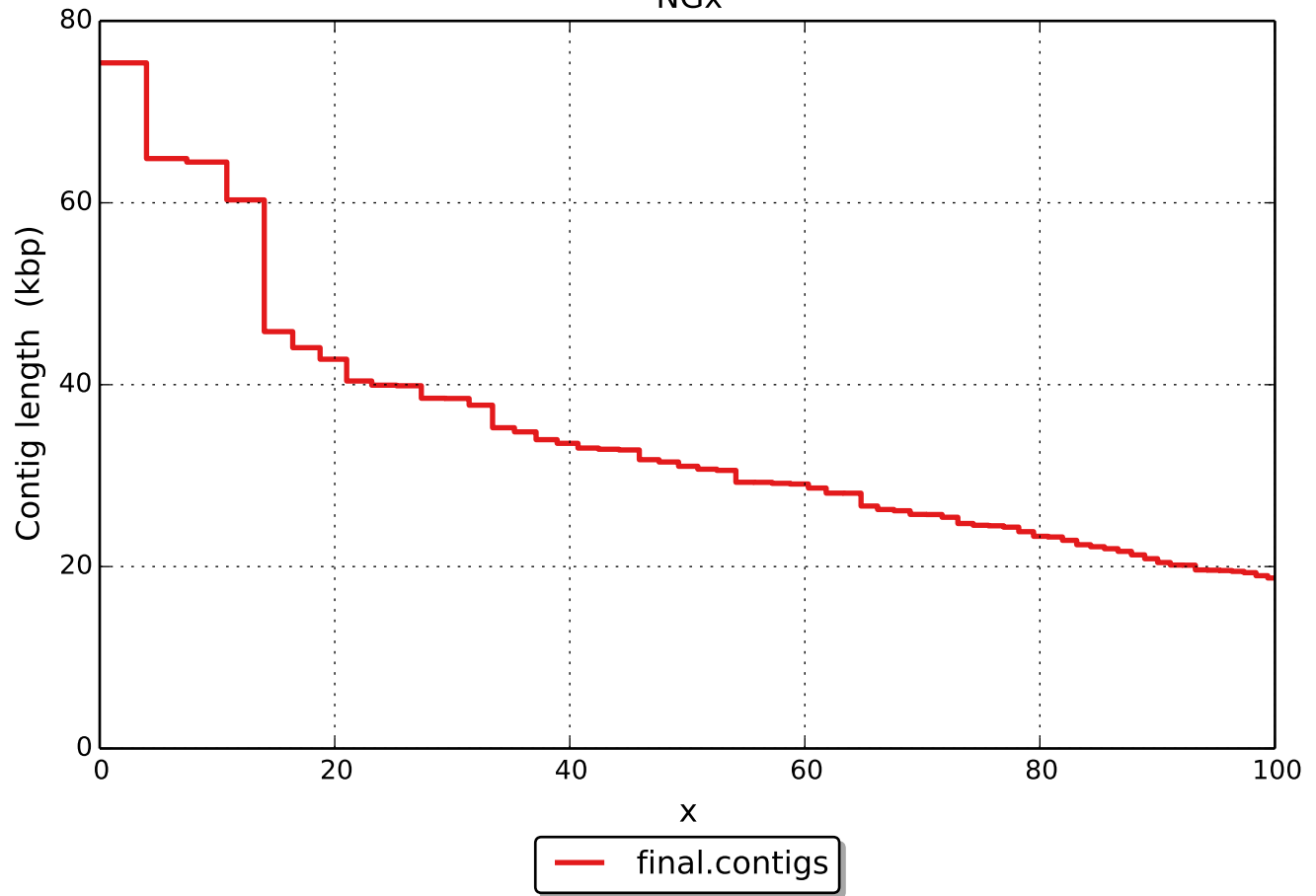


GC content





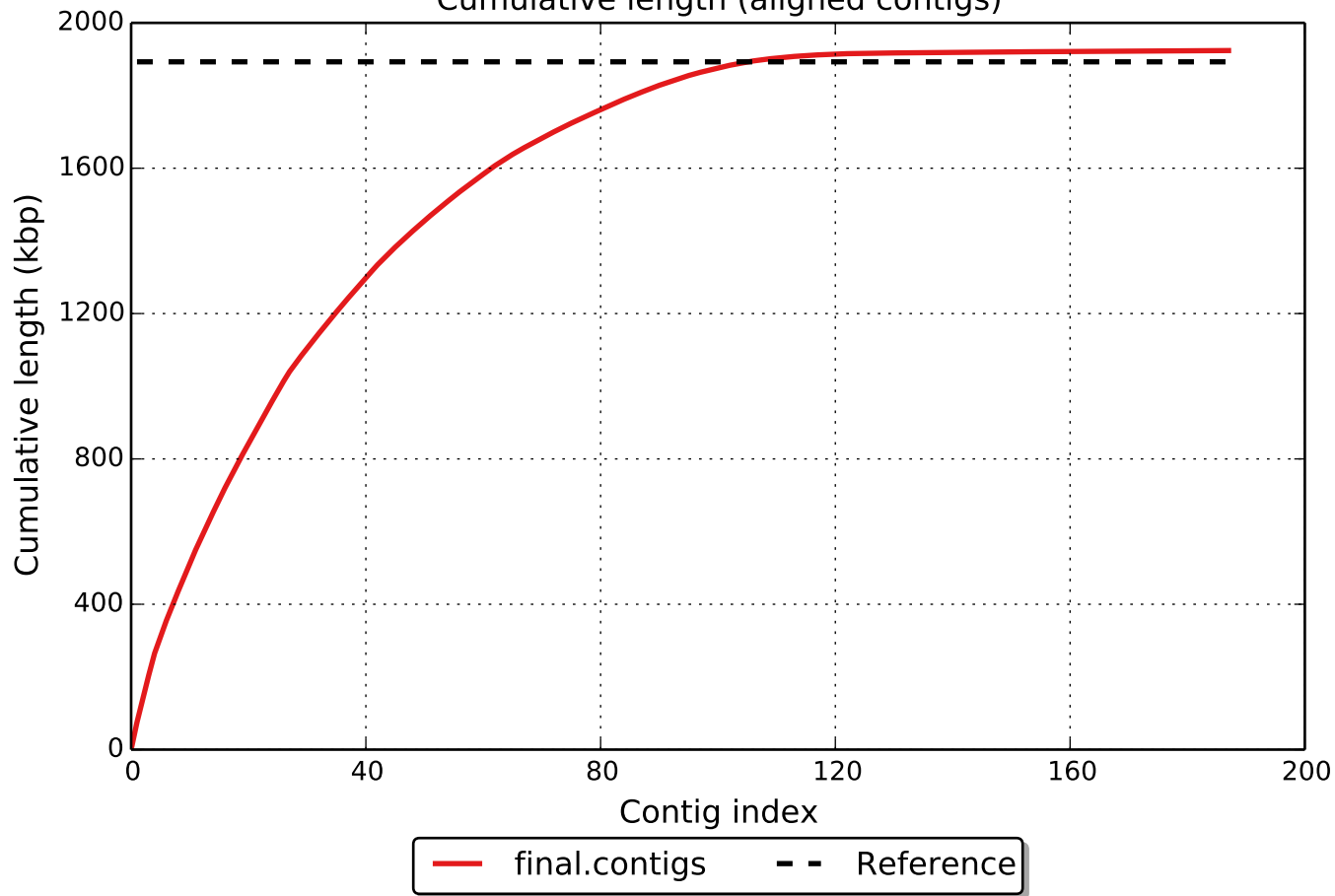
NGx

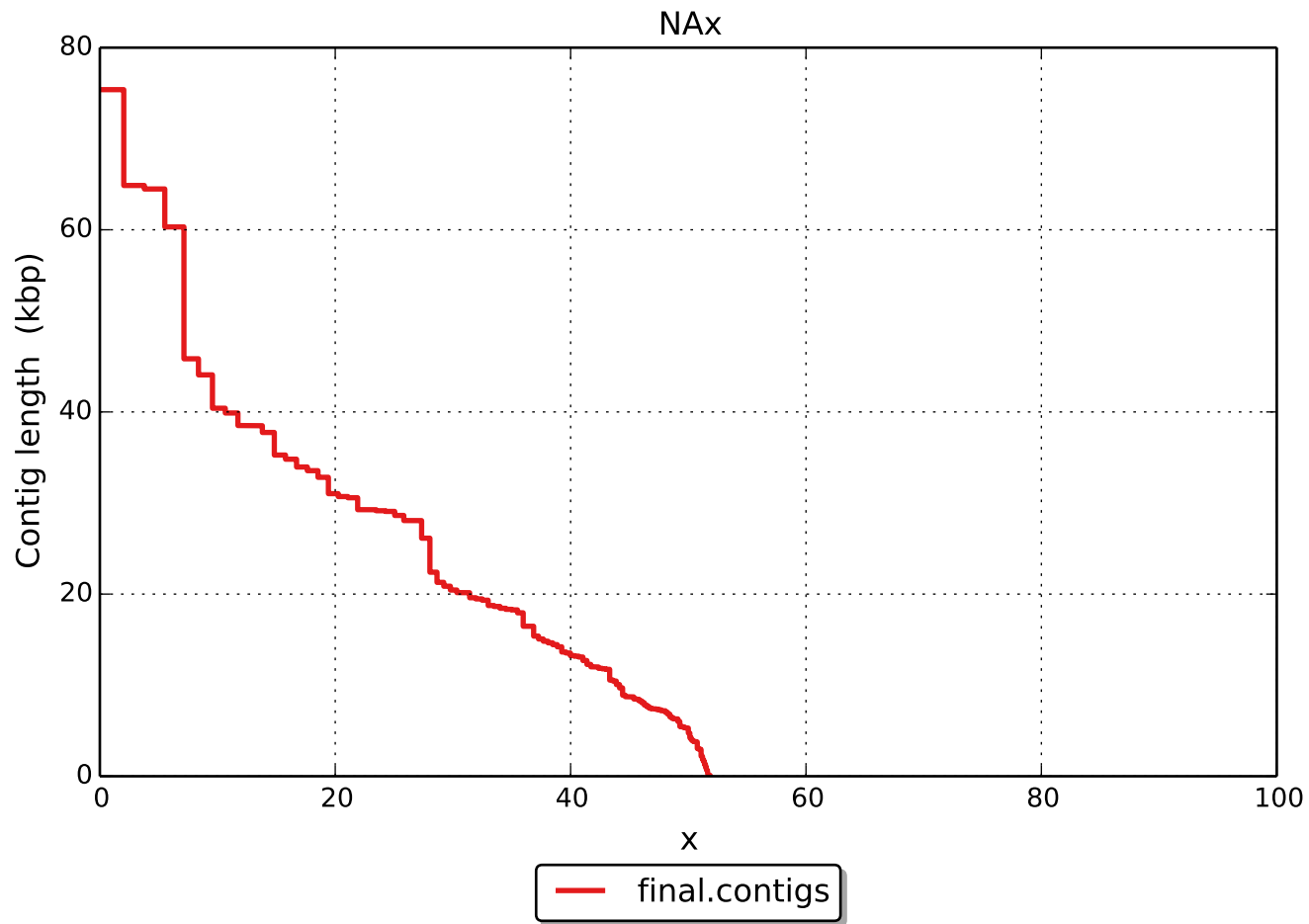


Misassemblies



Cumulative length (aligned contigs)





NGAx

