

Report

	final.contigs
# contigs (≥ 0 bp)	1343
# contigs (≥ 1000 bp)	1095
Total length (≥ 0 bp)	5243699
Total length (≥ 1000 bp)	5066798
# contigs	1343
Largest contig	25863
Total length	5243699
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	6355
NG50	6060
N75	3412
NG75	2995
L50	253
LG50	277
L75	540
LG75	611
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6203
# local misassemblies	4
# unaligned contigs	0 + 2 part
Unaligned length	13809
Genome fraction (%)	92.459
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	27.00
# indels per 100 kbp	0.41
Largest alignment	25863
NA50	6331
NGA50	6016
NA75	3395
NGA75	2962
LA50	255
LGA50	279
LA75	544
LGA75	616

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

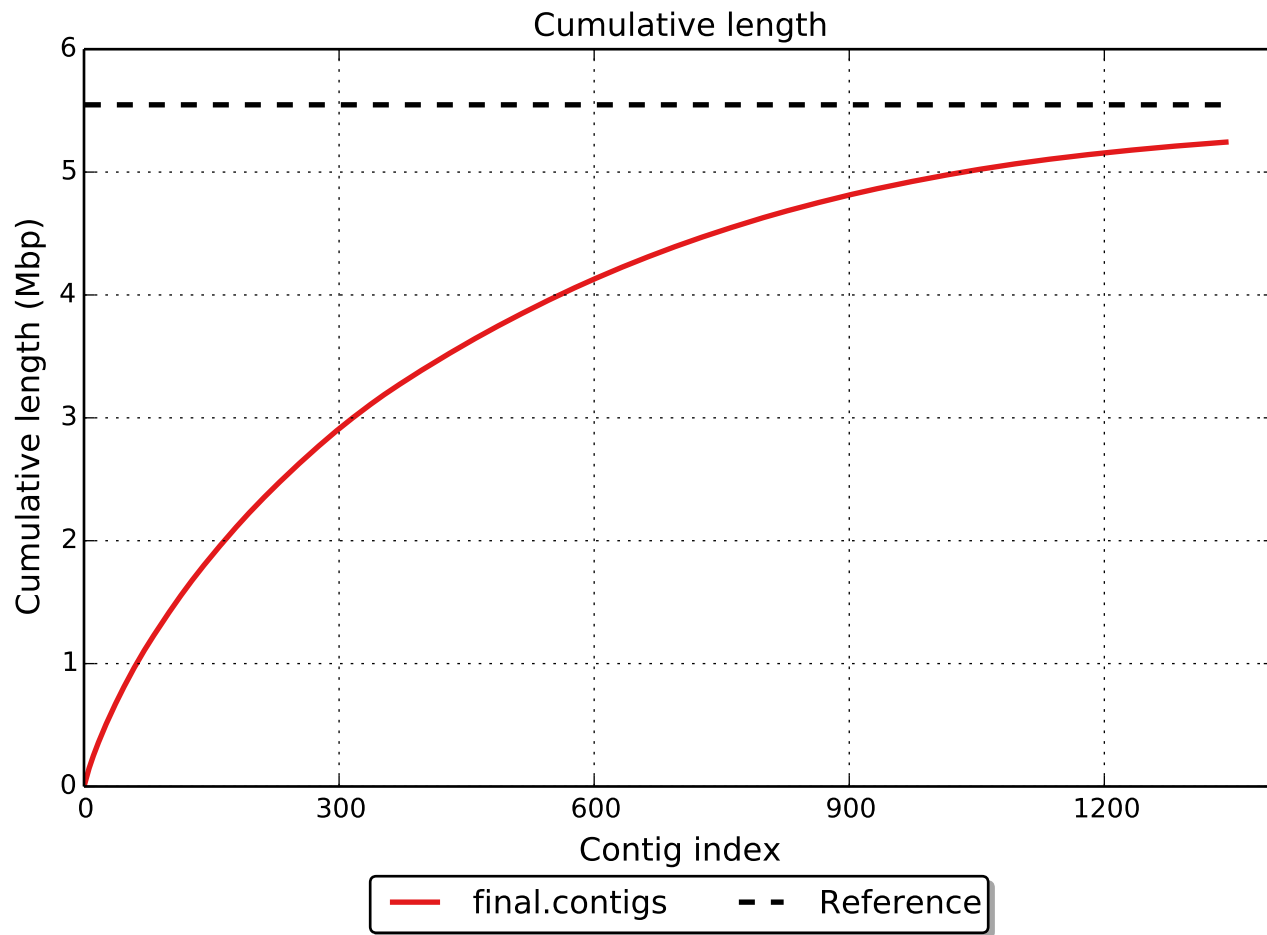
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	6203
# local misassemblies	4
# mismatches	1385
# indels	21
# short indels	17
# long indels	4
Indels length	142

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).

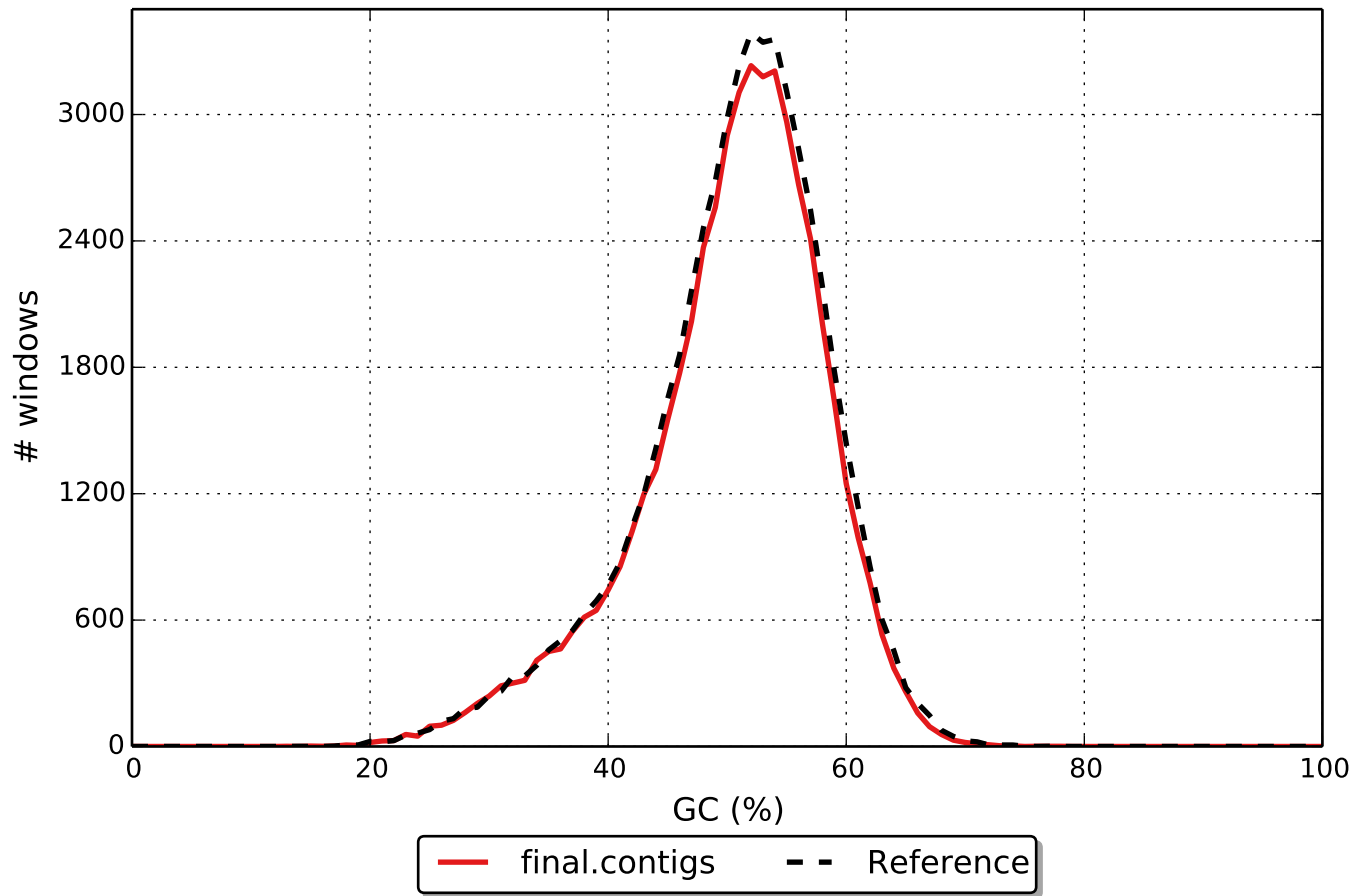
Unaligned report

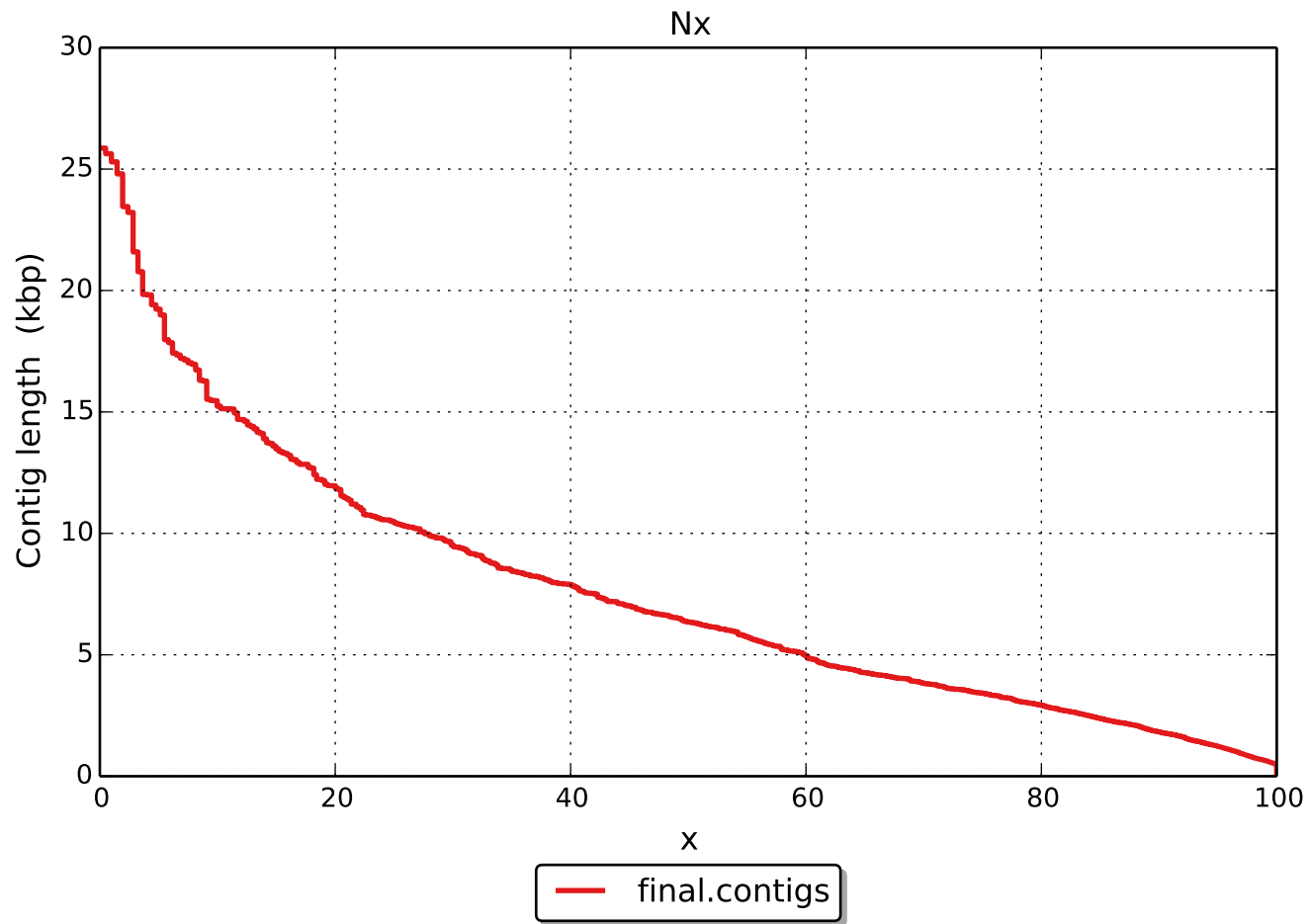
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	13809
# N's	0

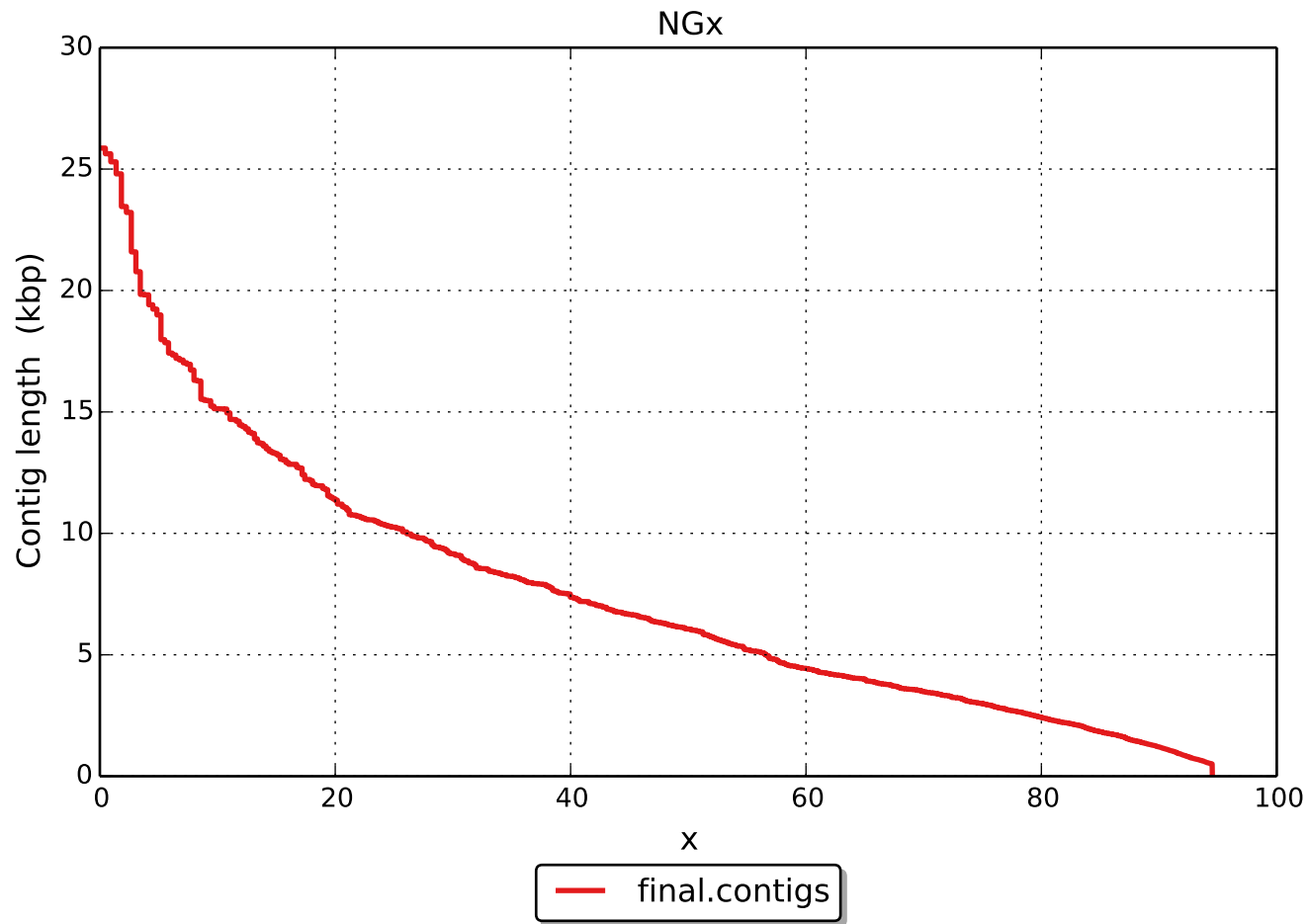
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

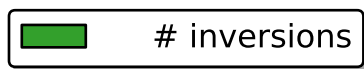
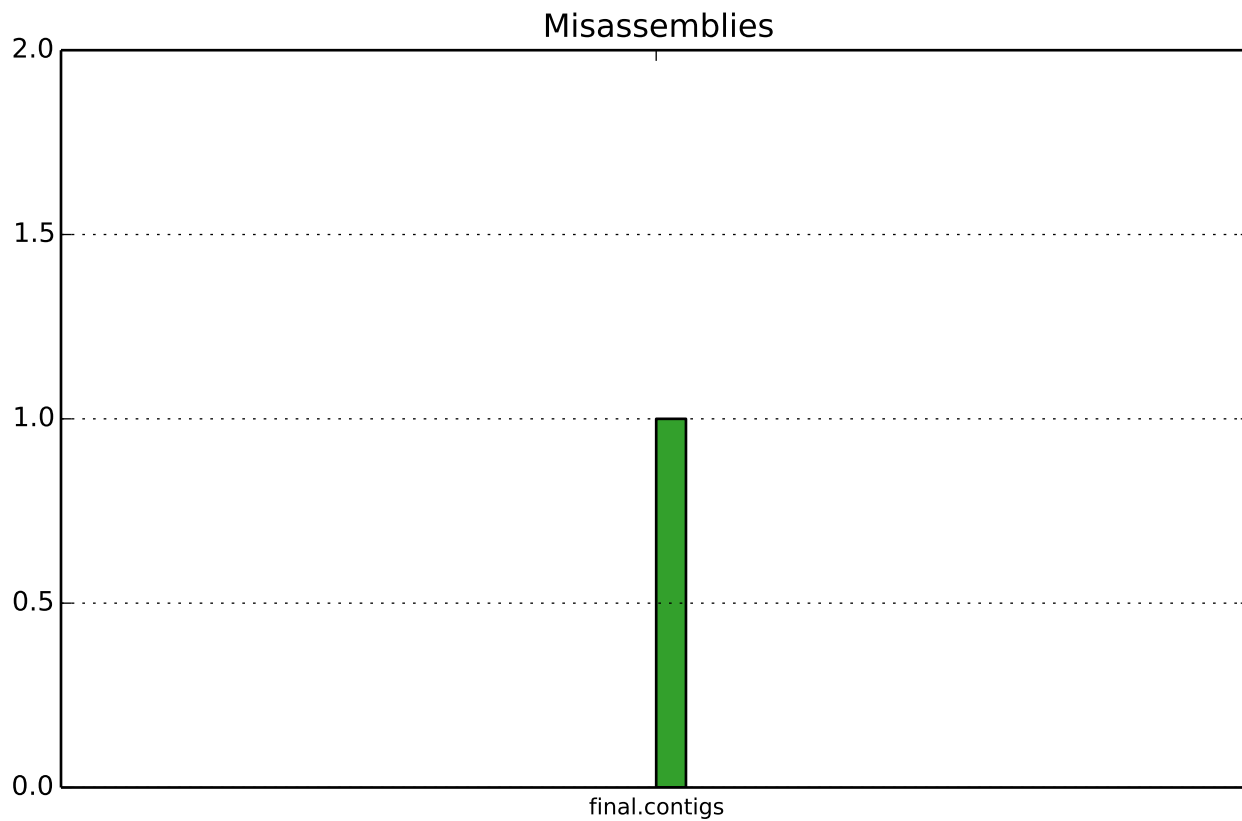


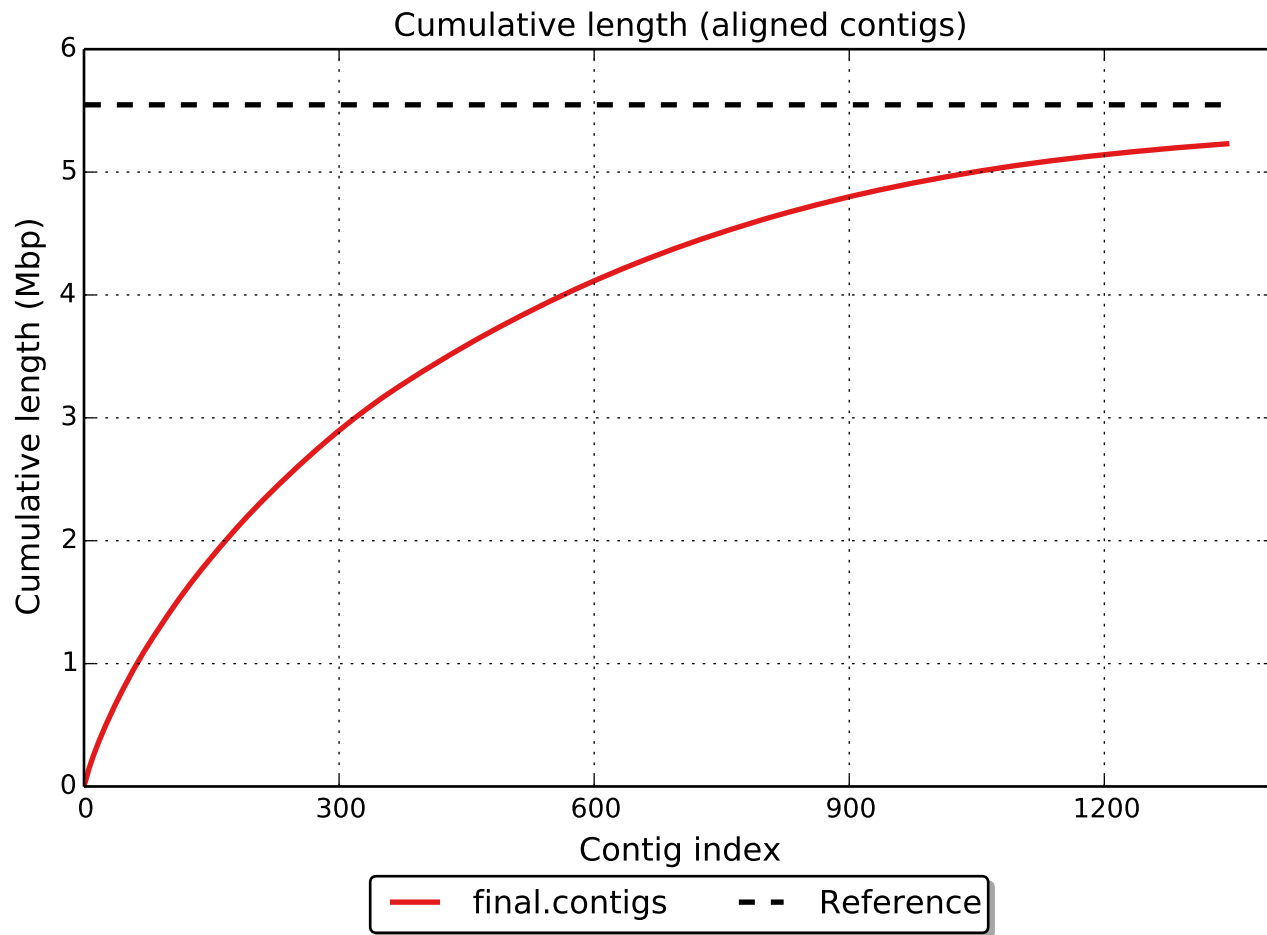
GC content

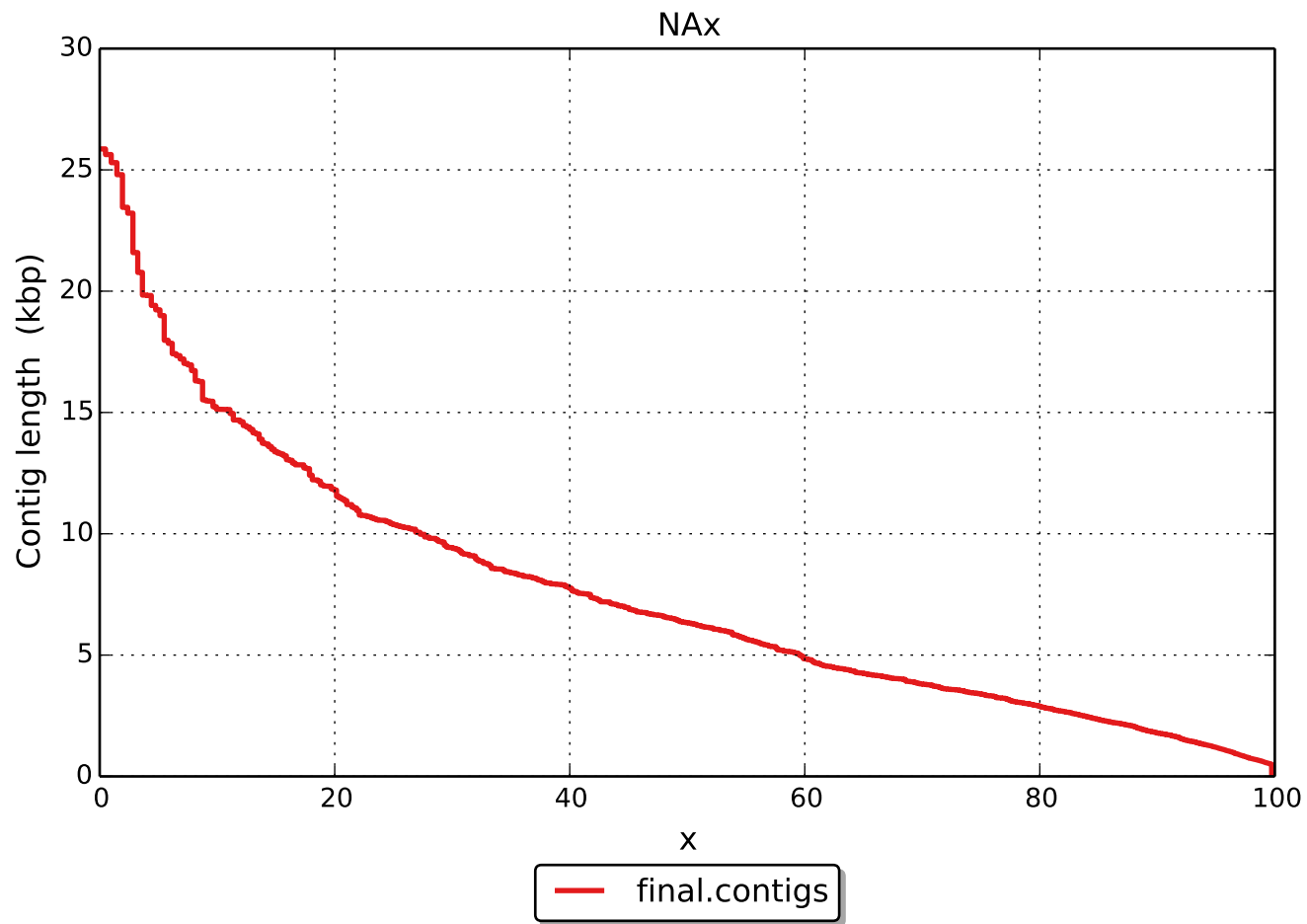












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