

Report

	final.contigs
# contigs (≥ 0 bp)	2610
# contigs (≥ 1000 bp)	1775
Total length (≥ 0 bp)	10954809
Total length (≥ 1000 bp)	10586235
# contigs	2044
Largest contig	38712
Total length	10778791
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	8527
NG50	8412
N75	4819
NG75	4626
L50	400
LG50	410
L75	817
LG75	845
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.425
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	12.64
# indels per 100 kbp	0.08
Largest alignment	38712
NA50	8527
NGA50	8412
NA75	4819
NGA75	4626
LA50	400
LGA50	410
LA75	817
LGA75	845

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

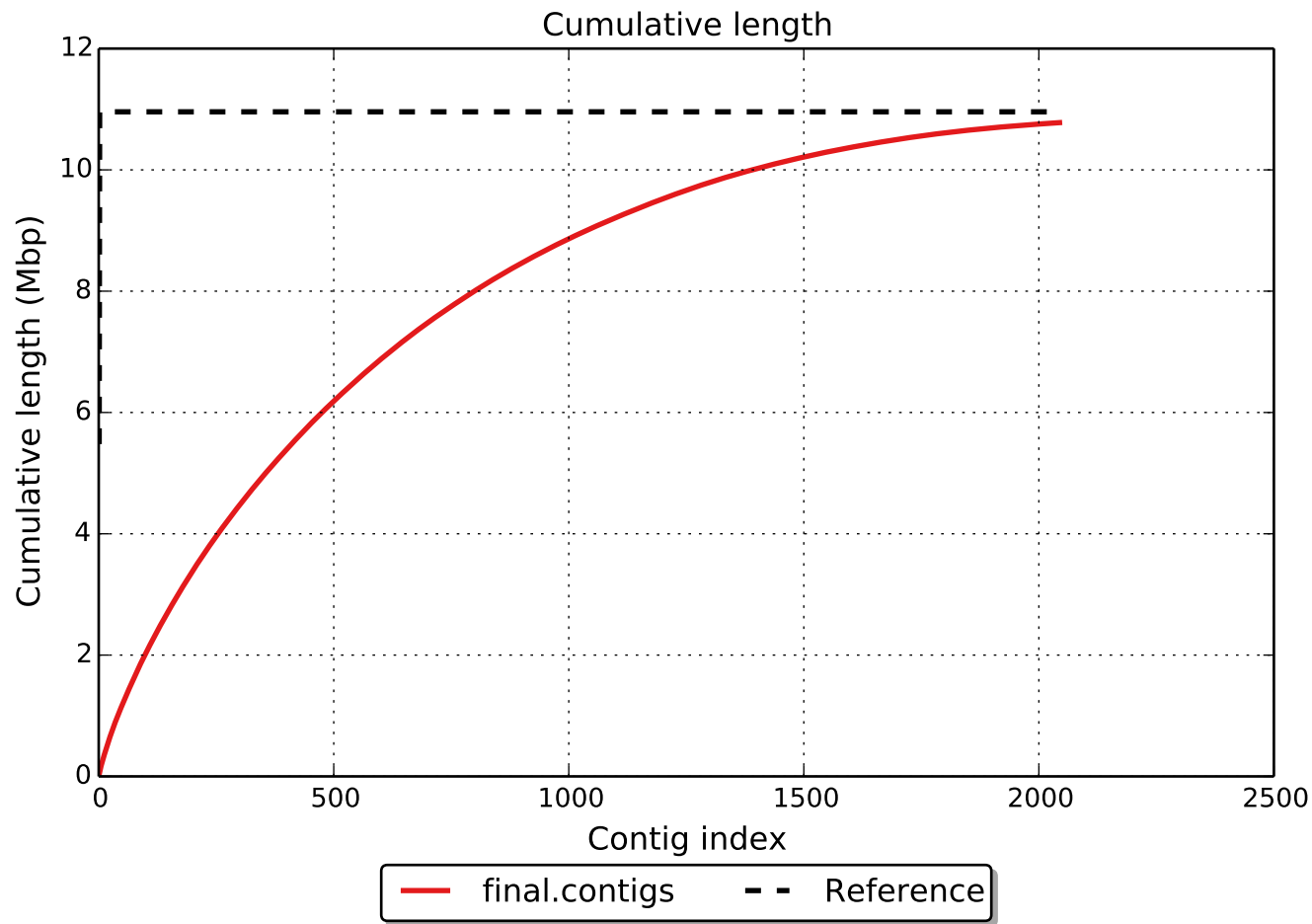
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1349
# indels	9
# short indels	7
# long indels	2
Indels length	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).

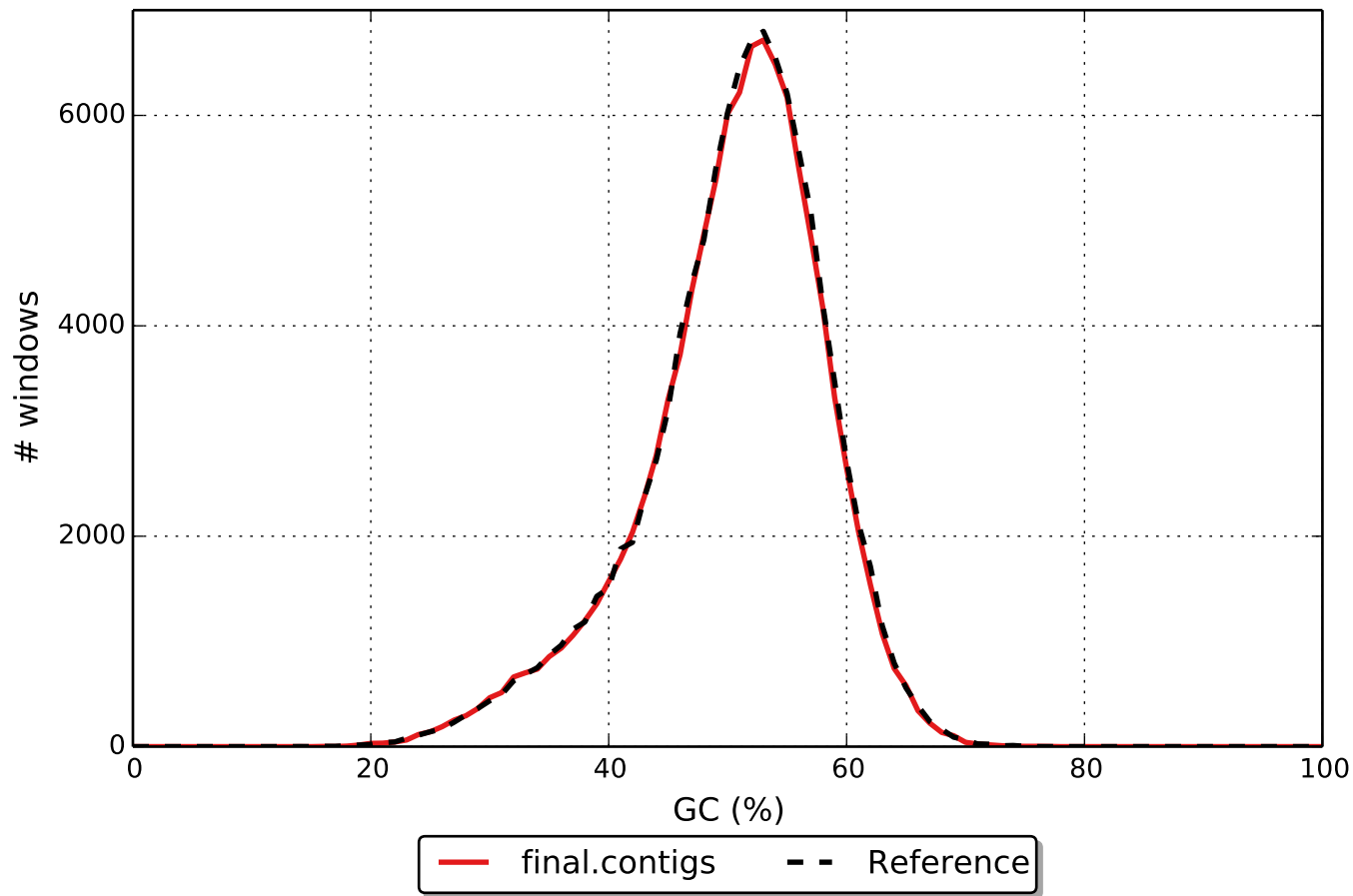
Unaligned report

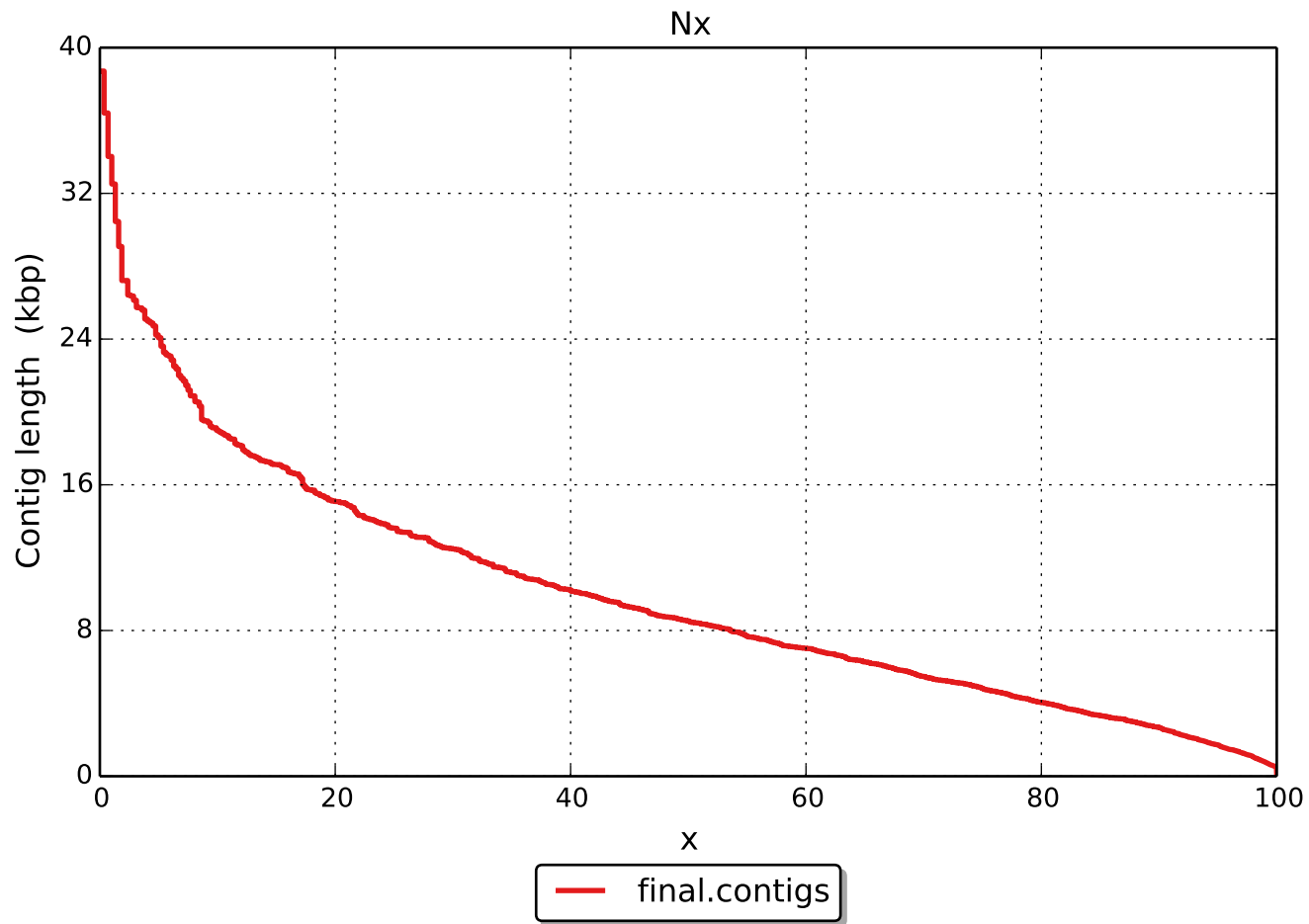
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

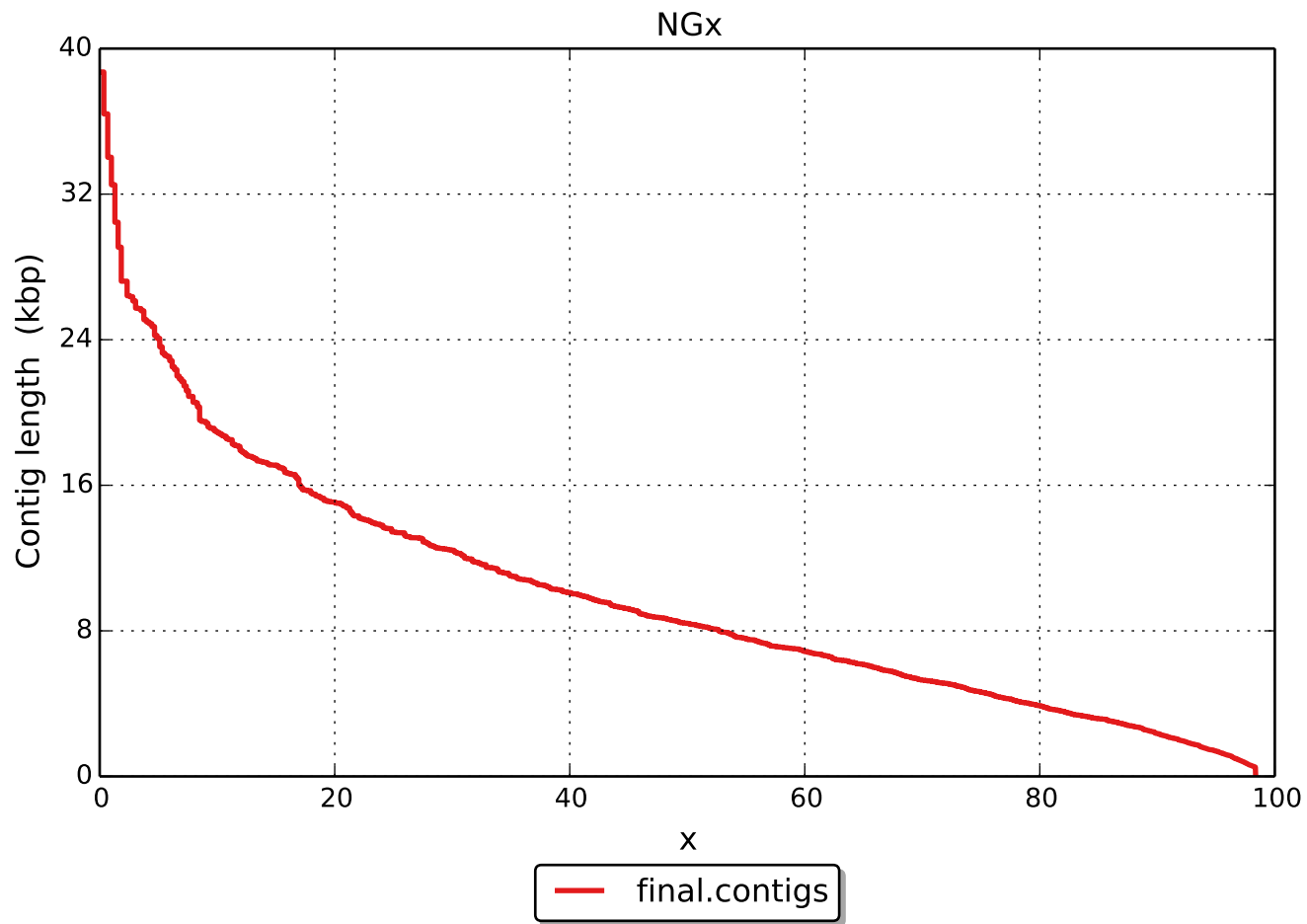
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

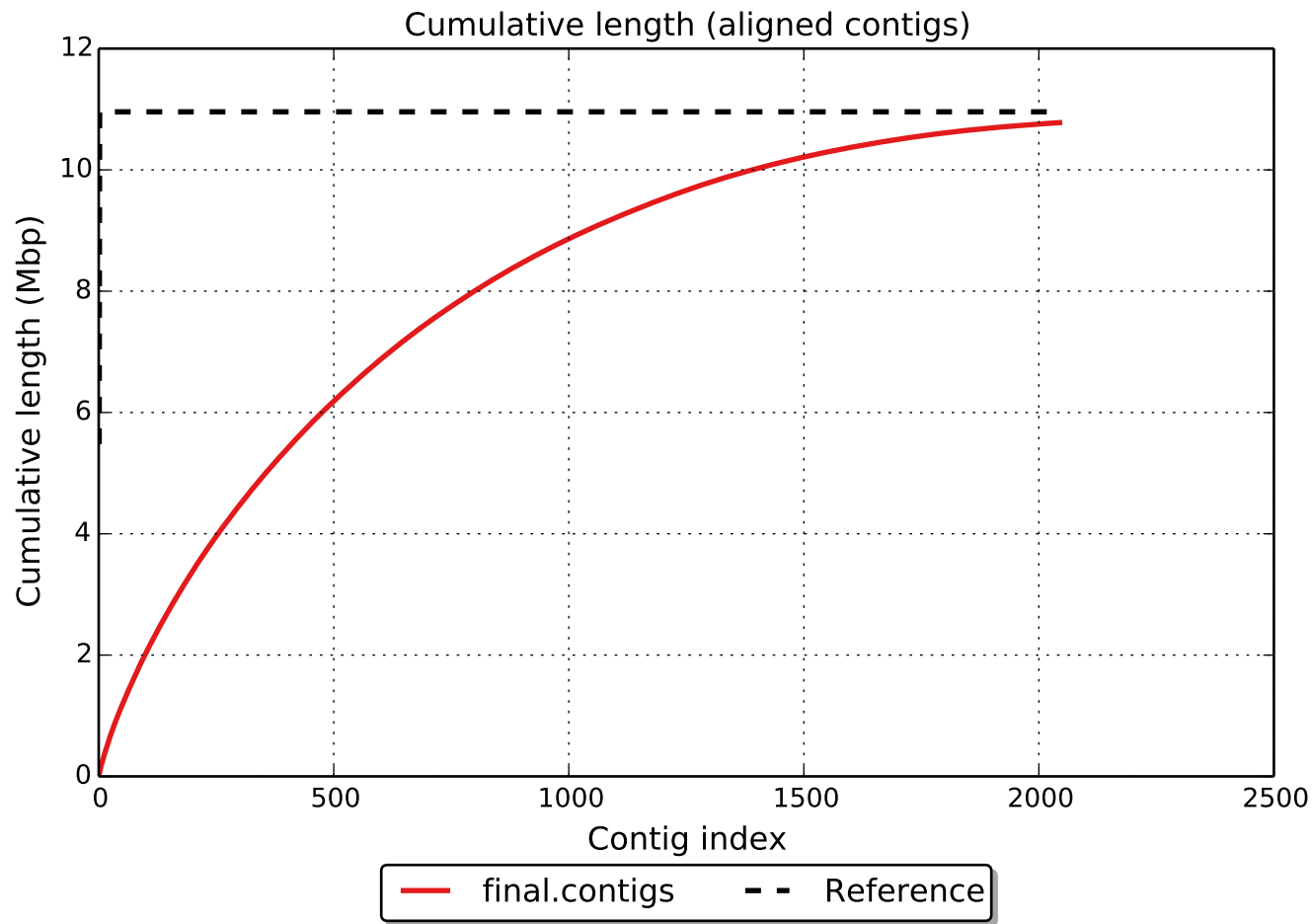


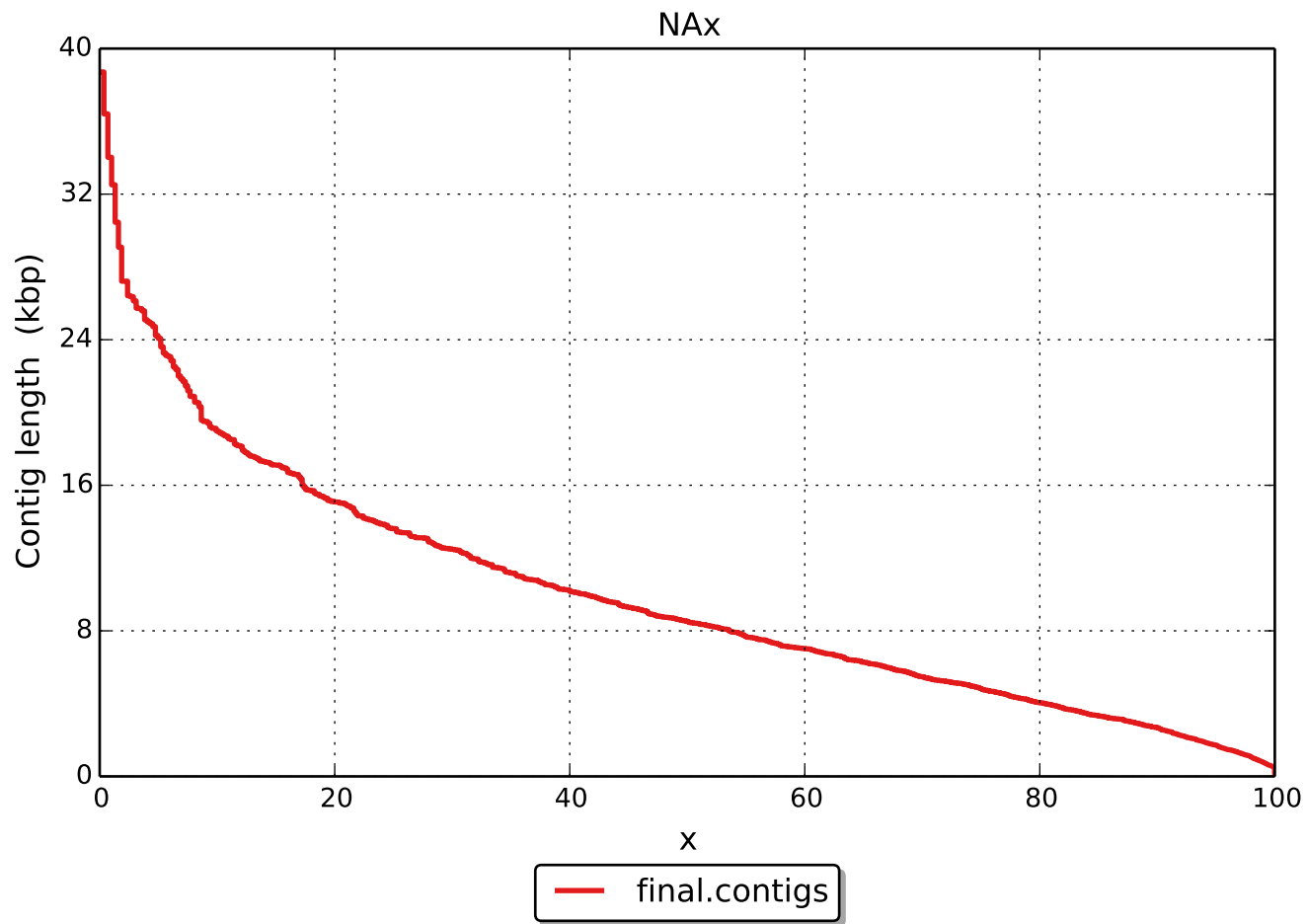




Misassemblies







NGAx

