

Report

	final.contigs
# contigs (≥ 0 bp)	1628
# contigs (≥ 1000 bp)	1351
Total length (≥ 0 bp)	5639428
Total length (≥ 1000 bp)	5429894
# contigs	1628
Largest contig	23946
Total length	5639428
Reference length	5547323
GC (%)	50.47
Reference GC (%)	50.49
N50	5187
NG50	5220
N75	2956
NG75	3103
L50	347
LG50	338
L75	703
LG75	680
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	1459
Genome fraction (%)	98.993
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	35.27
# indels per 100 kbp	0.00
Largest alignment	23946
NA50	5187
NGA50	5220
NA75	2956
NGA75	3103
LA50	347
LGA50	338
LA75	703
LGA75	680

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

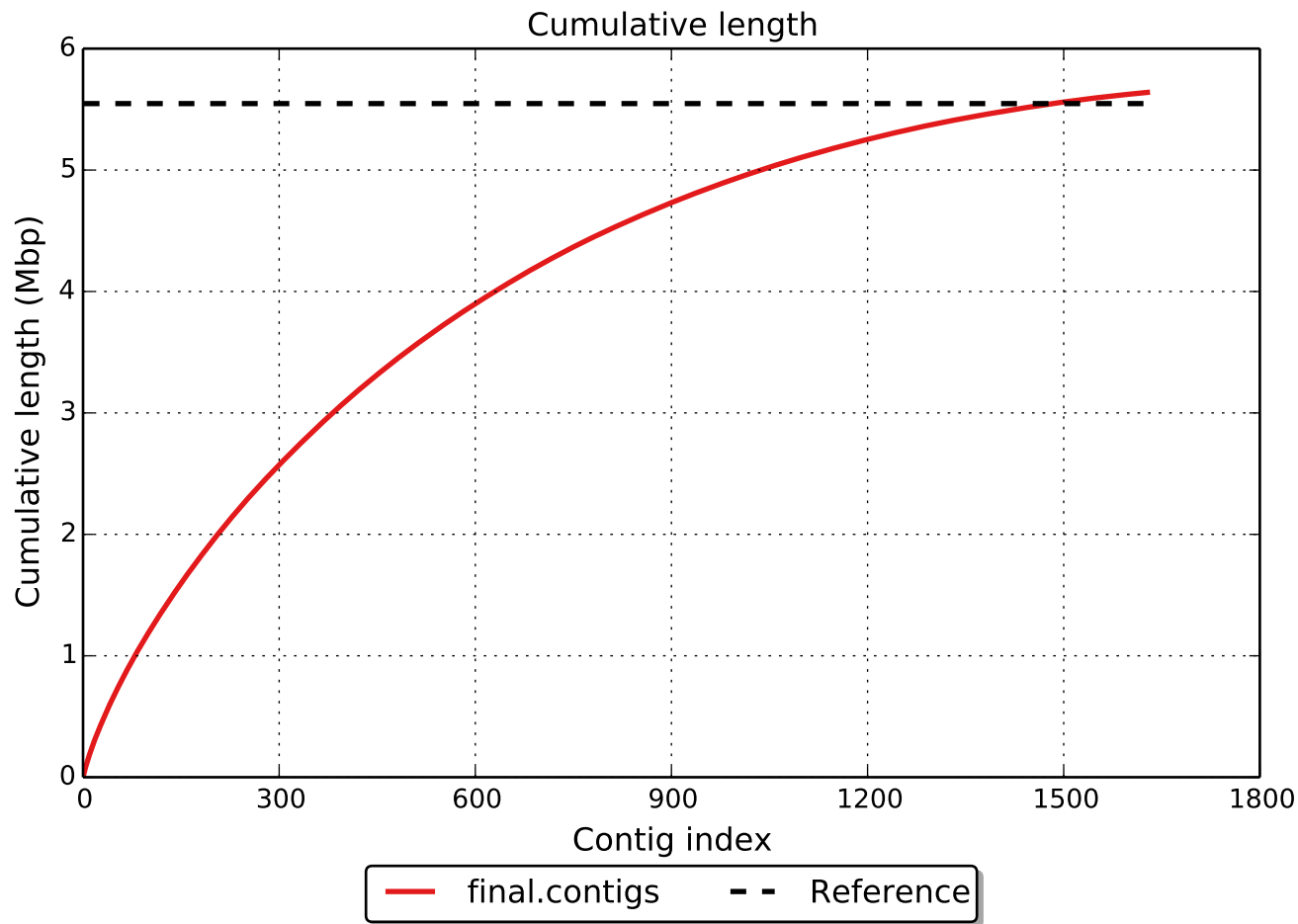
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1937
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

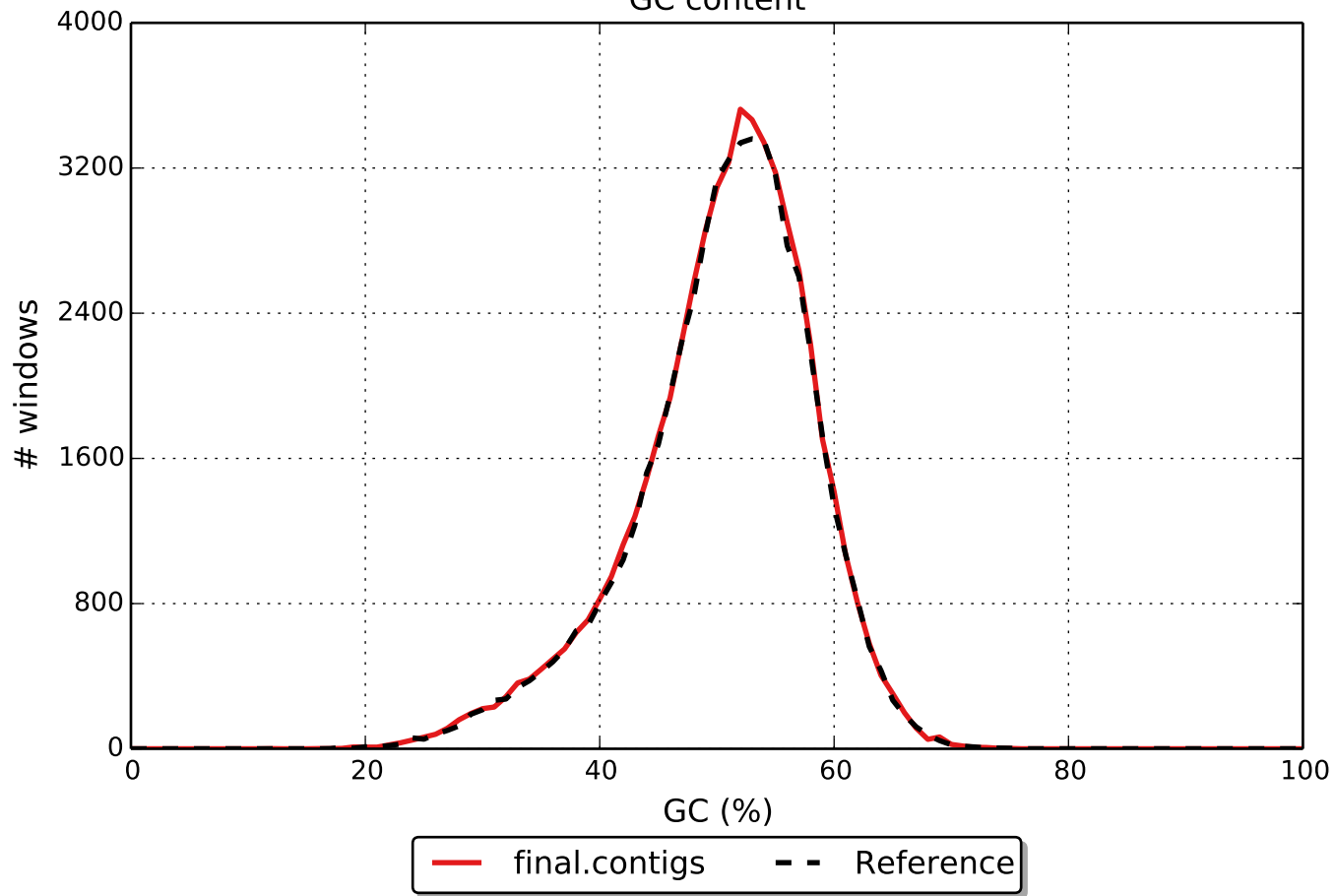
Unaligned report

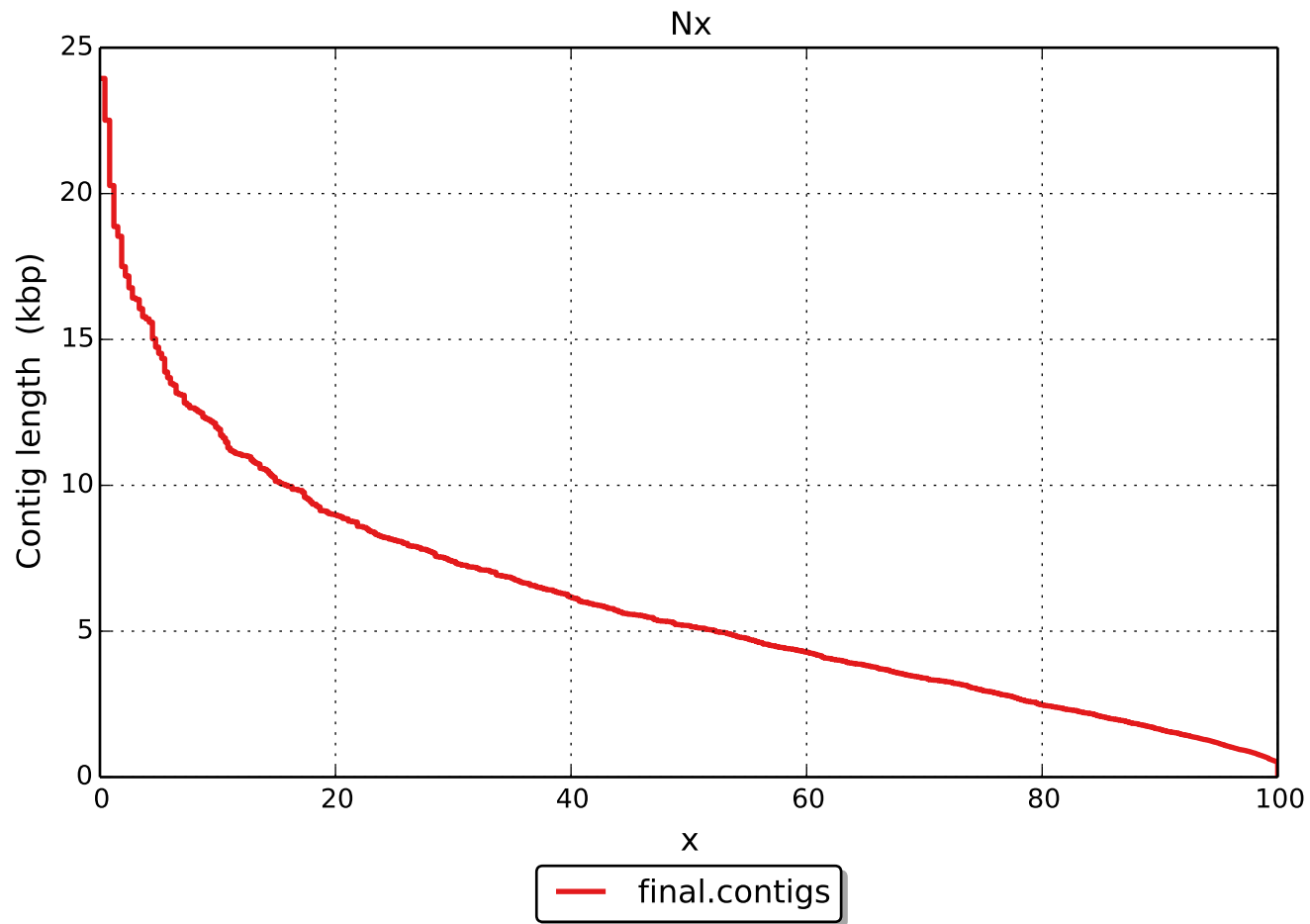
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	1
Partially unaligned length	1459
# N's	0

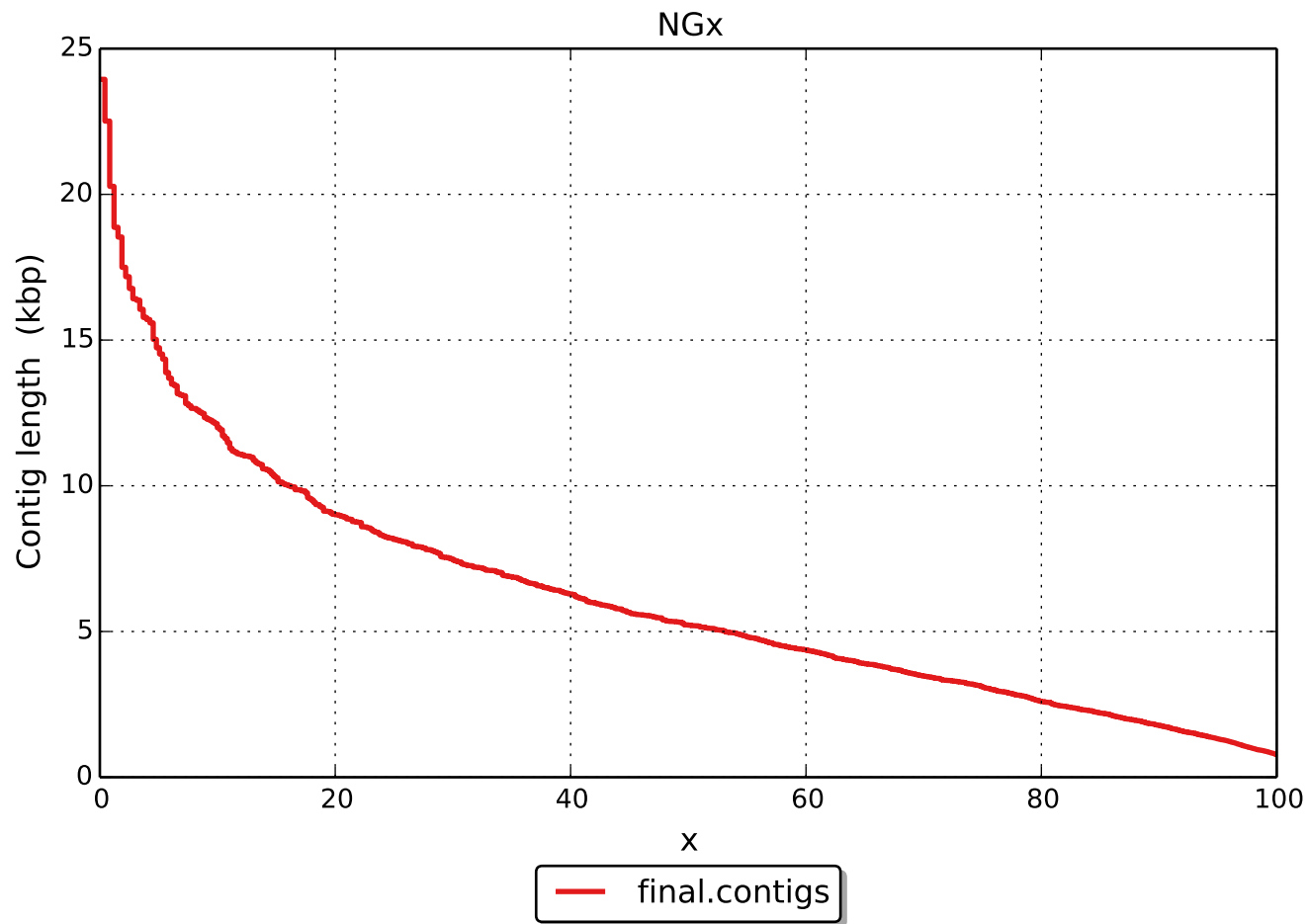
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

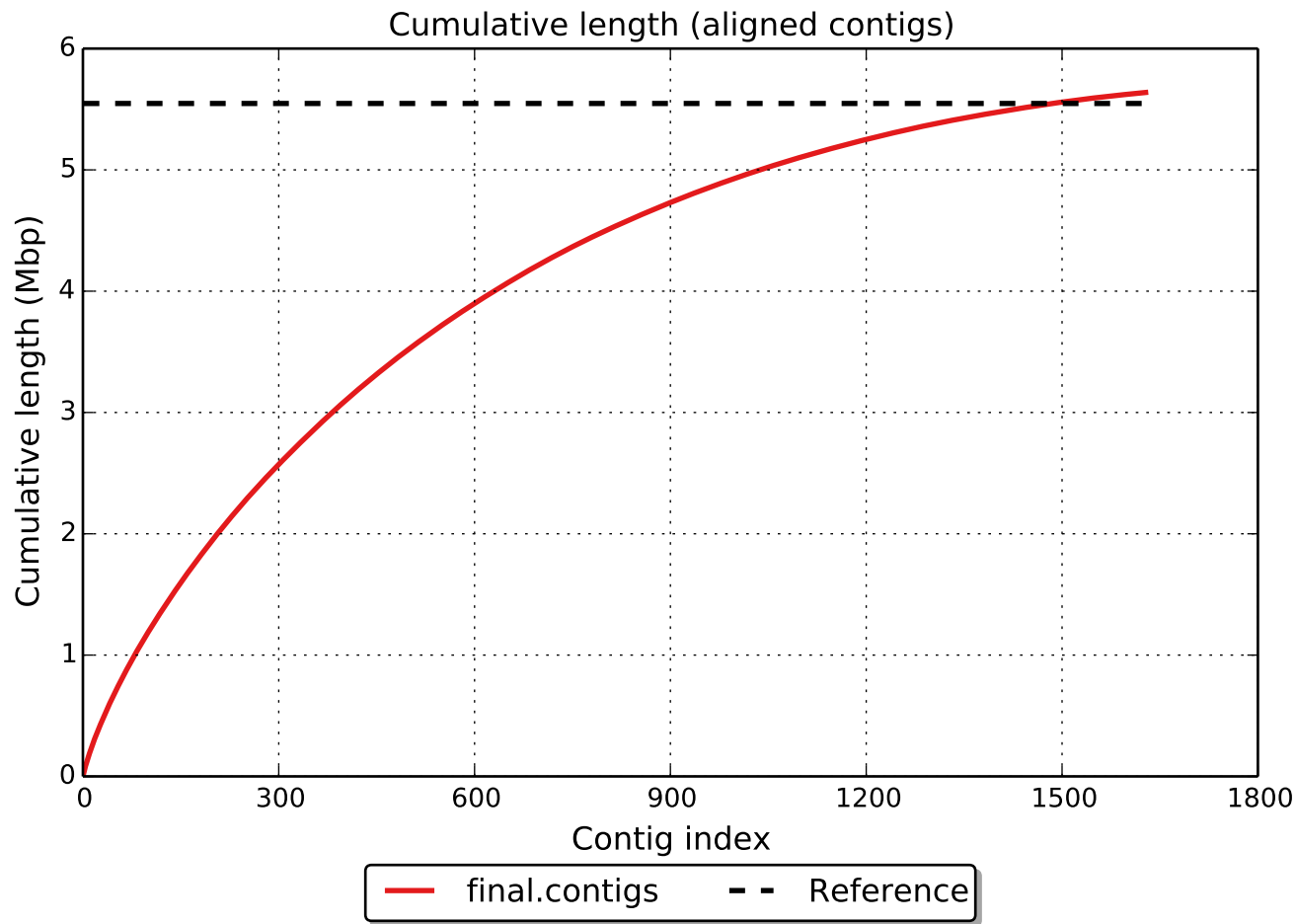


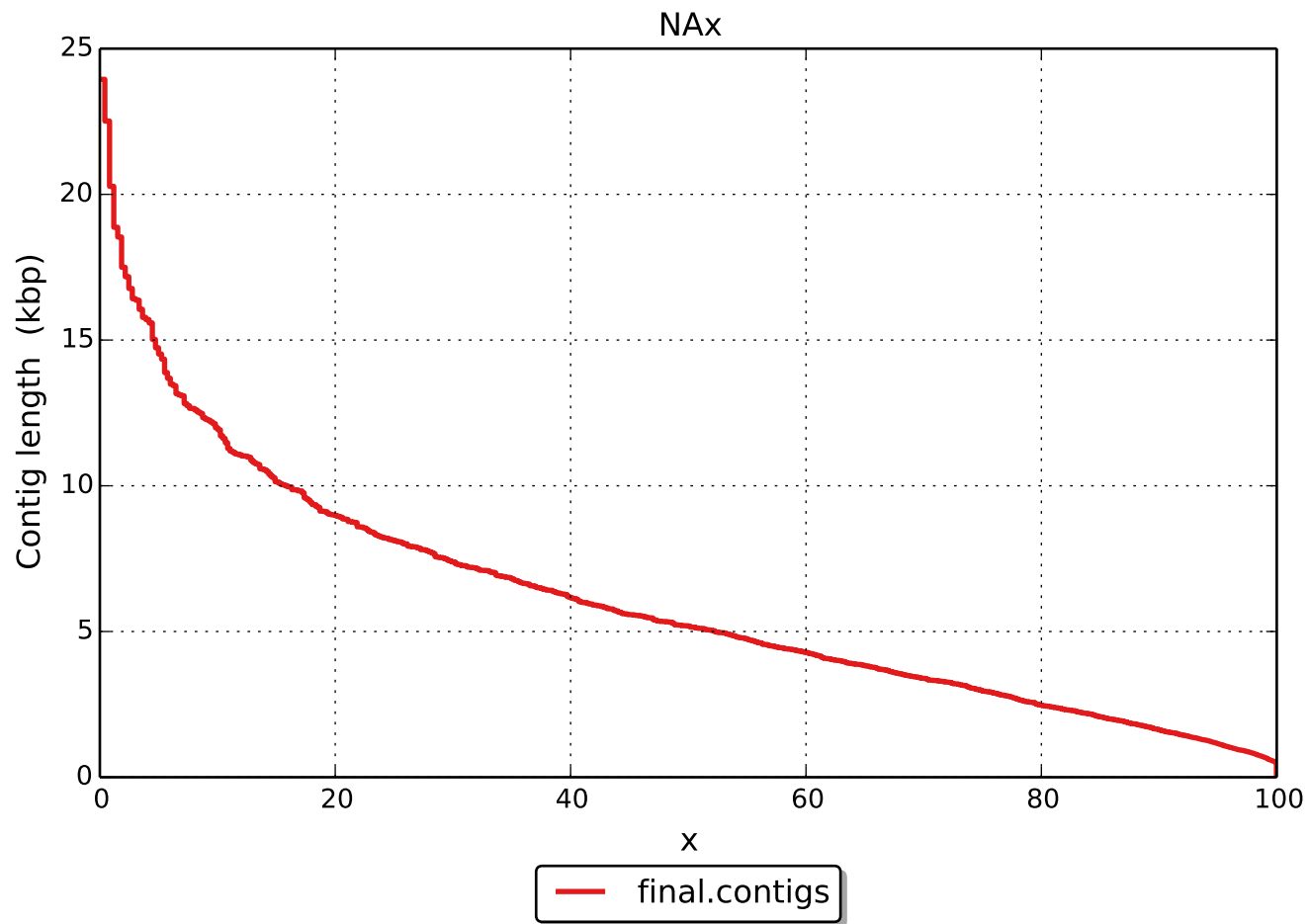




Misassemblies







NGAx

