

Report

	final.contigs
# contigs (≥ 0 bp)	3790
# contigs (≥ 1000 bp)	2026
Total length (≥ 0 bp)	4981006
Total length (≥ 1000 bp)	3695851
# contigs	3790
Largest contig	6941
Total length	4981006
Reference length	5478683
GC (%)	50.26
Reference GC (%)	50.49
N50	1541
NG50	1419
N75	985
NG75	849
L50	1055
LG50	1223
L75	2067
LG75	2475
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	86.983
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	54.10
# indels per 100 kbp	0.13
Largest alignment	6941
NA50	1541
NGA50	1419
NA75	985
NGA75	849
LA50	1055
LGA50	1223
LA75	2067
LGA75	2475

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

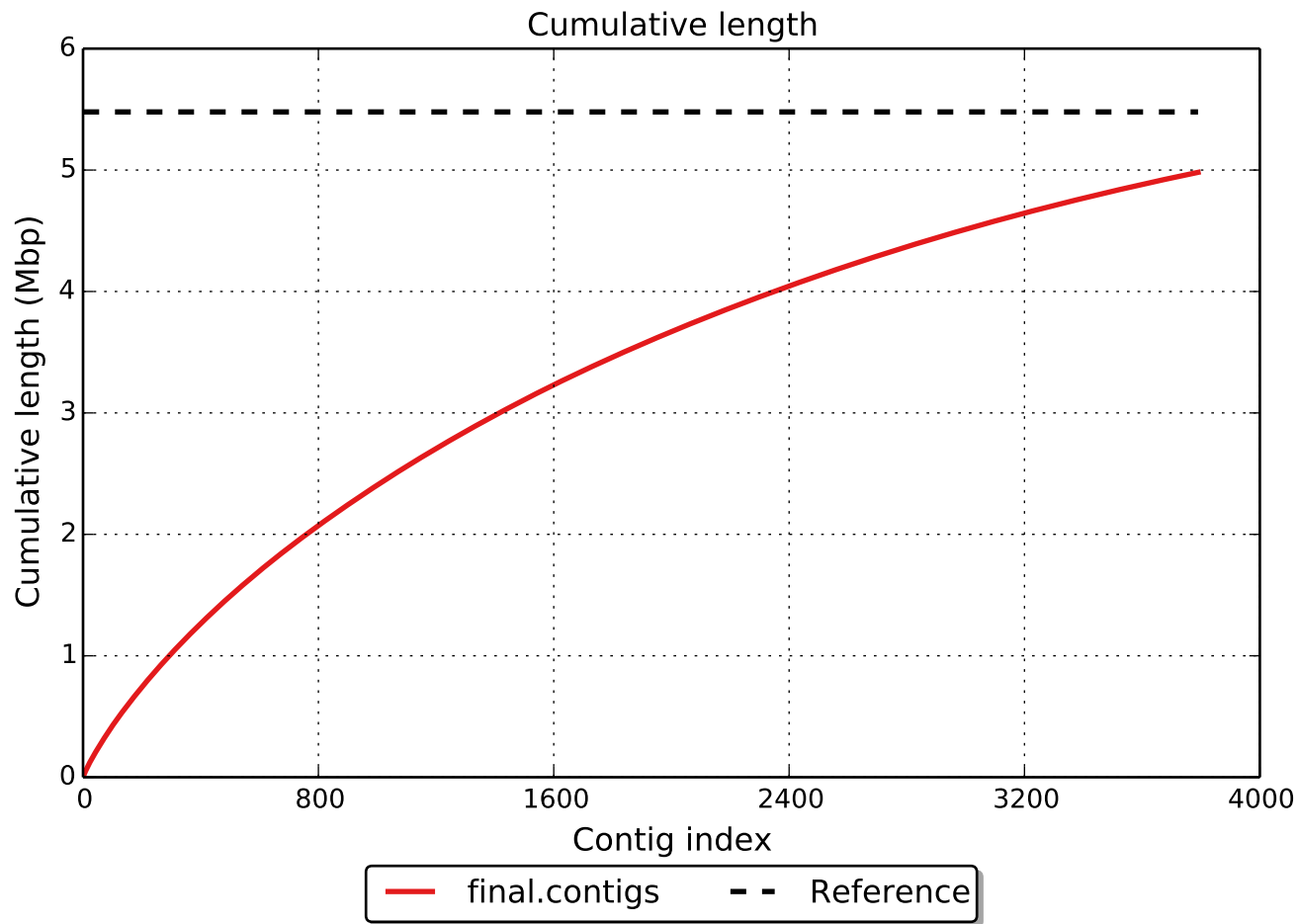
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	2578
# indels	6
# short indels	5
# long indels	1
Indels length	13

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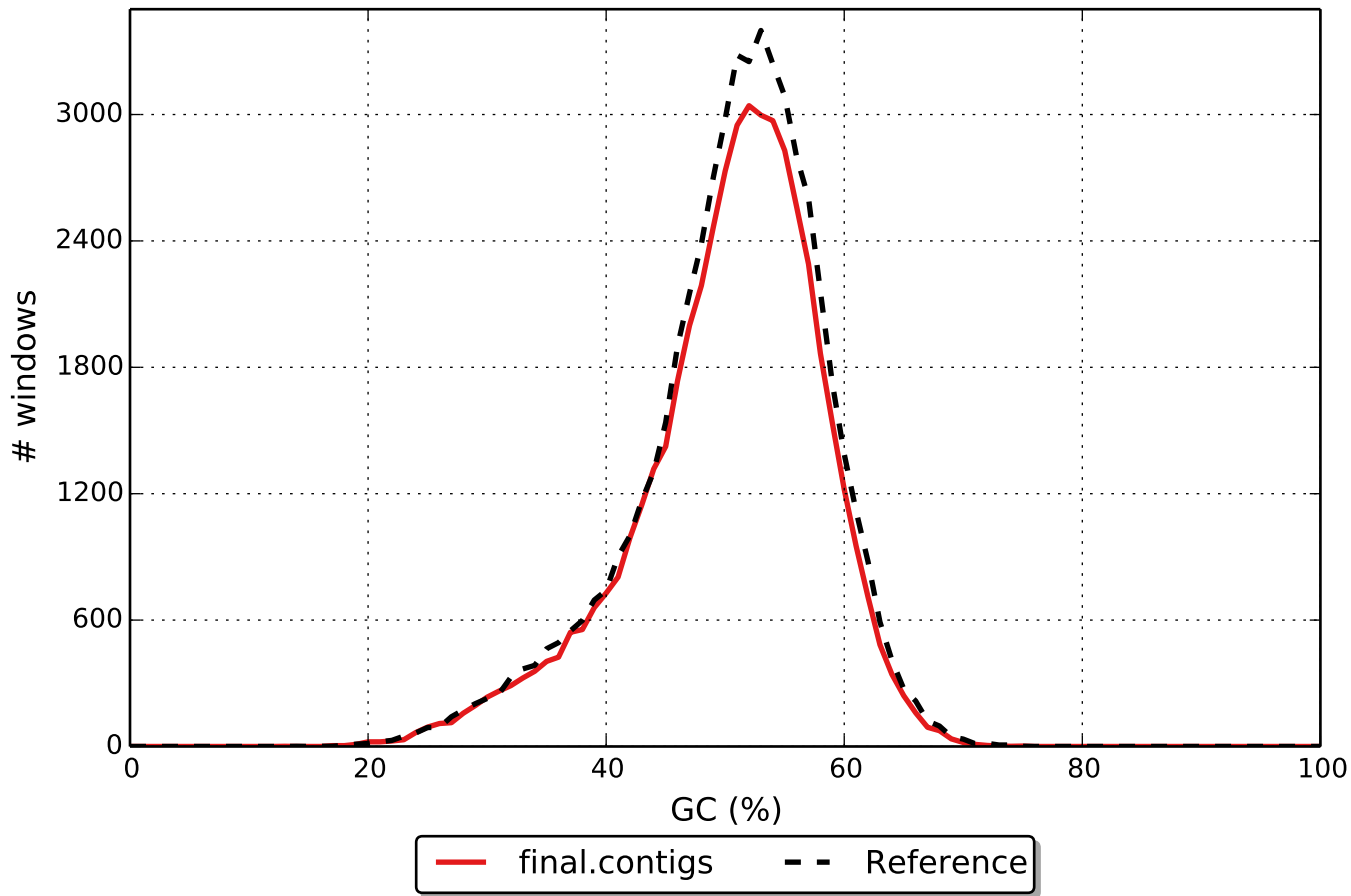
Unaligned report

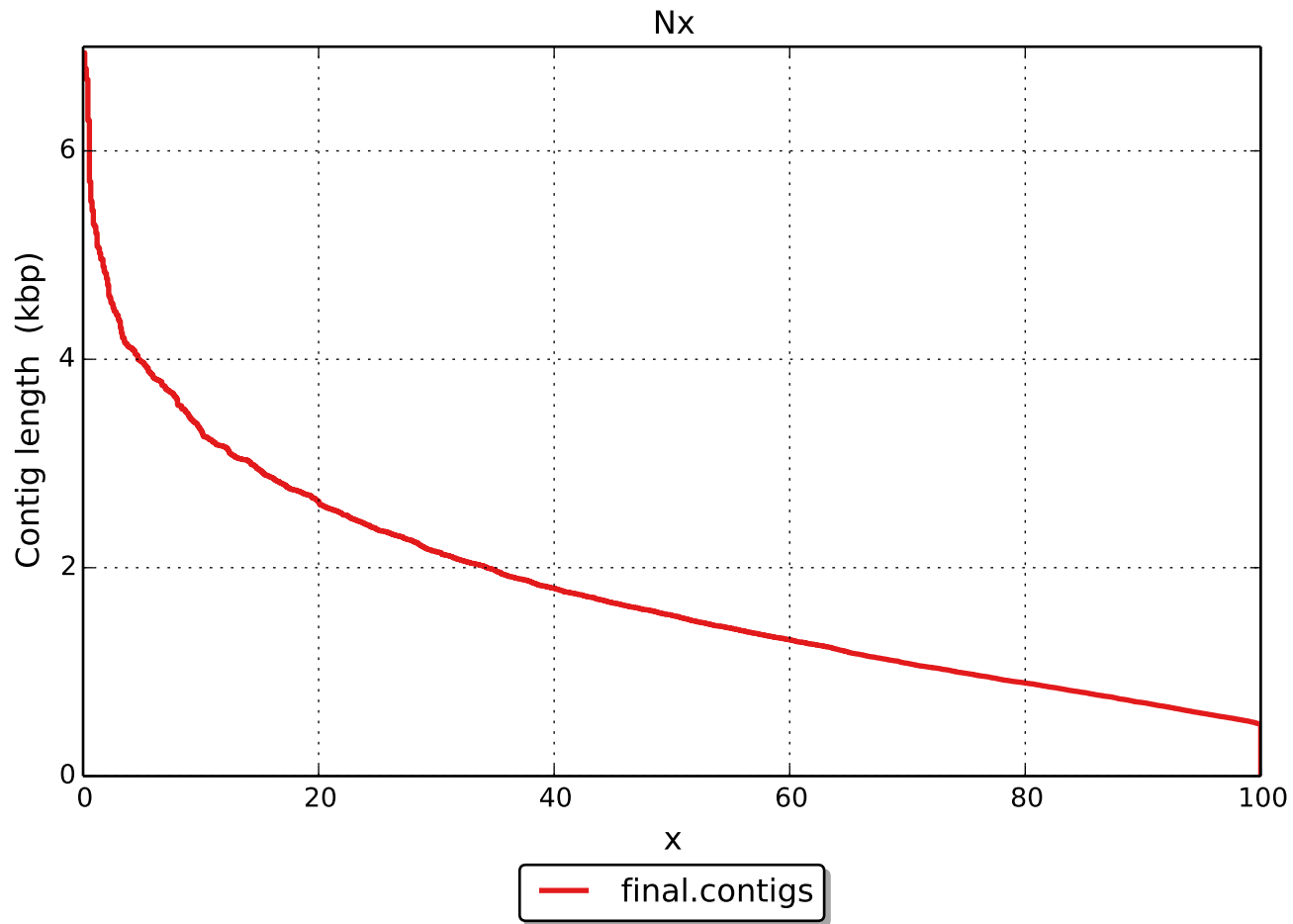
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

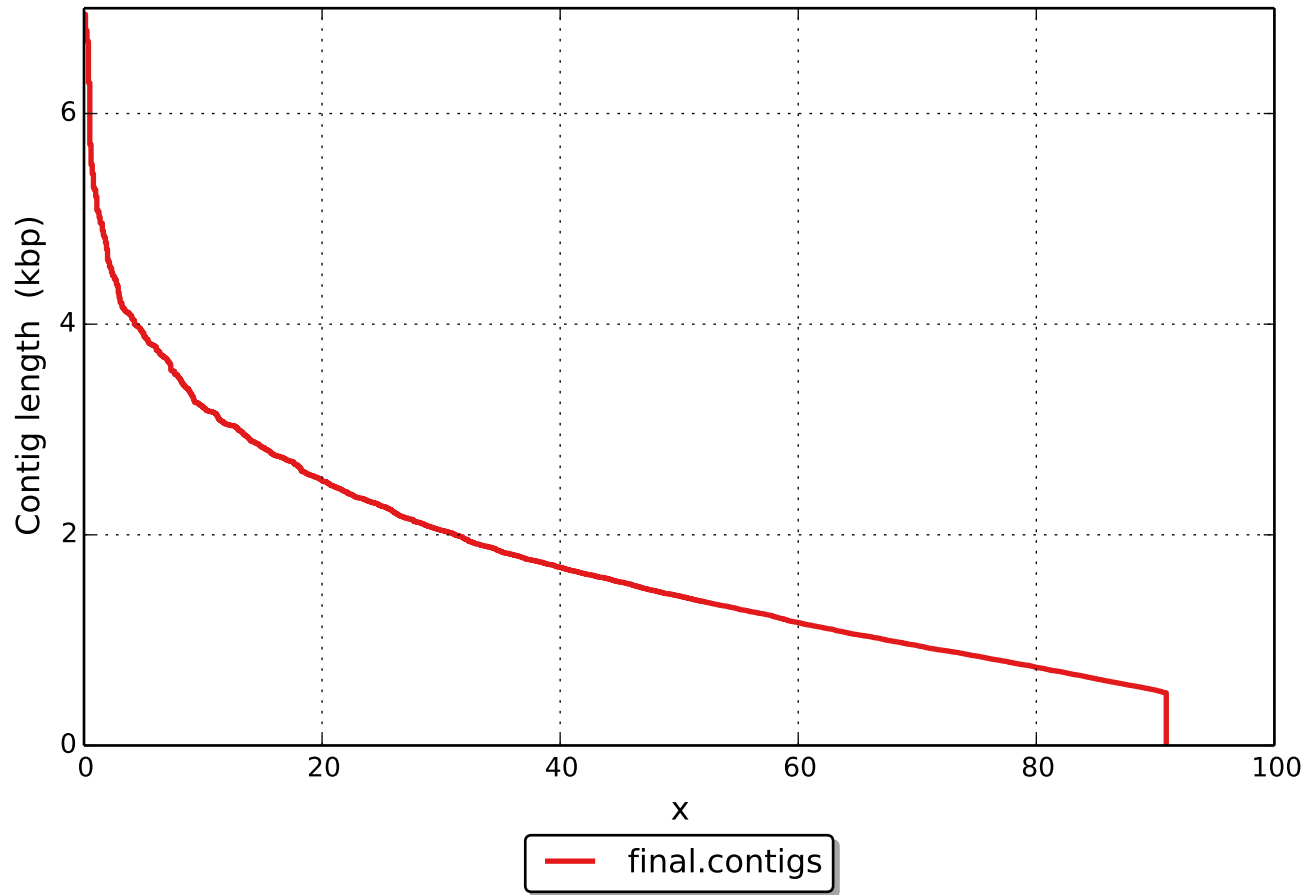


GC content



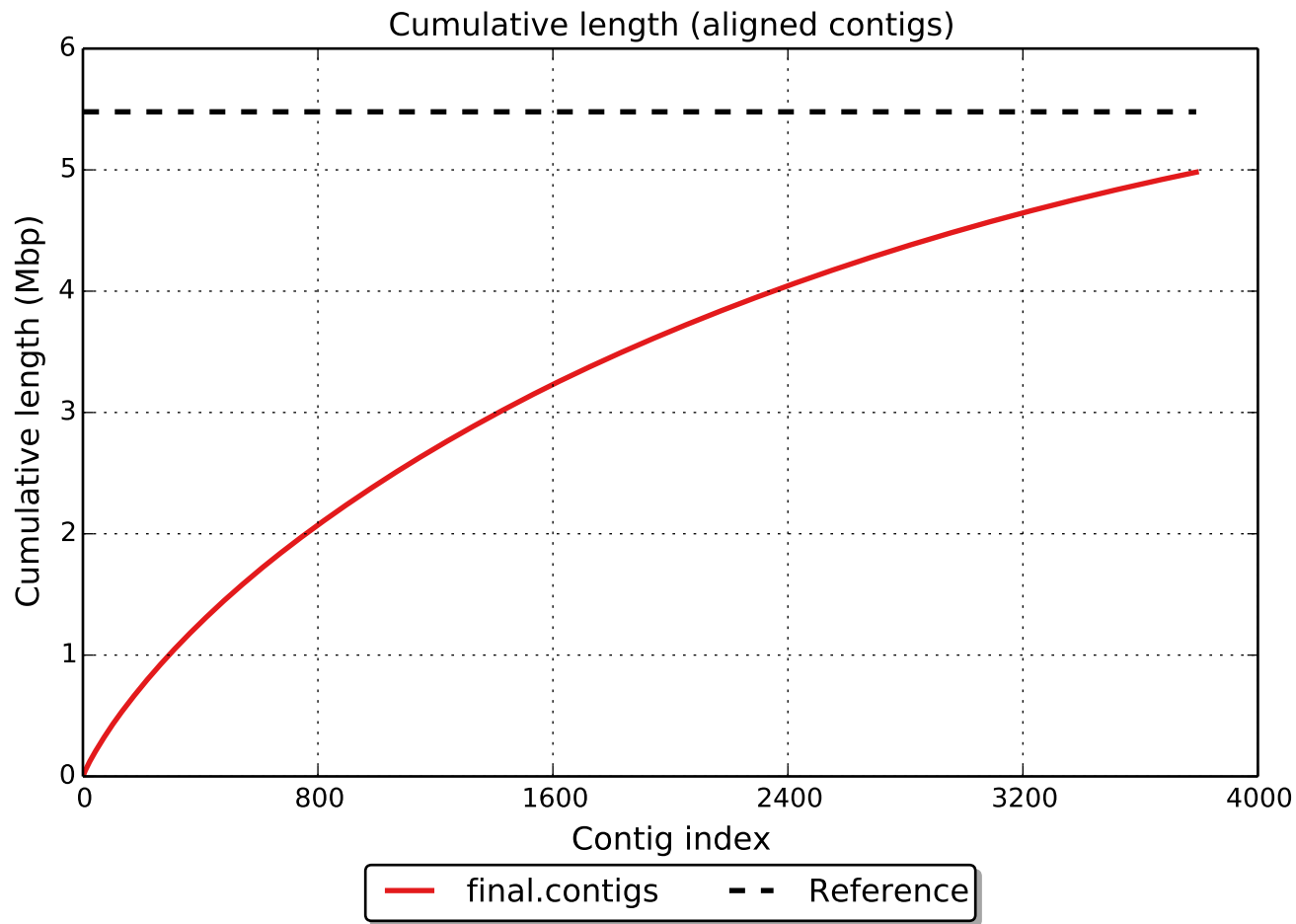


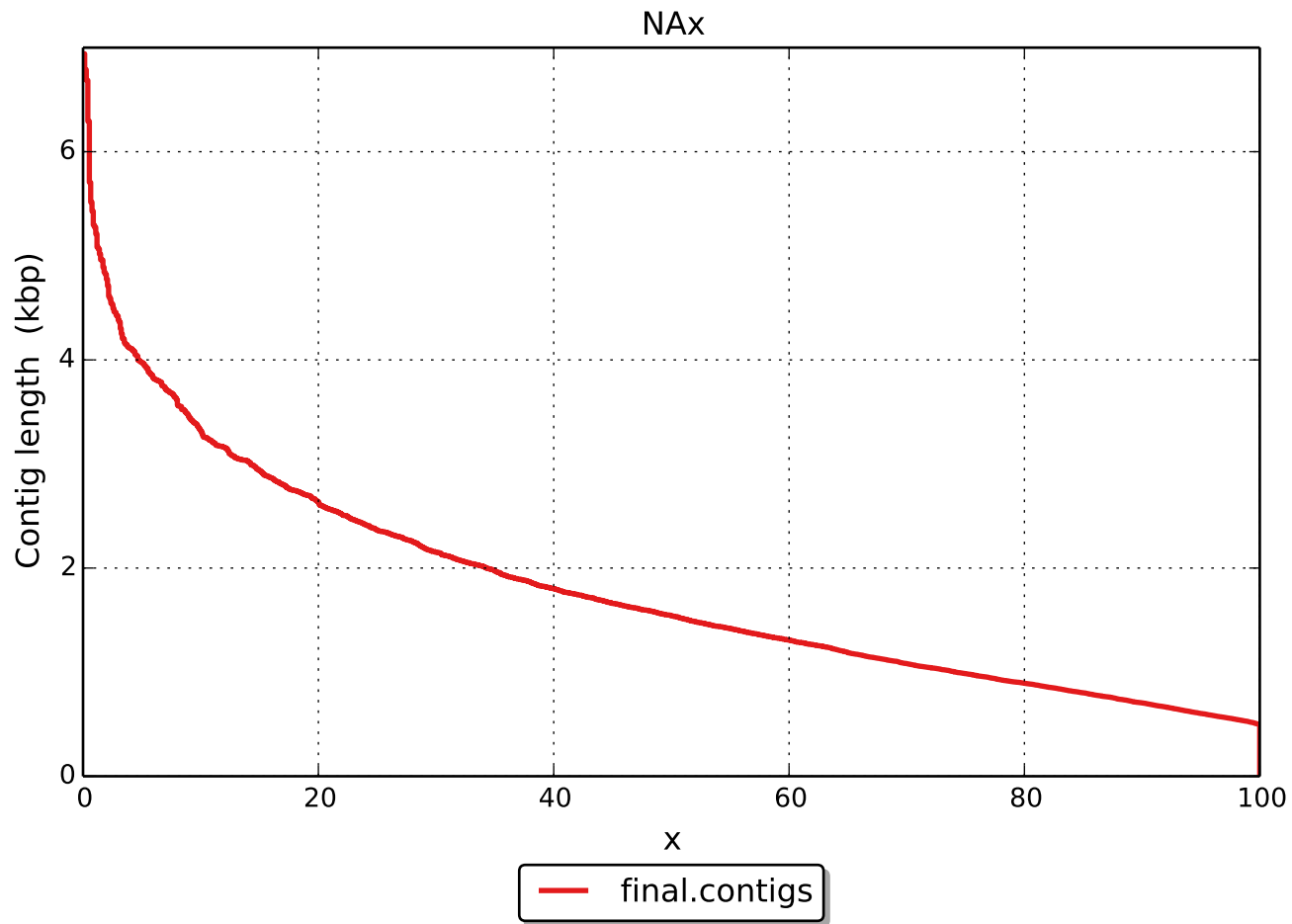
NGx



Misassemblies







NGAx

