

Report

	final.contigs
# contigs (>= 0 bp)	1232
# contigs (>= 1000 bp)	879
Total length (>= 0 bp)	3784812
Total length (>= 1000 bp)	3595334
# contigs	1058
Largest contig	21305
Total length	3728635
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.25
N50	5431
NG50	5372
N75	3048
NG75	2955
L50	213
LG50	218
L75	442
LG75	456
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.416
Duplication ratio	1.022
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.69
# indels per 100 kbp	0.08
Largest alignment	21305
NA50	5431
NGA50	5372
NA75	3048
NGA75	2955
LA50	213
LGA50	218
LA75	442
LGA75	456

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

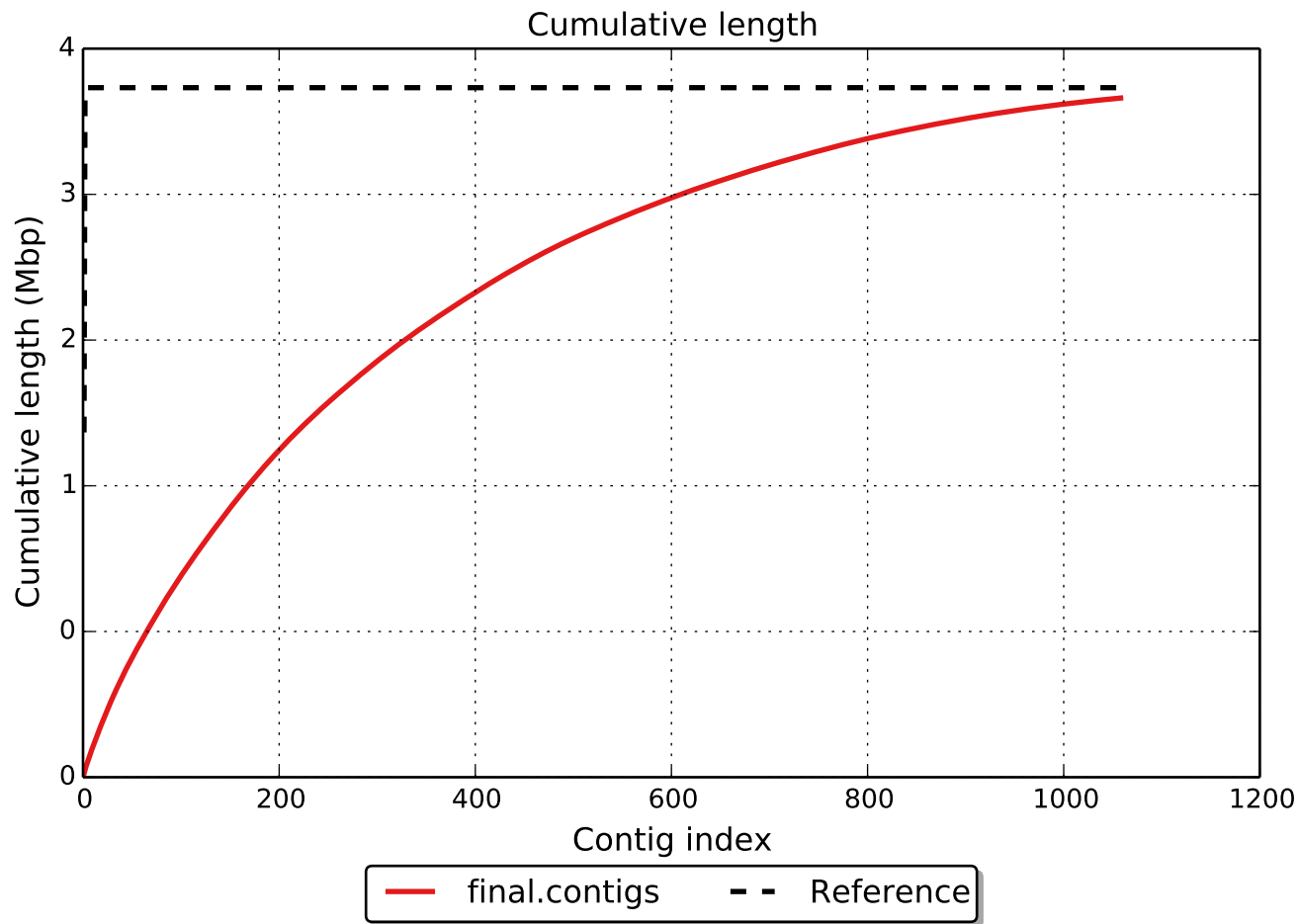
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	974
# indels	3
# short indels	2
# long indels	1
Indels length	26

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).

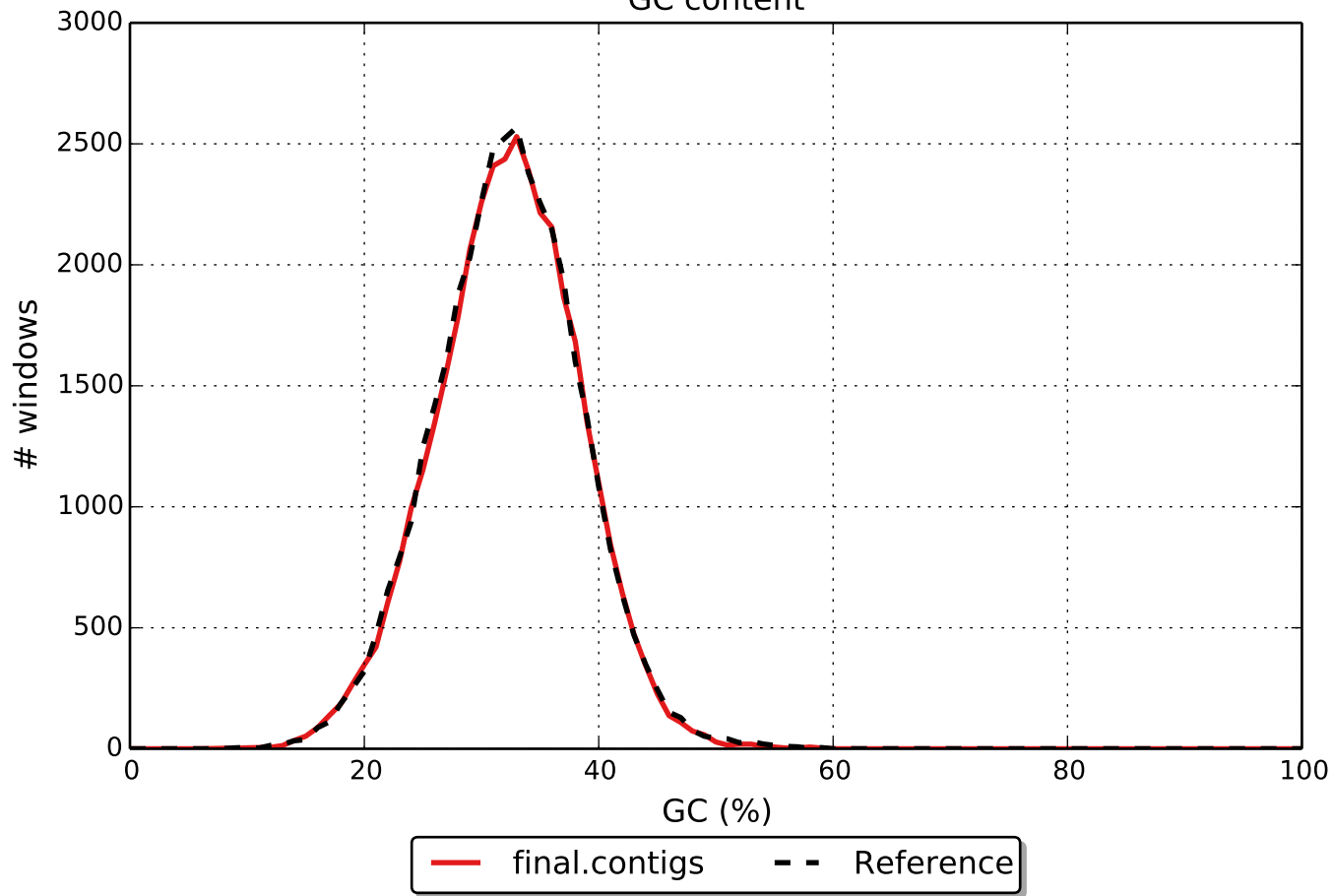
Unaligned report

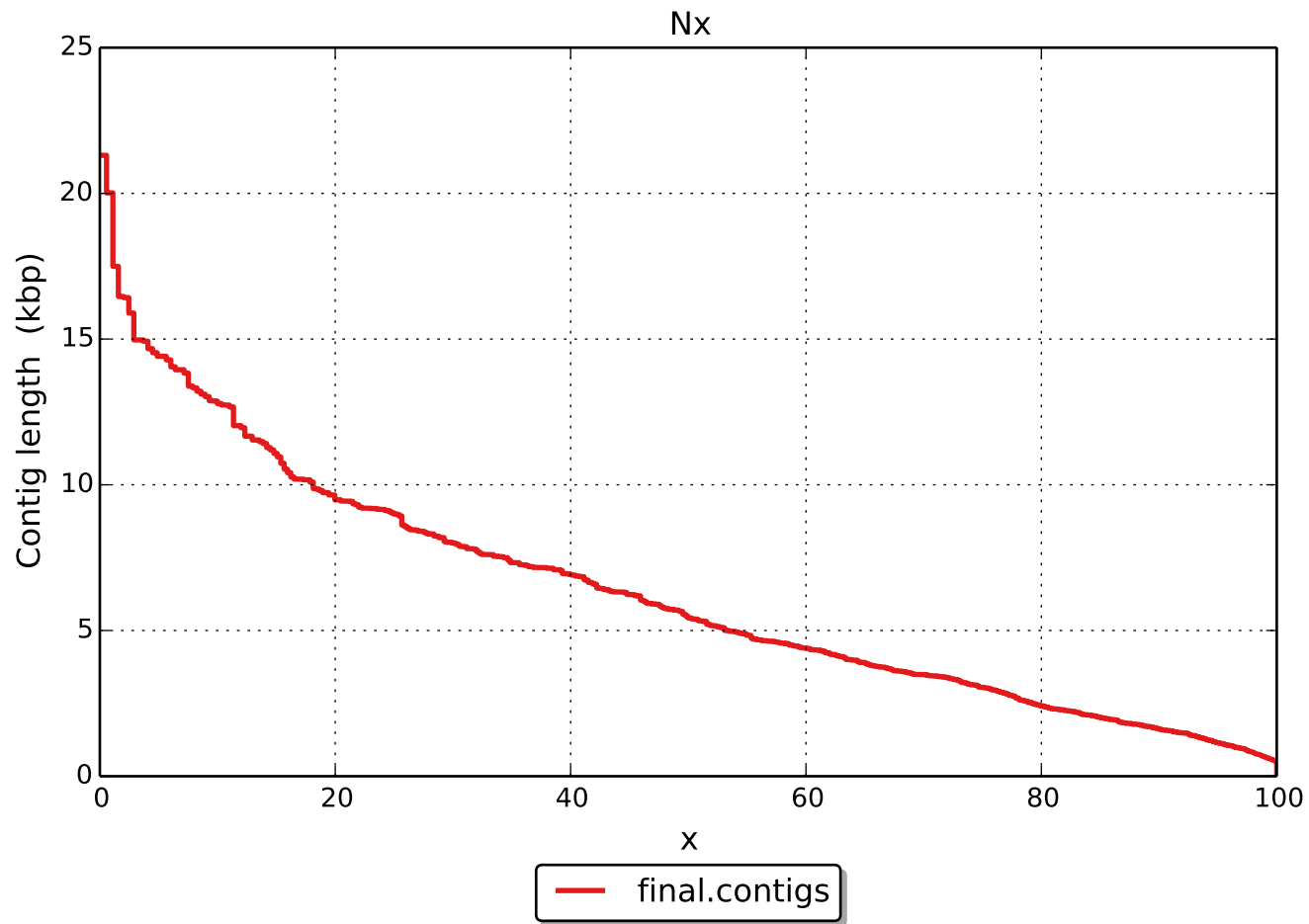
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

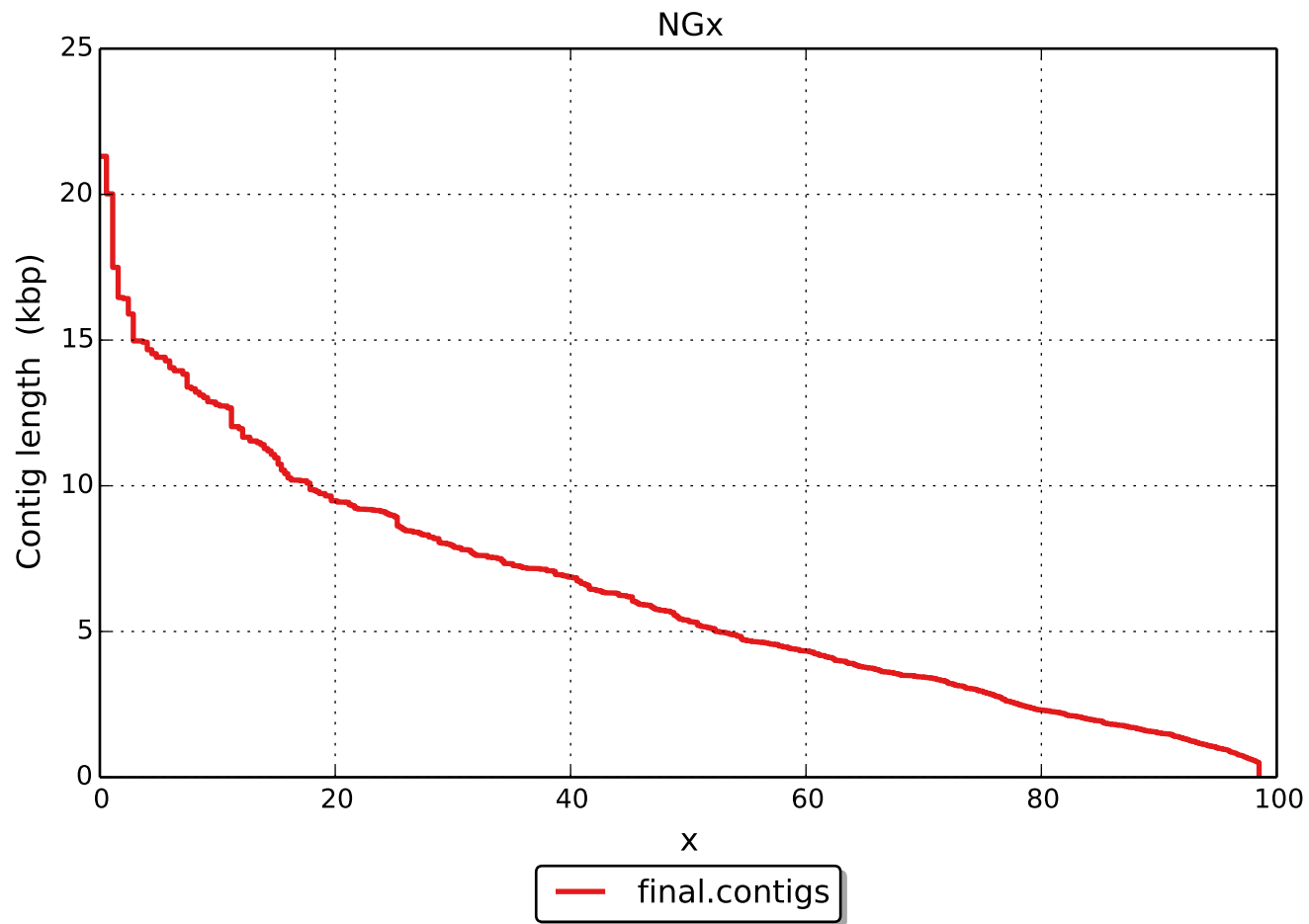
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

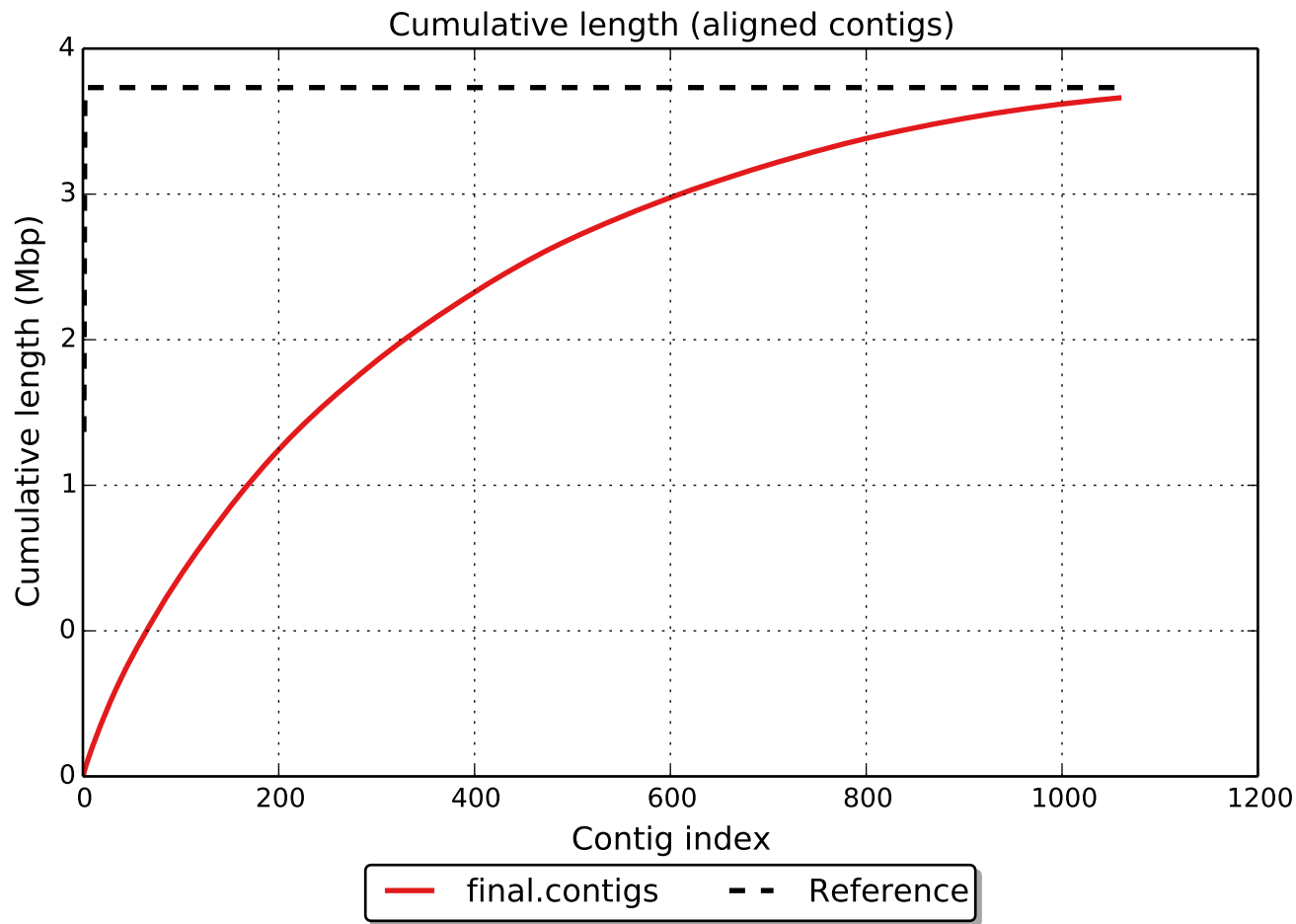


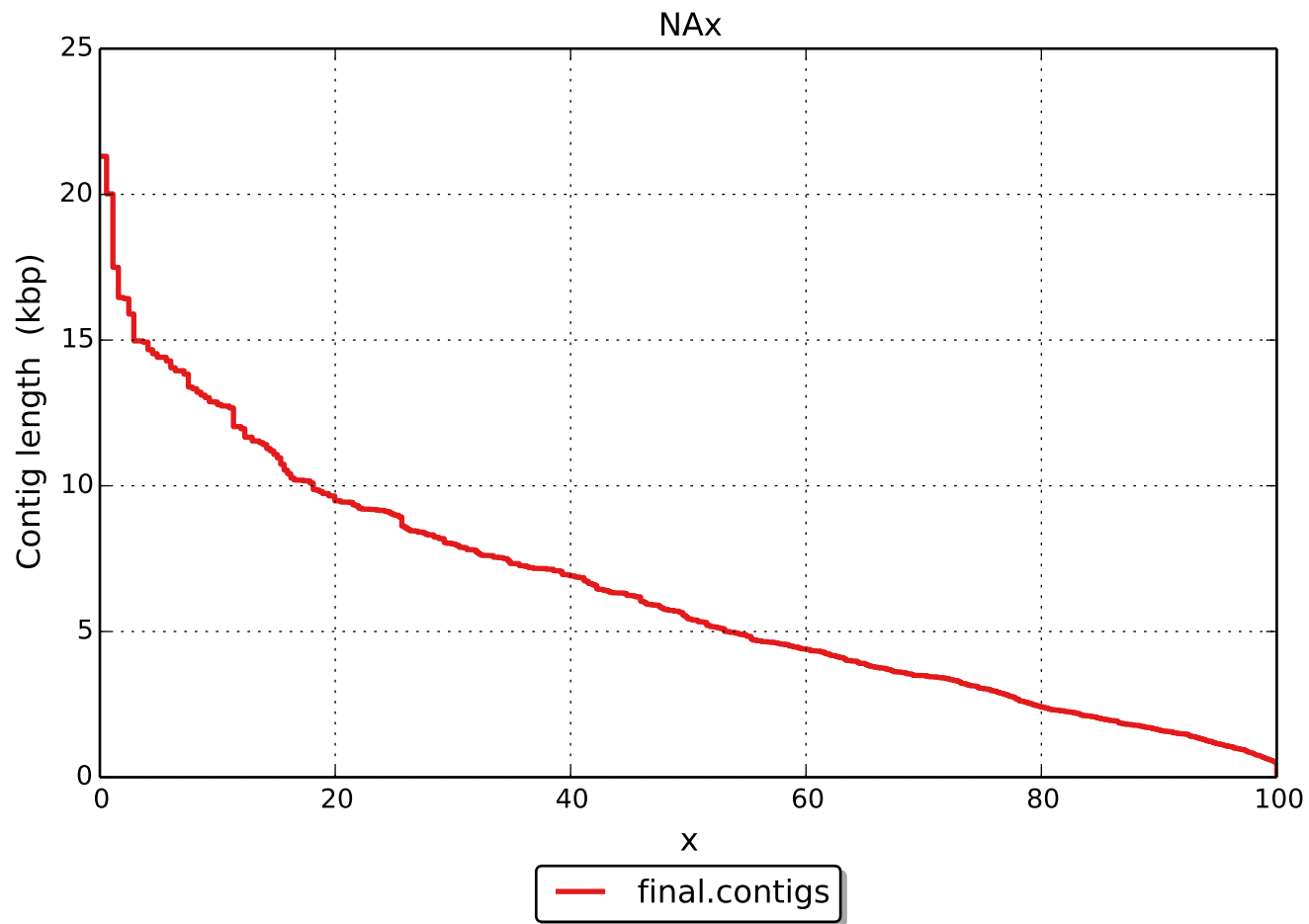




Misassemblies







NGAx

