

## Report

	final.contigs
# contigs (>= 0 bp)	1344
# contigs (>= 1000 bp)	1096
Total length (>= 0 bp)	5255672
Total length (>= 1000 bp)	5078771
# contigs	1344
Largest contig	25863
Total length	5255672
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	6359
NG50	6068
N75	3426
NG75	3001
L50	253
LG50	276
L75	540
LG75	608
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	6203
# local misassemblies	4
# unaligned contigs	0 + 2 part
Unaligned length	13809
Genome fraction (%)	92.553
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.89
# indels per 100 kbp	0.45
Largest alignment	25863
NA50	6339
NGA50	6058
NA75	3405
NGA75	2982
LA50	255
LGA50	278
LA75	544
LGA75	613

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

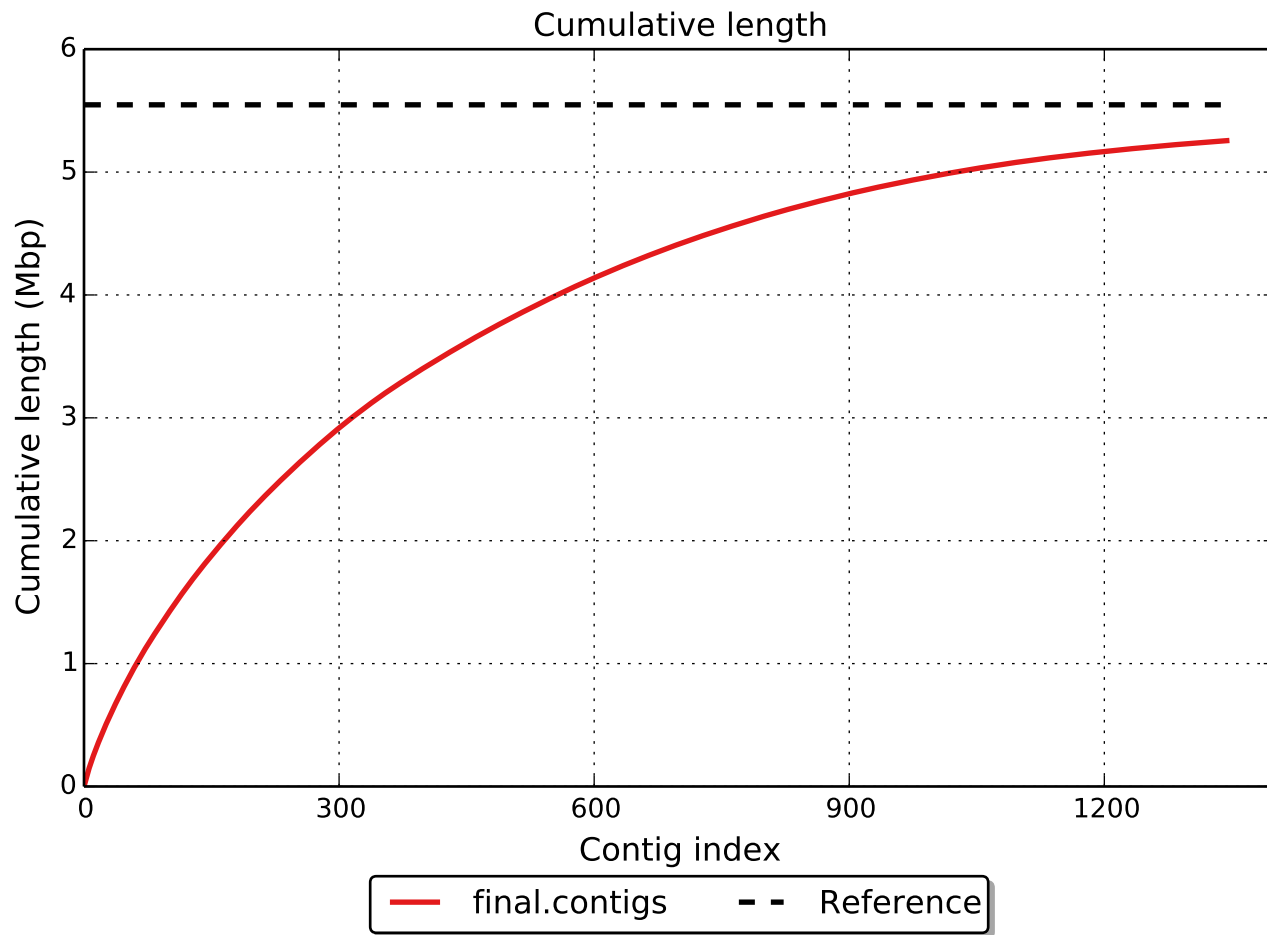
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	6203
# local misassemblies	4
# mismatches	1740
# indels	23
# short indels	19
# long indels	4
Indels length	144

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

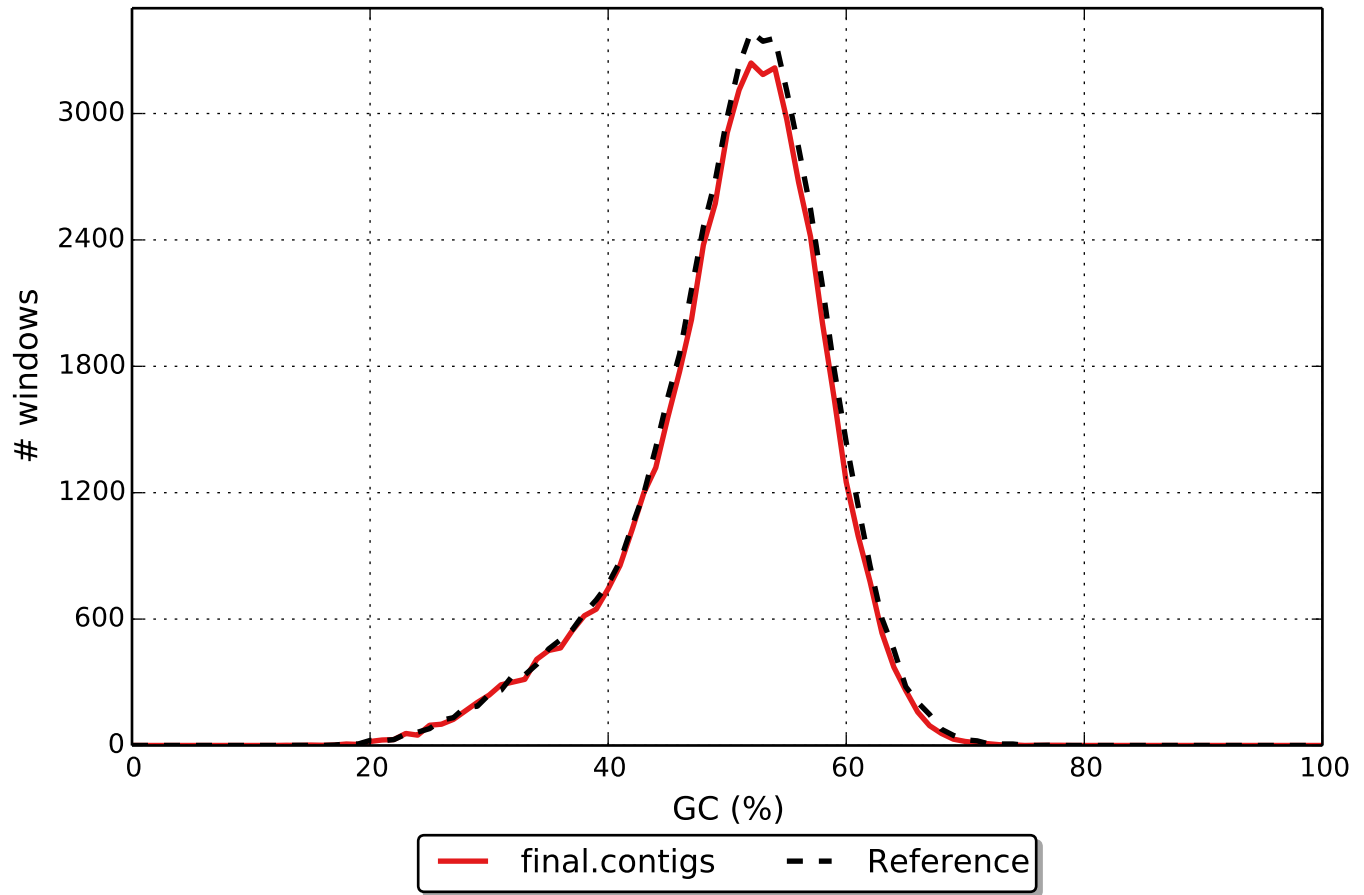
## Unaligned report

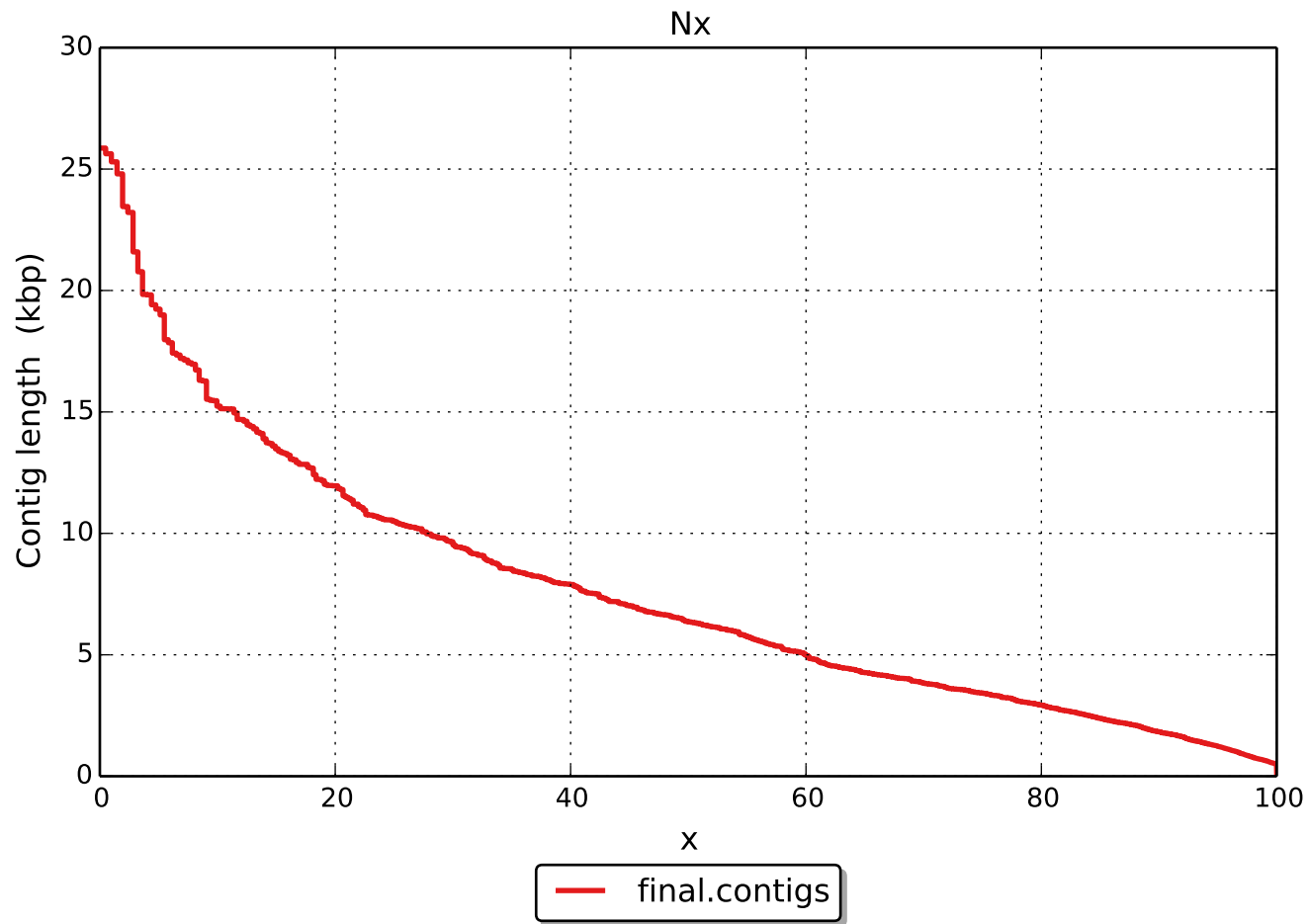
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	13809
# N's	0

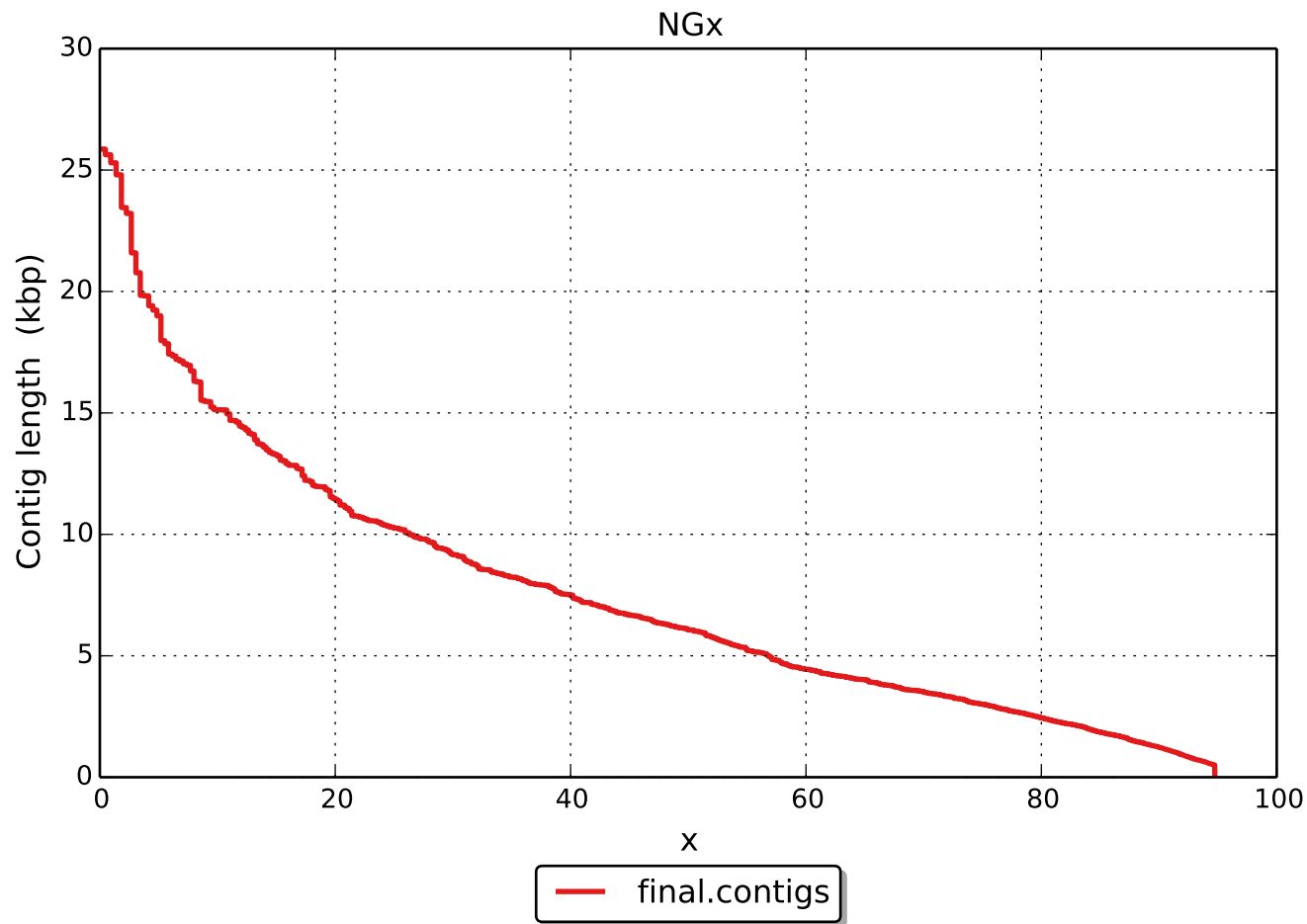
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



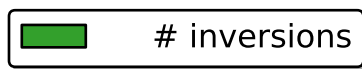
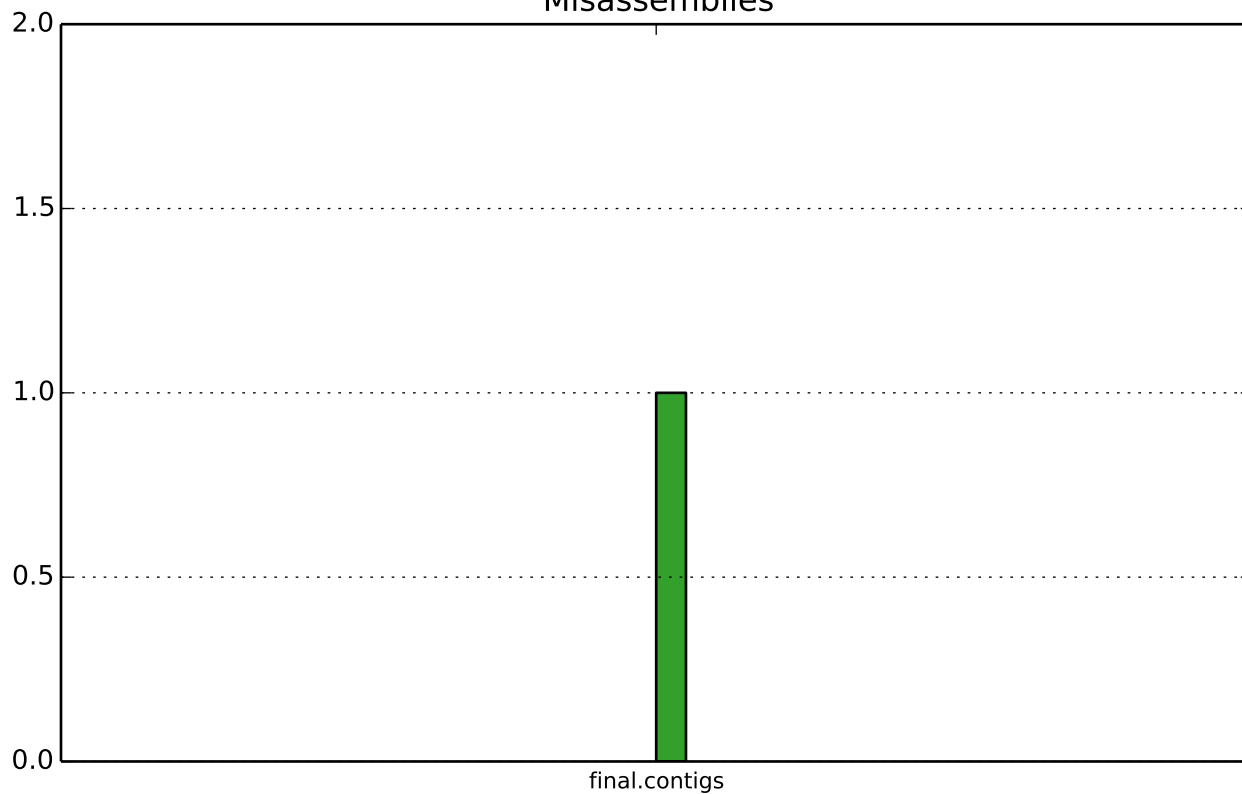
GC content



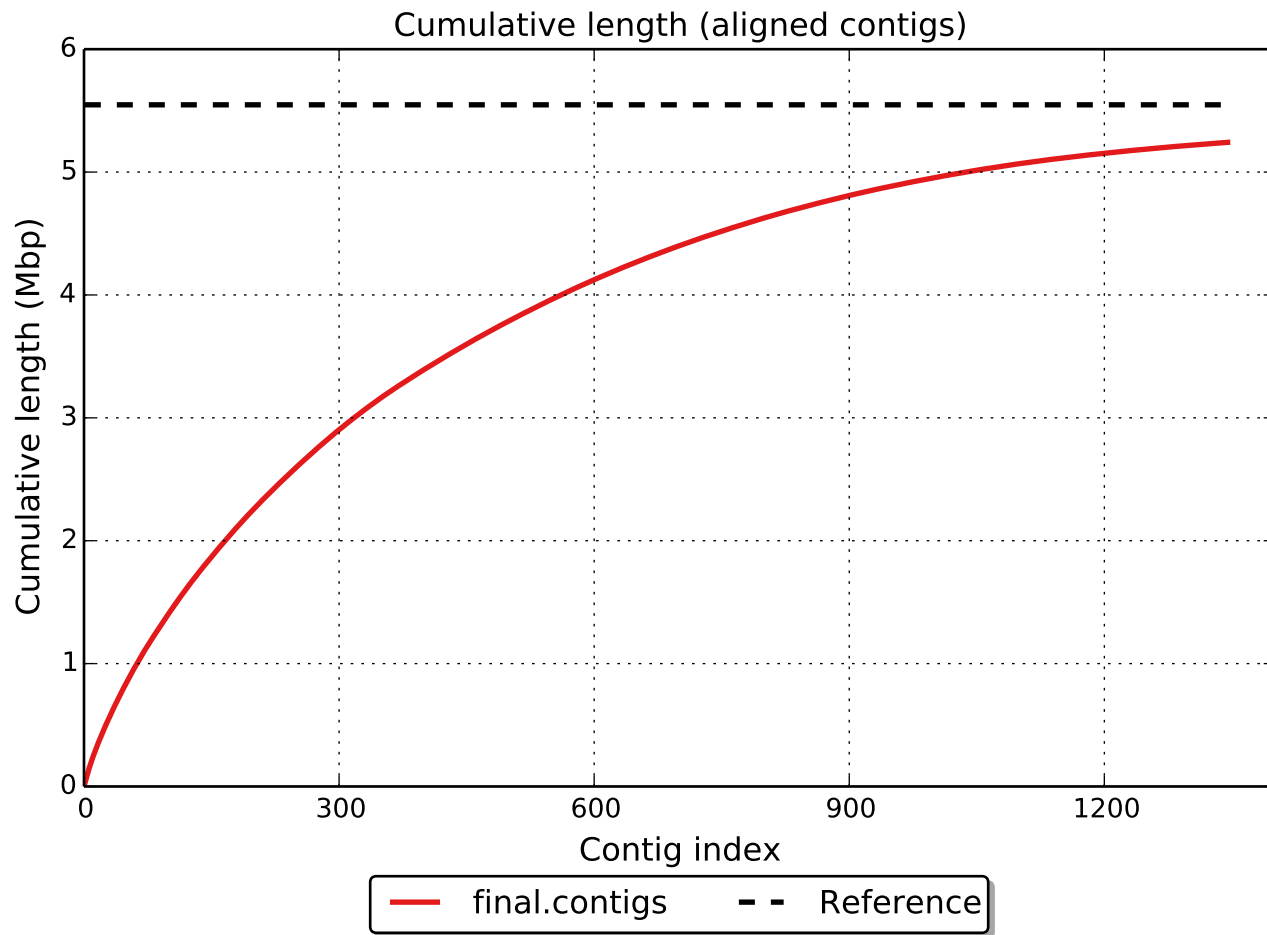


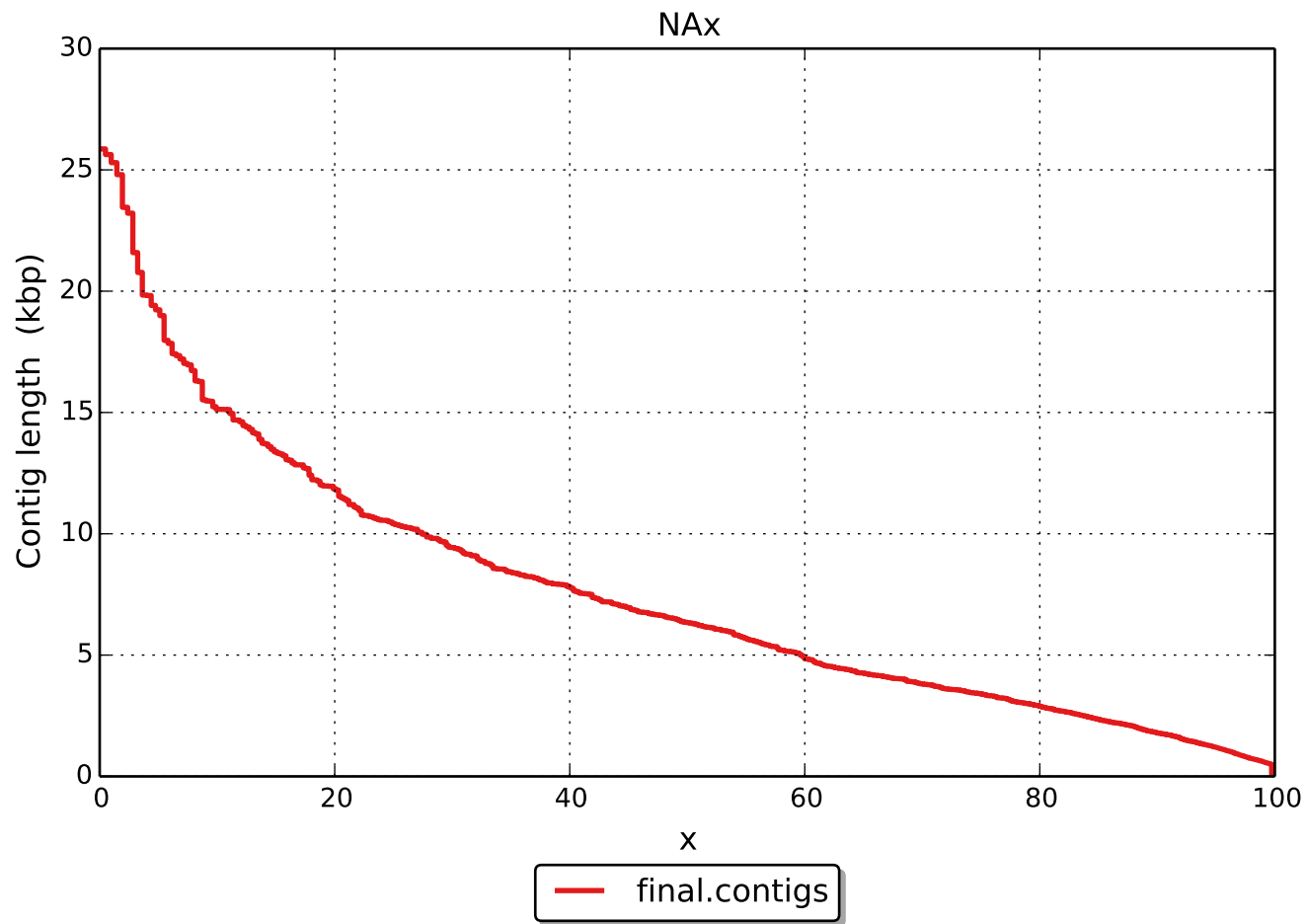


# Misassemblies









NGAx

