

Report

	final.contigs
# contigs (>= 1000 bp)	558
# contigs (>= 5000 bp)	305
# contigs (>= 10000 bp)	166
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	4557313
Total length (>= 5000 bp)	3876277
Total length (>= 10000 bp)	2886212
Total length (>= 25000 bp)	646507
Total length (>= 50000 bp)	54626
# contigs	599
Largest contig	54626
Total length	4587033
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	12933
NG50	12541
N75	6998
NG75	6856
L50	113
LG50	116
L75	233
LG75	239
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	51334
# local misassemblies	14
# unaligned contigs	0 + 2 part
Unaligned length	447
Genome fraction (℥)	97.896
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	147.56
# indels per 100 kbp	9.79
Largest alignment	54626
NA50	12897
NGA50	12541
NA75	6981
NGA75	6829
LA50	114
LGA50	116
LA75	234
LGA75	240

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

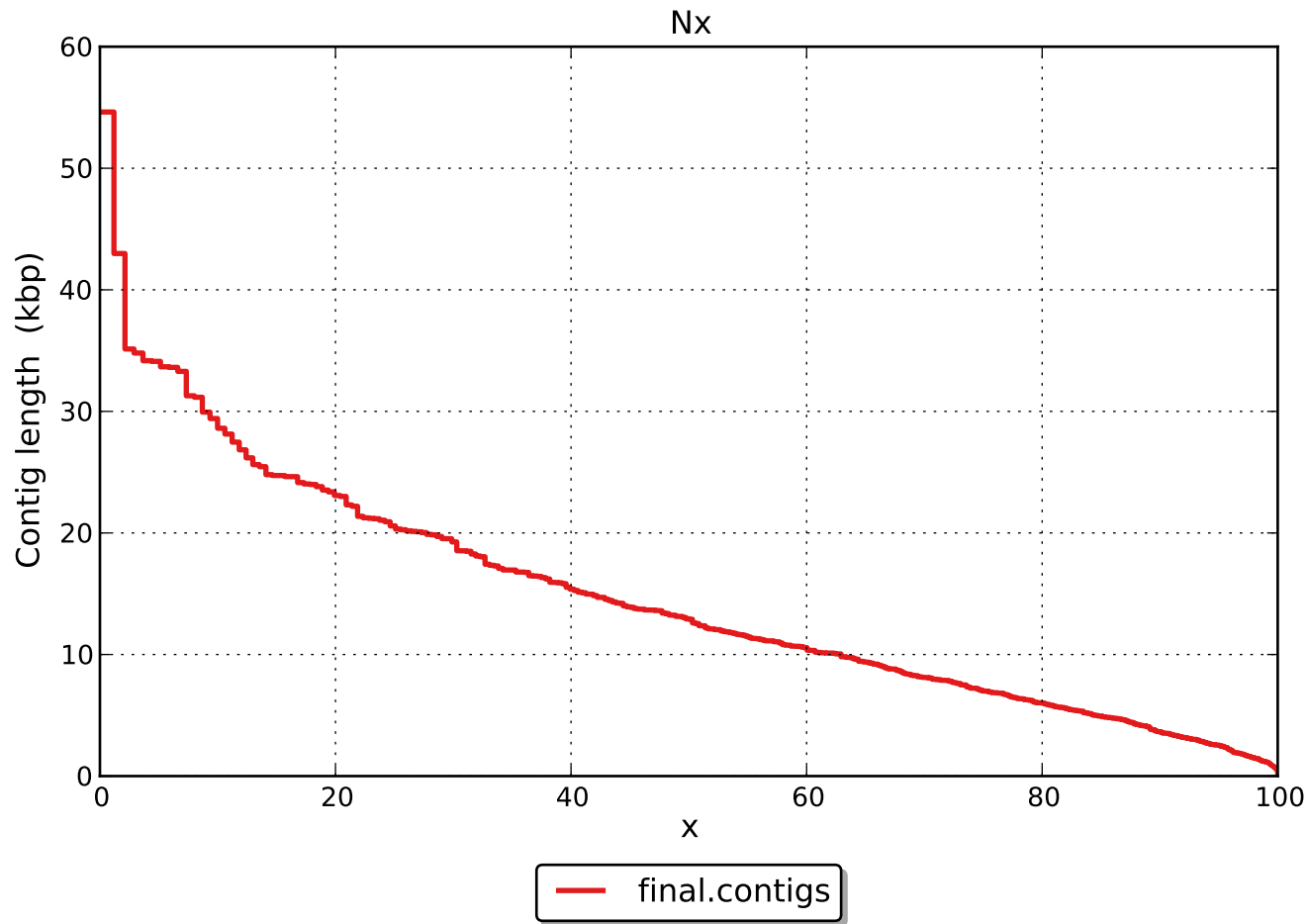
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	51334
# local misassemblies	14
# mismatches	6705
# indels	445
# short indels	443
# long indels	2
Indels length	696

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).

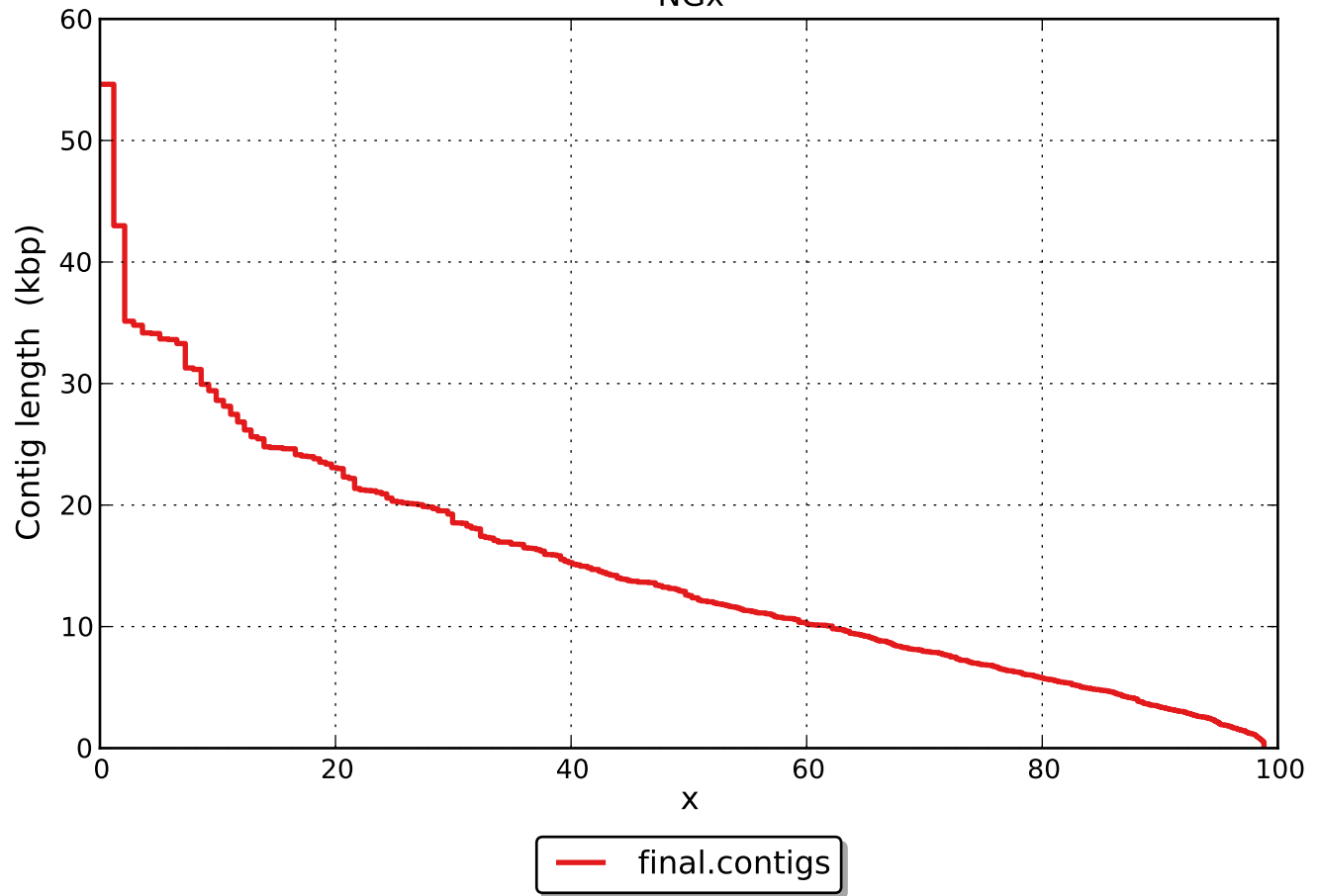
Unaligned report

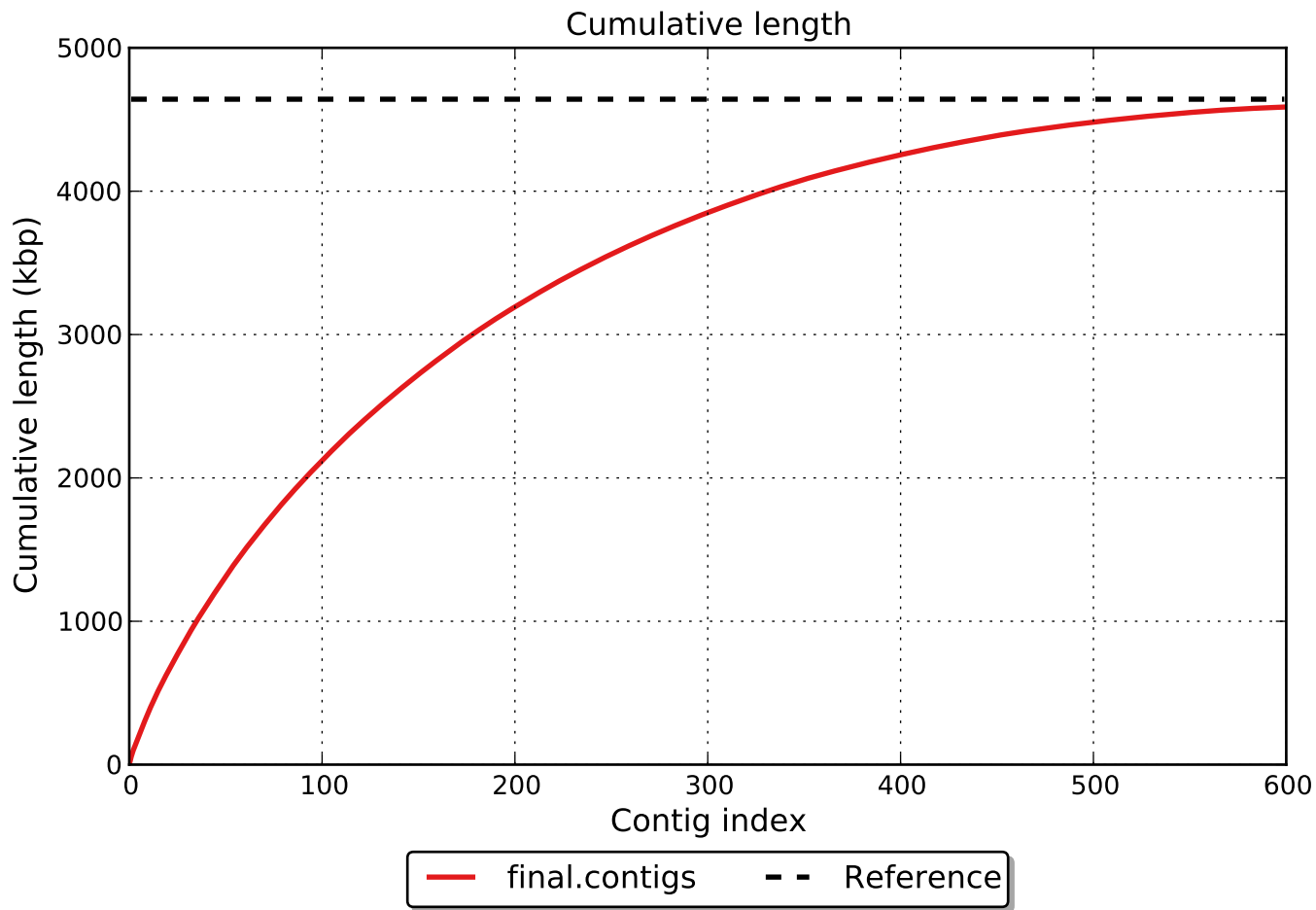
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	447
# N's	0

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).

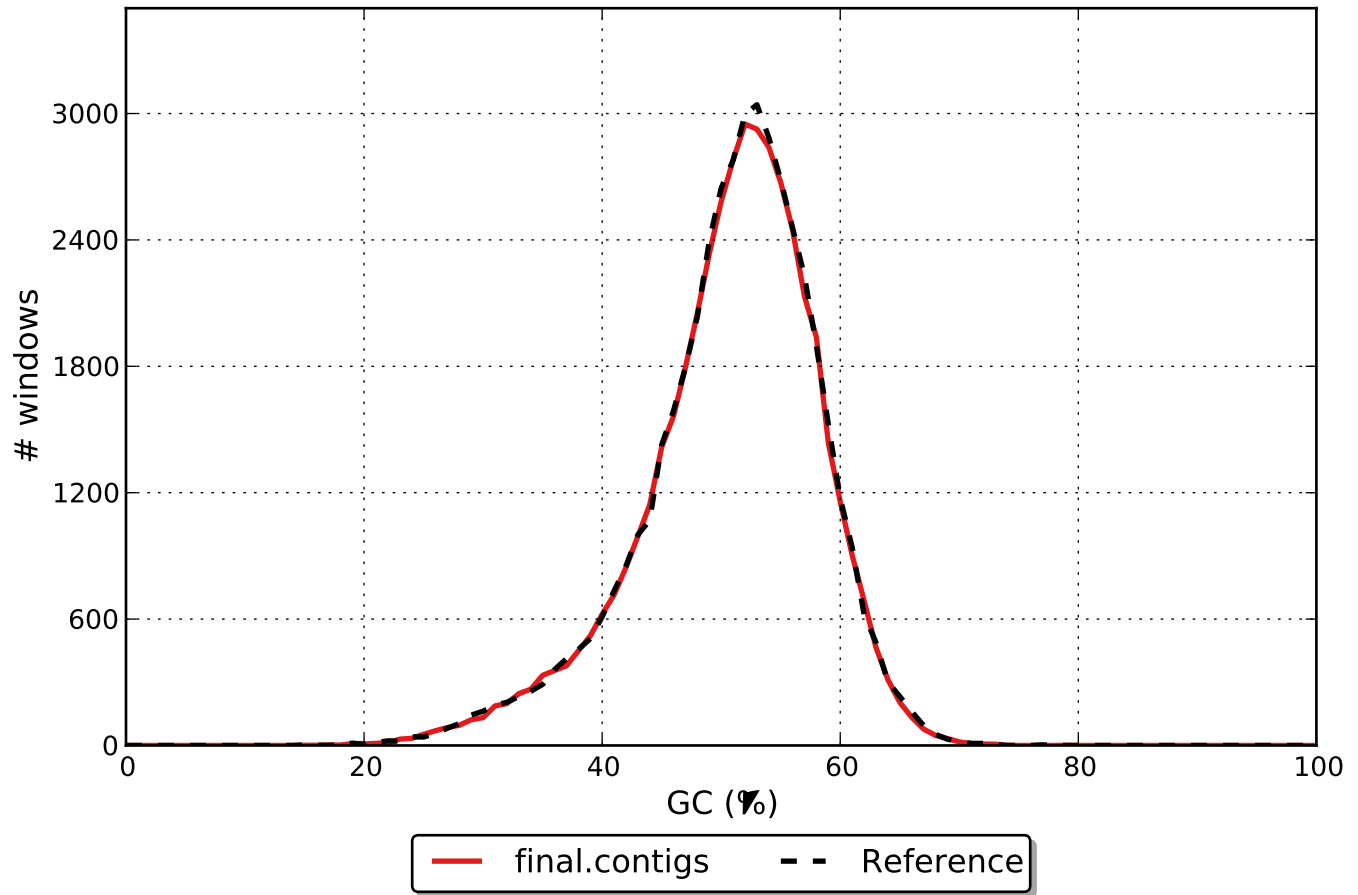


NGx

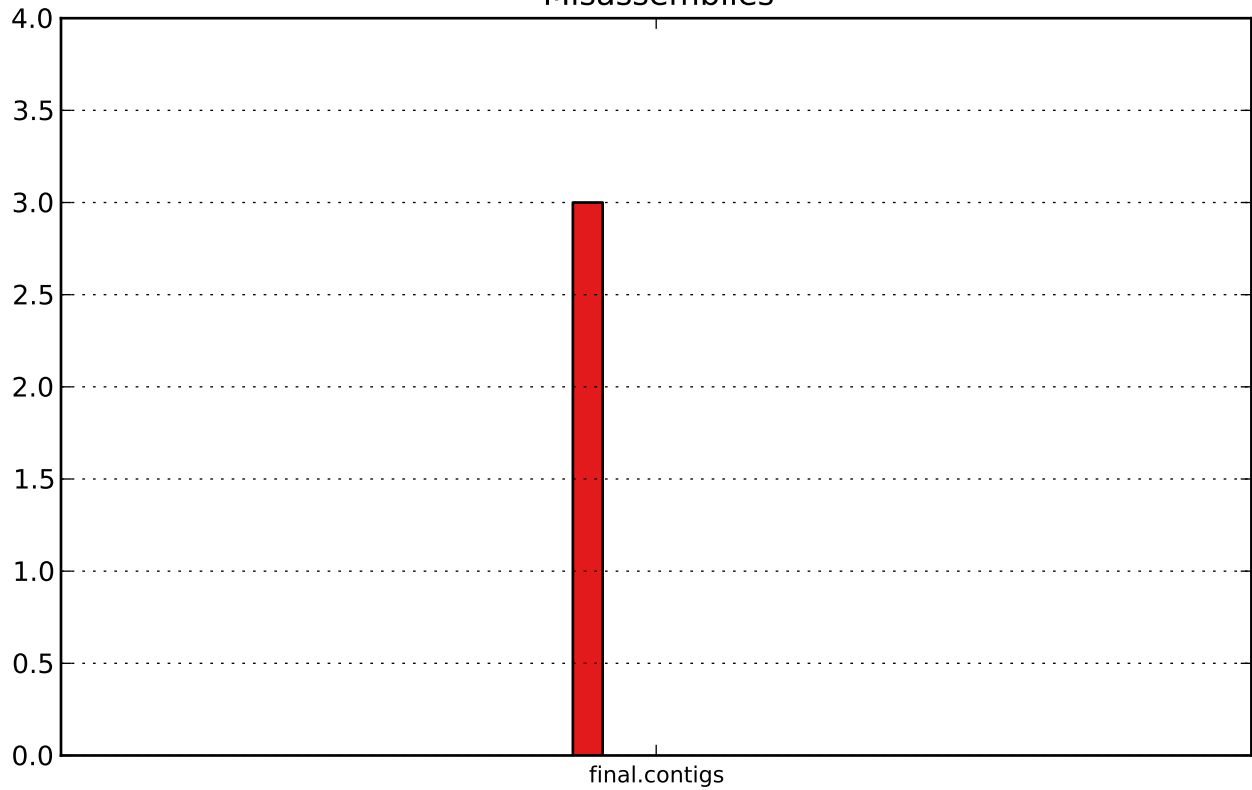




GC content

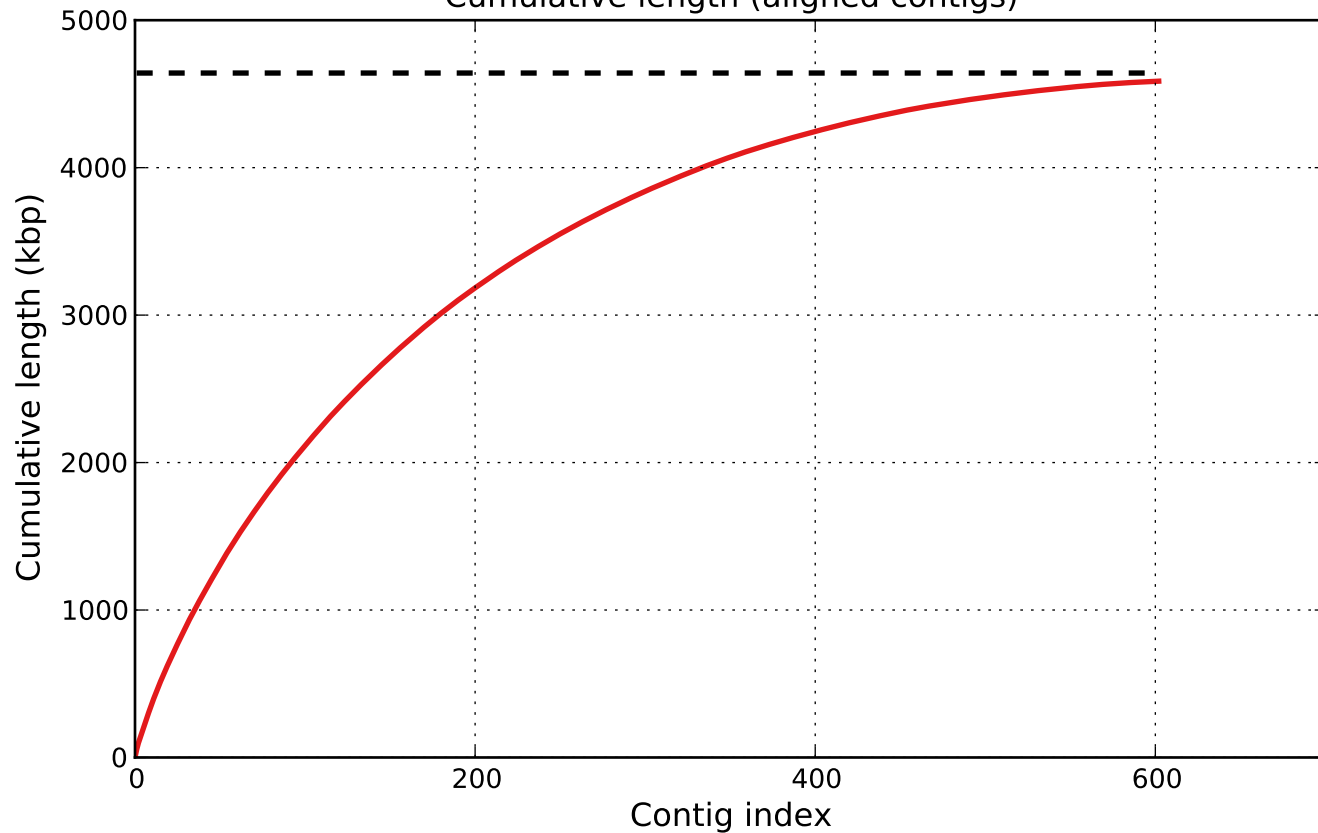


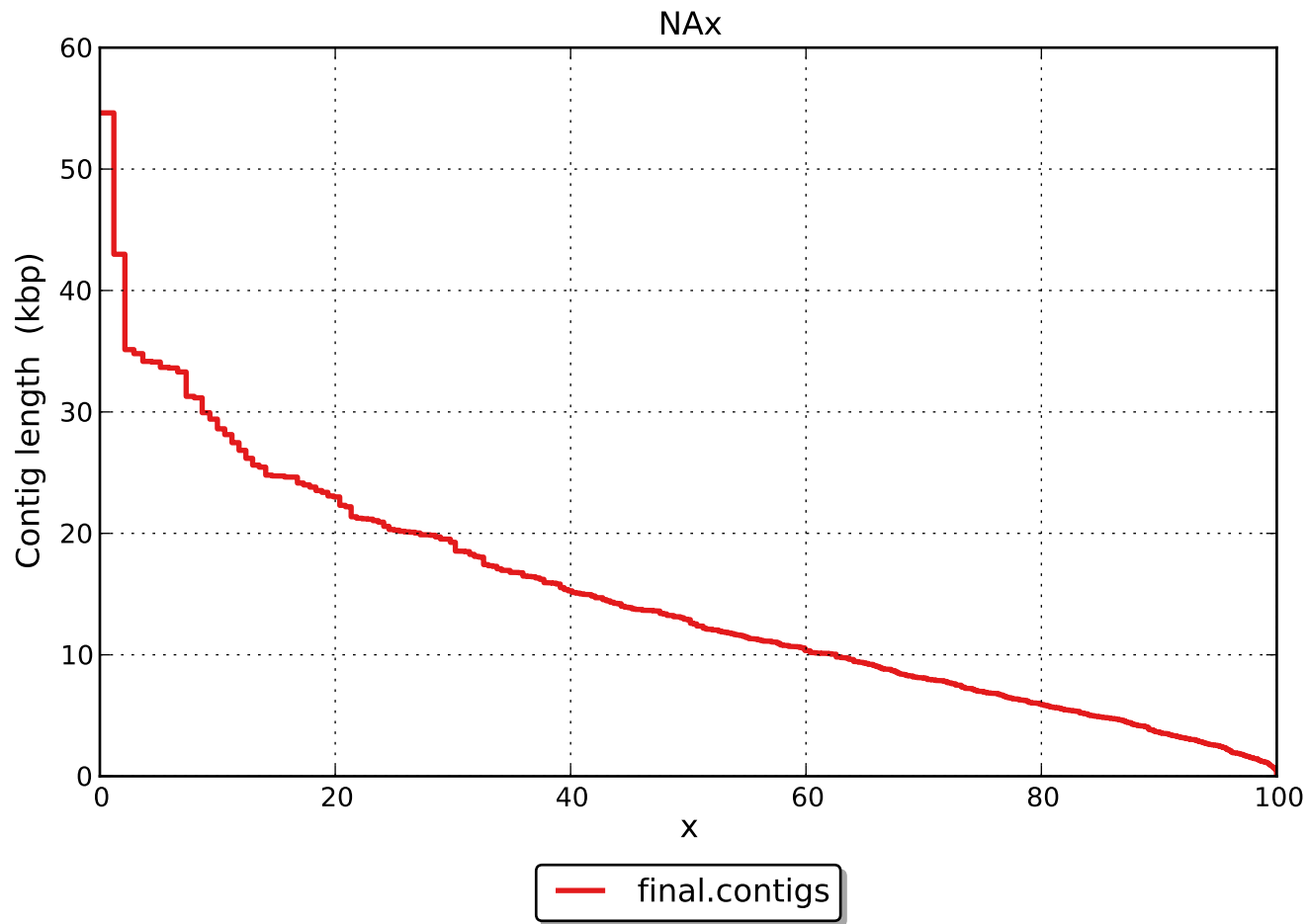
Misassemblies



 # relocations

Cumulative length (aligned contigs)





NGAx

