

Report

	final.contigs
# contigs (≥ 0 bp)	509
# contigs (≥ 1000 bp)	378
Total length (≥ 0 bp)	1299661
Total length (≥ 1000 bp)	1202336
# contigs	509
Largest contig	18135
Total length	1299661
Reference length	641799
GC (%)	26.30
Reference GC (%)	26.30
N50	3618
NG50	5513
N75	2097
NG75	4384
L50	116
LG50	41
L75	231
LG75	74
# misassemblies	30
# misassembled contigs	29
Misassembled contigs length	120593
# local misassemblies	0
# unaligned contigs	20 + 18 part
Unaligned length	105815
Genome fraction (%)	98.911
Duplication ratio	1.881
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1486.44
# indels per 100 kbp	2.52
Largest alignment	14070
NA50	3117
NGA50	4808
NA75	1540
NGA75	4021
LA50	133
LGA50	48
LA75	279
LGA75	85

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	30
# relocations	30
# translocations	0
# inversions	0
# possibly misassembled contigs	13
# misassembled contigs	29
Misassembled contigs length	120593
# local misassemblies	0
# mismatches	9436
# indels	16
# short indels	16
# long indels	0
Indels length	16

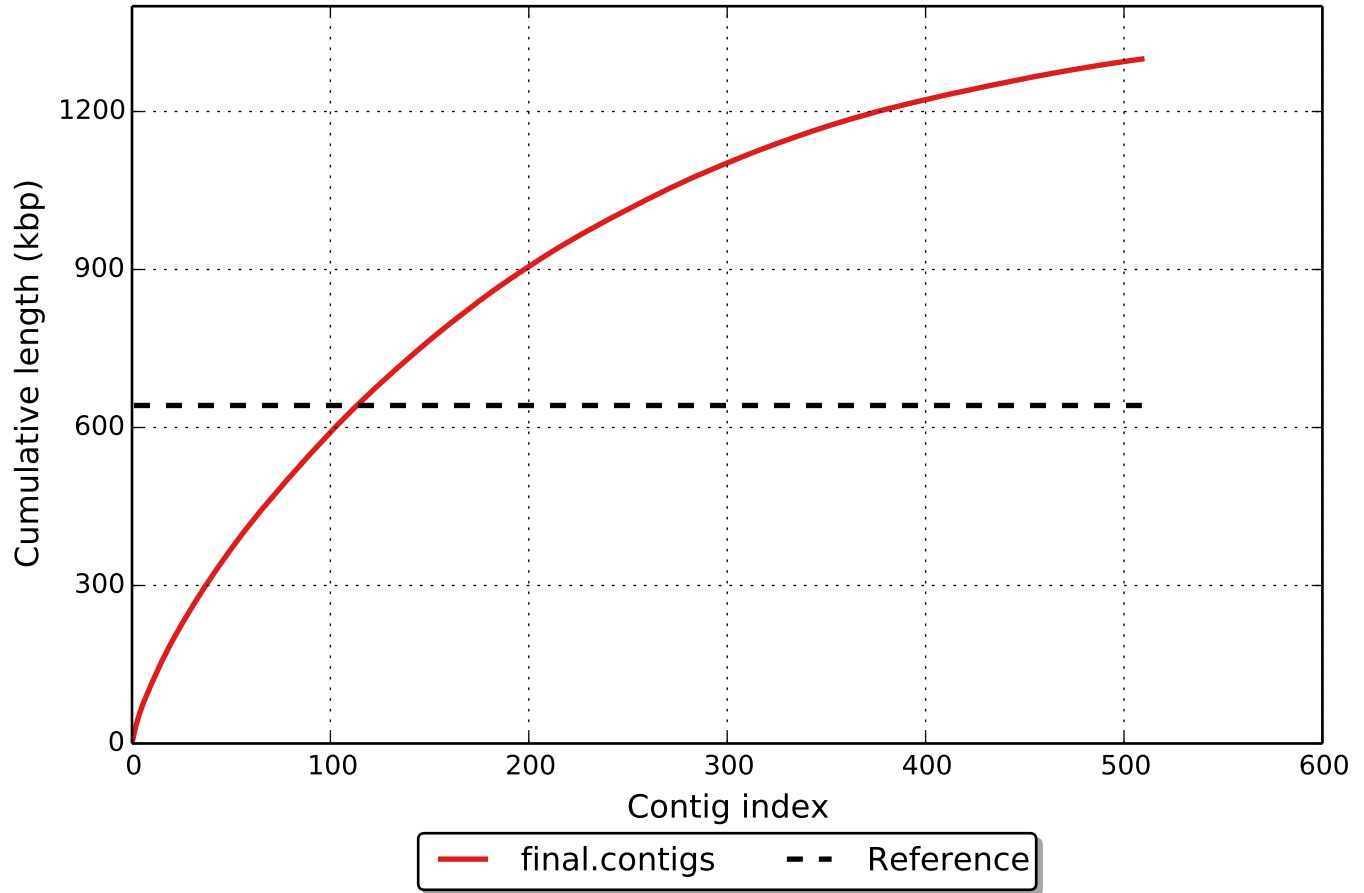
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

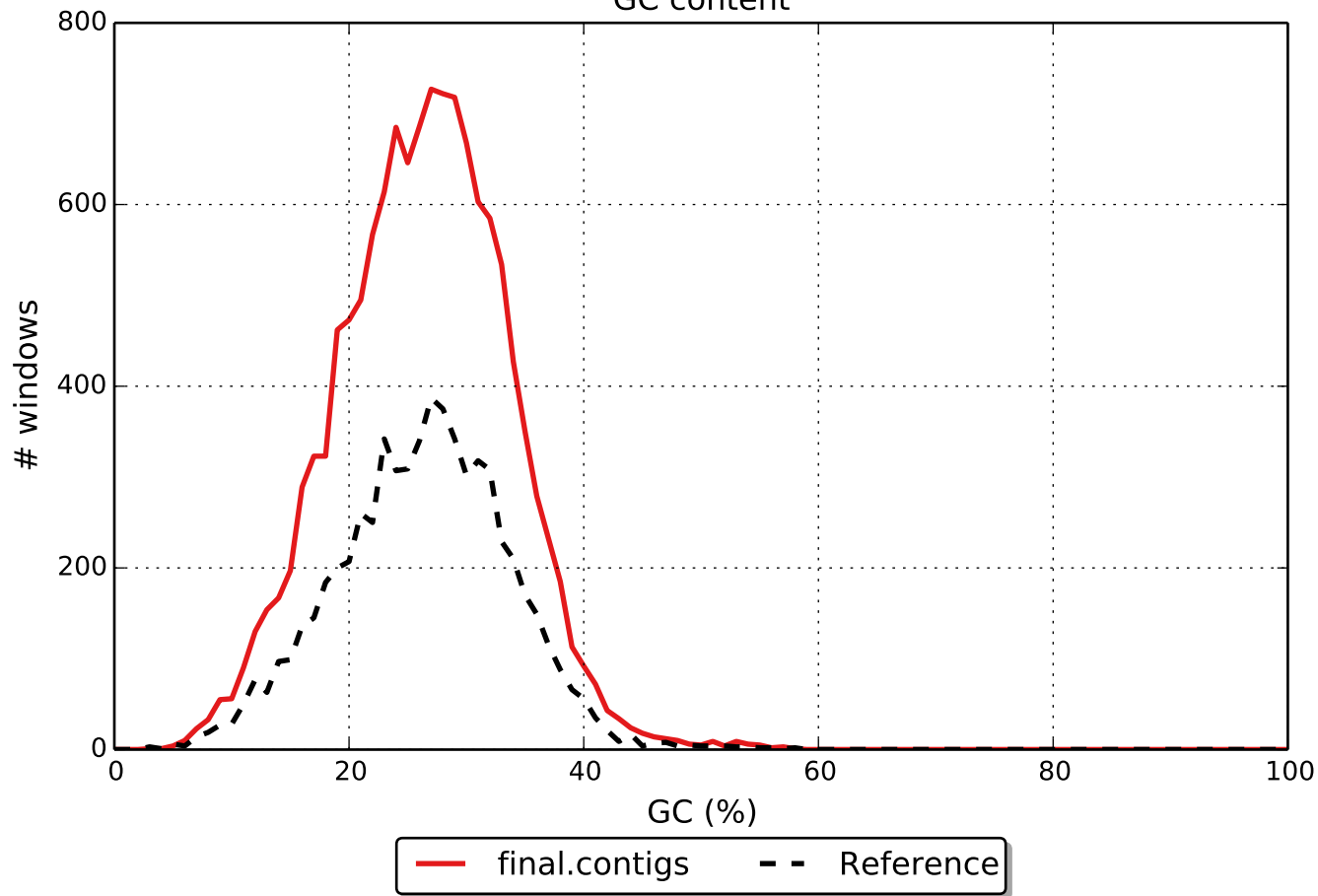
	final.contigs
# fully unaligned contigs	20
Fully unaligned length	56342
# partially unaligned contigs	18
# with misassembly	0
# both parts are significant	12
Partially unaligned length	49473
# N's	0

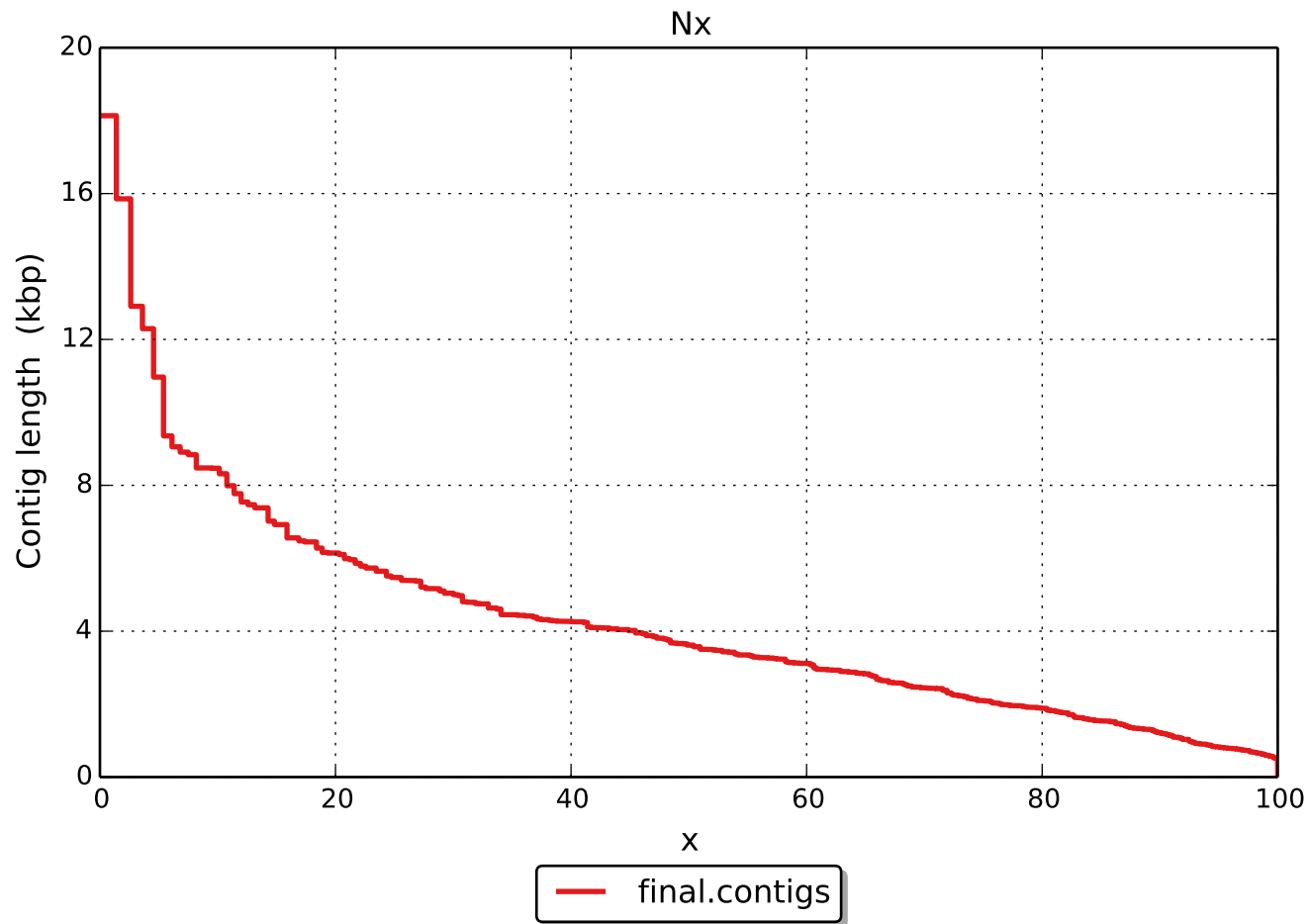
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

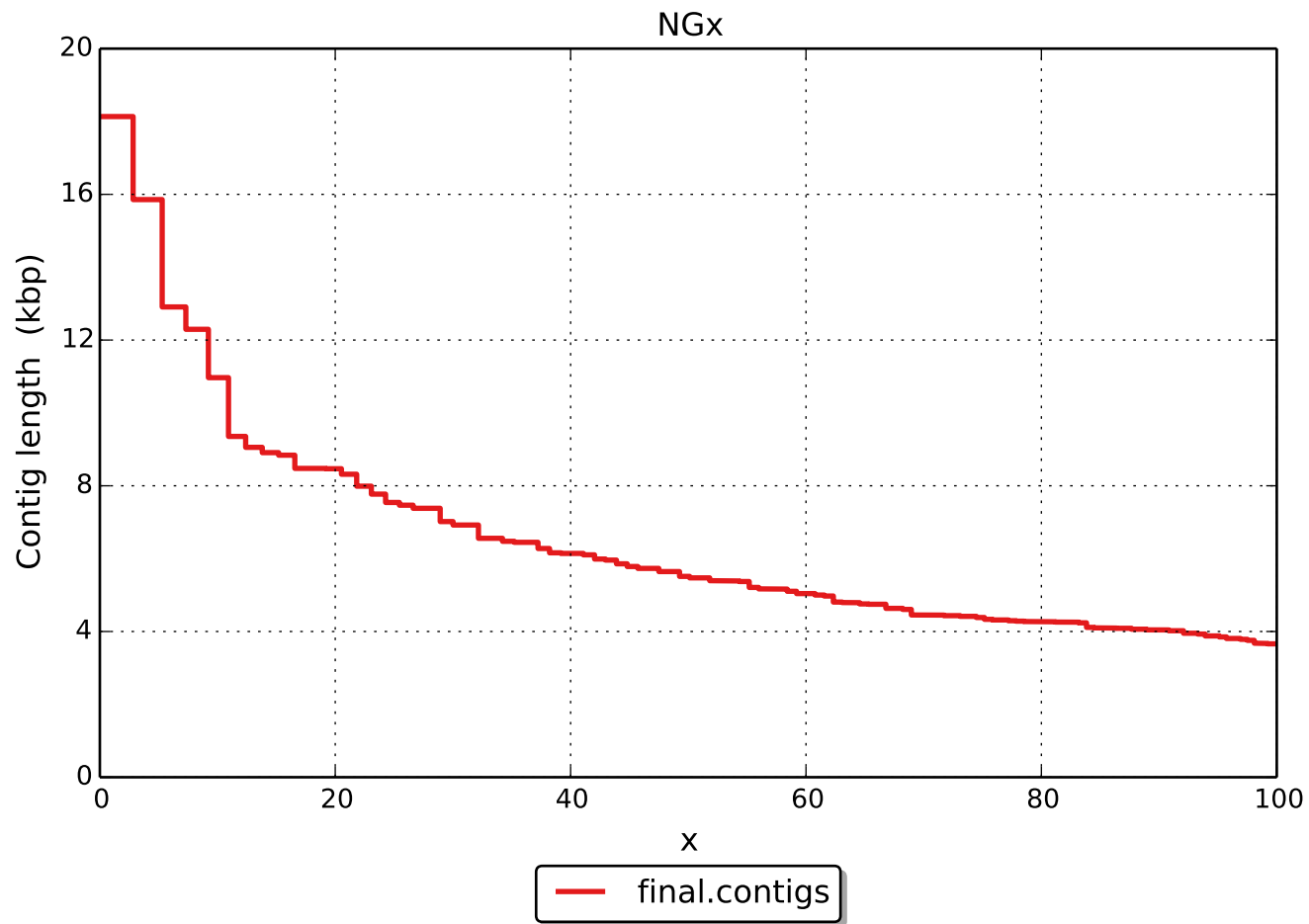
Cumulative length



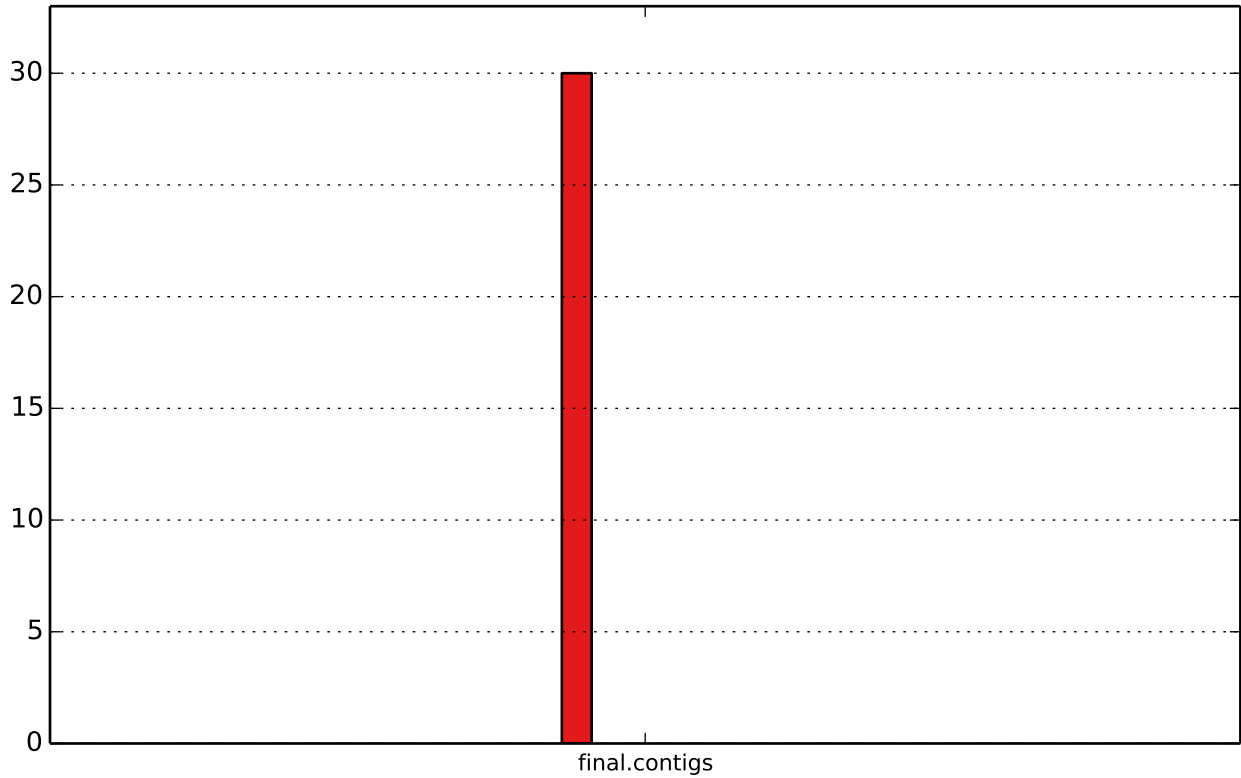
GC content





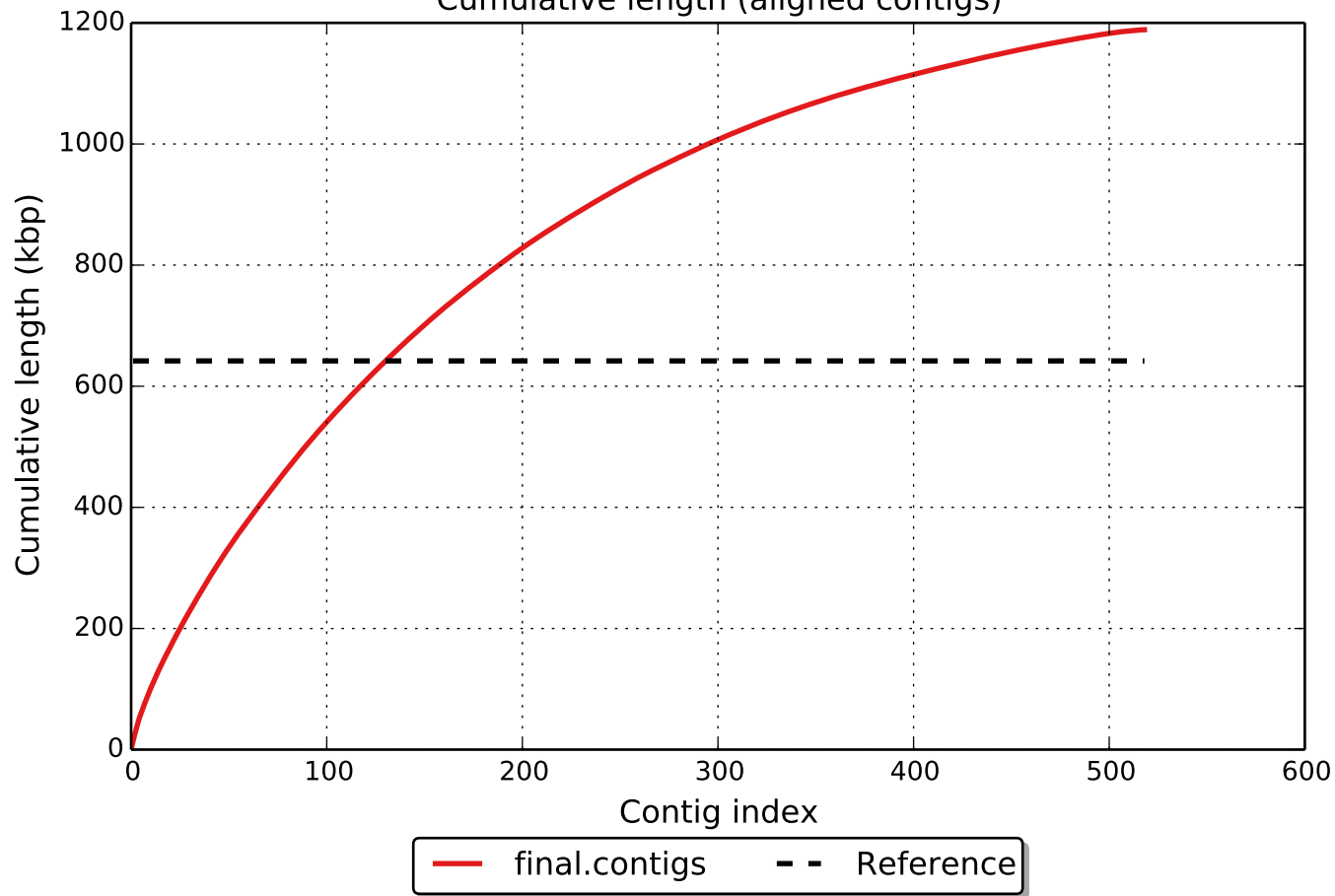


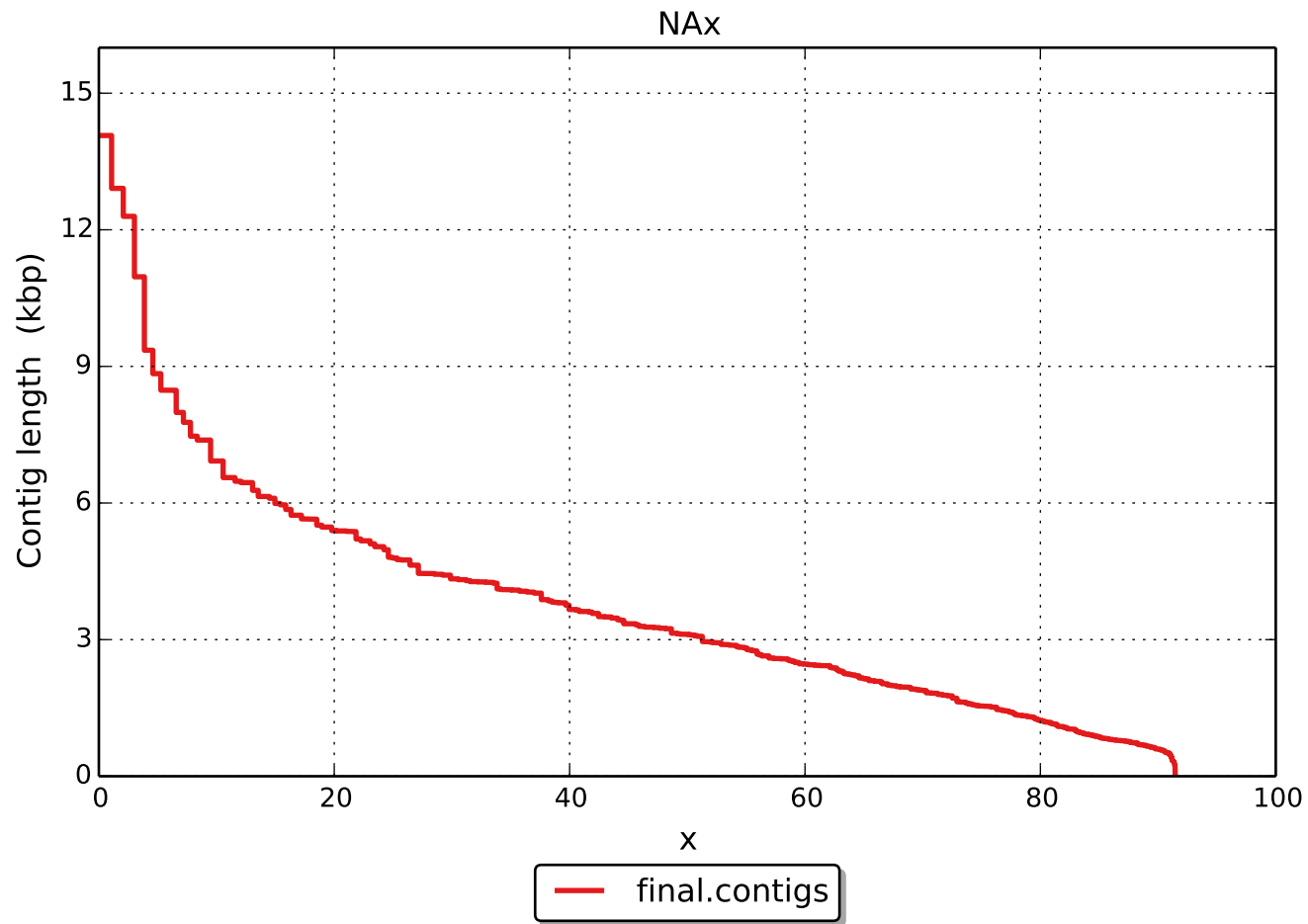
Misassemblies



 # relocations

Cumulative length (aligned contigs)





NGAx

