

Report

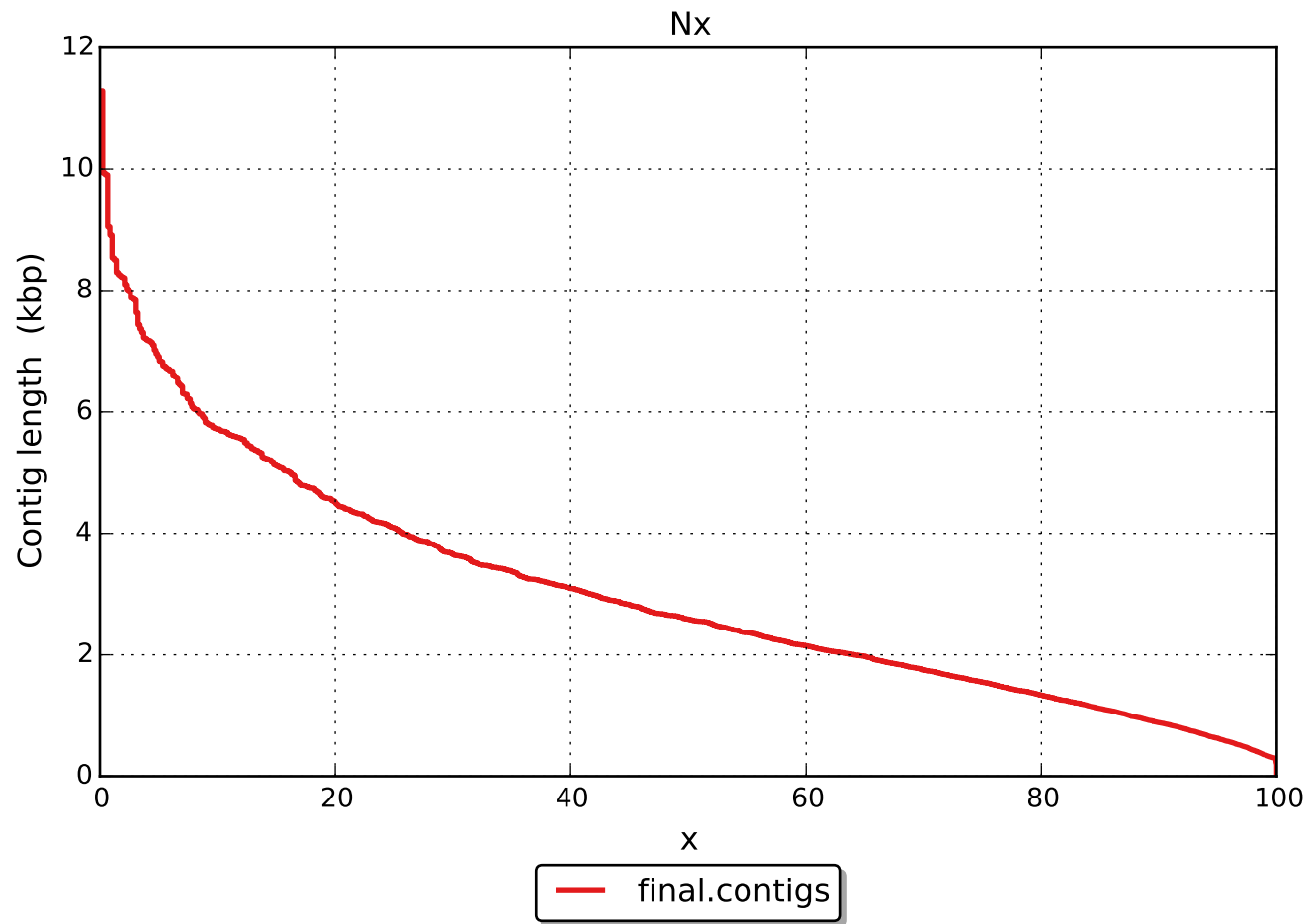
	final.contigs
# contigs (>= 0 bp)	2635
# contigs (>= 1000 bp)	1647
# contigs (>= 5000 bp)	122
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4745529
Total length (>= 1000 bp)	4152352
Total length (>= 5000 bp)	766717
Total length (>= 10000 bp)	11288
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2635
Largest contig	11288
Total length	4745529
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	2587
NG50	2639
N75	1548
NG75	1616
L50	588
LG50	568
L75	1177
LG75	1128
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	7148
# local misassemblies	2
# unaligned contigs	555 + 20 part
Unaligned length	388035
Genome fraction (%)	91.118
Duplication ratio	1.030
# N's per 100 kbp	0.00
# mismatches per 100 kbp	373.86
# indels per 100 kbp	0.38
Largest alignment	11288
NA50	2562
NGA50	2618
NA75	1484
NGA75	1564
LA50	591
LGA50	571
LA75	1190
LGA75	1139

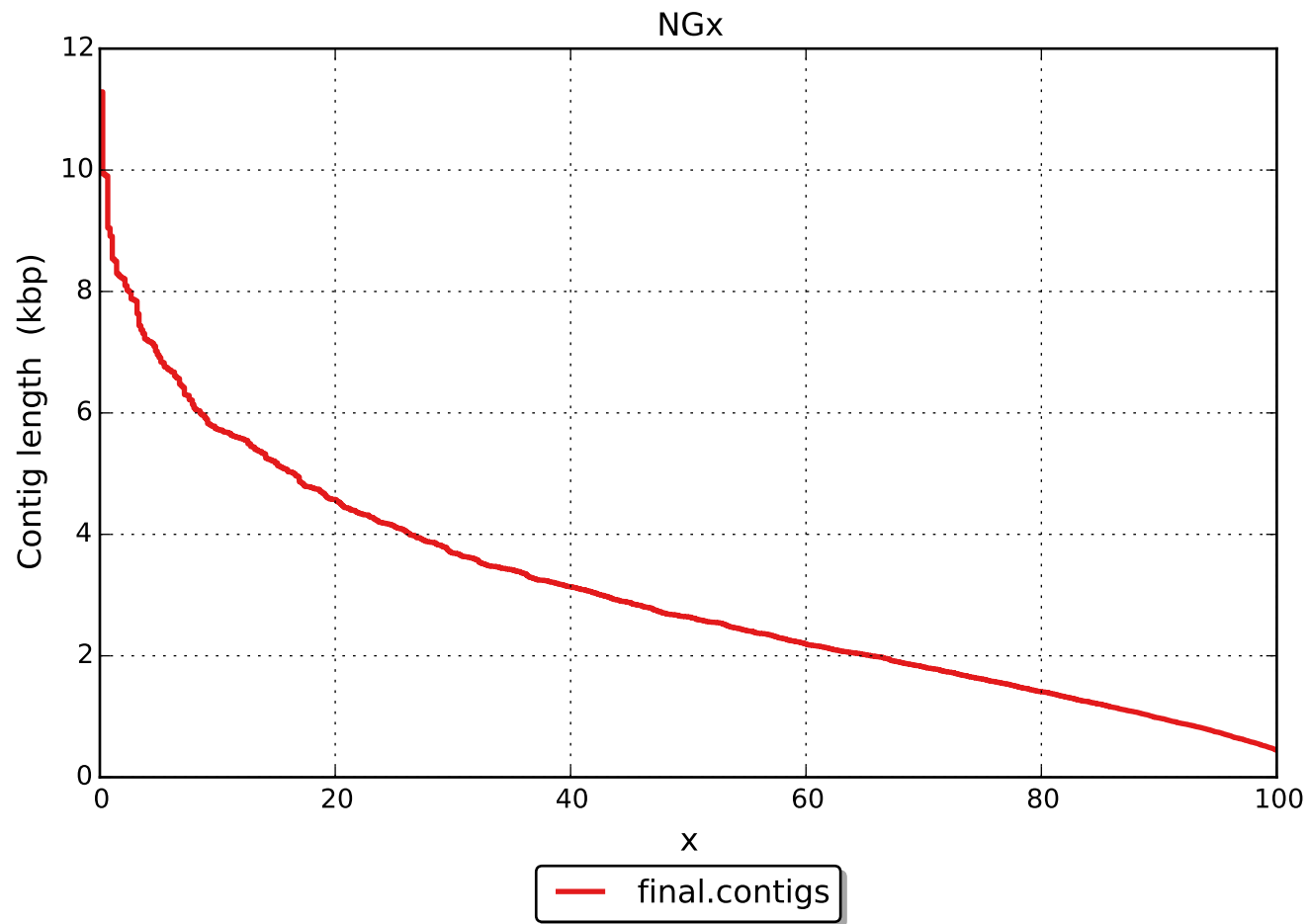
Misassemblies report

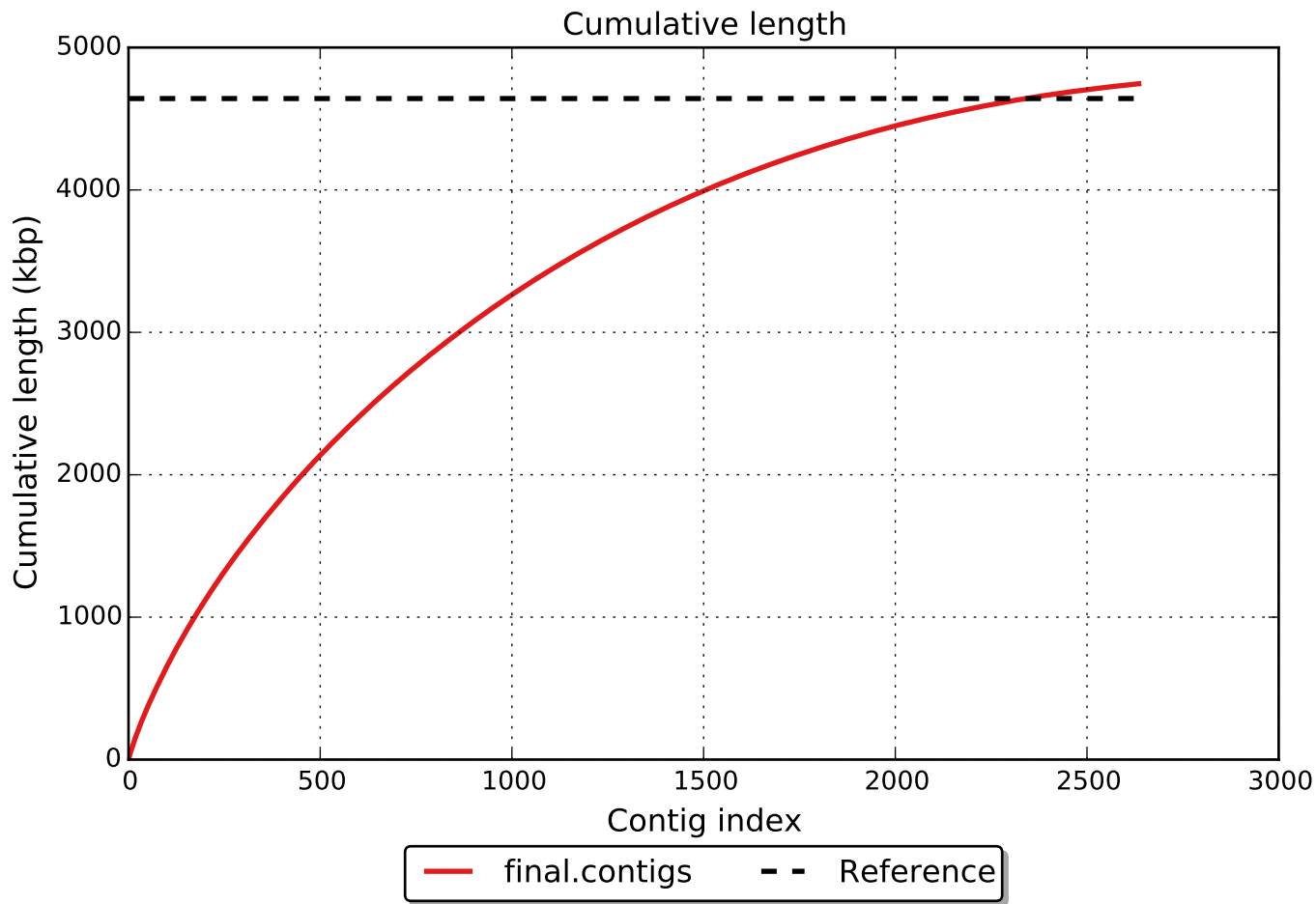
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	7148
# local misassemblies	2
# mismatches	15812
# indels	16
# short indels	15
# long indels	1
Indels length	99

Unaligned report

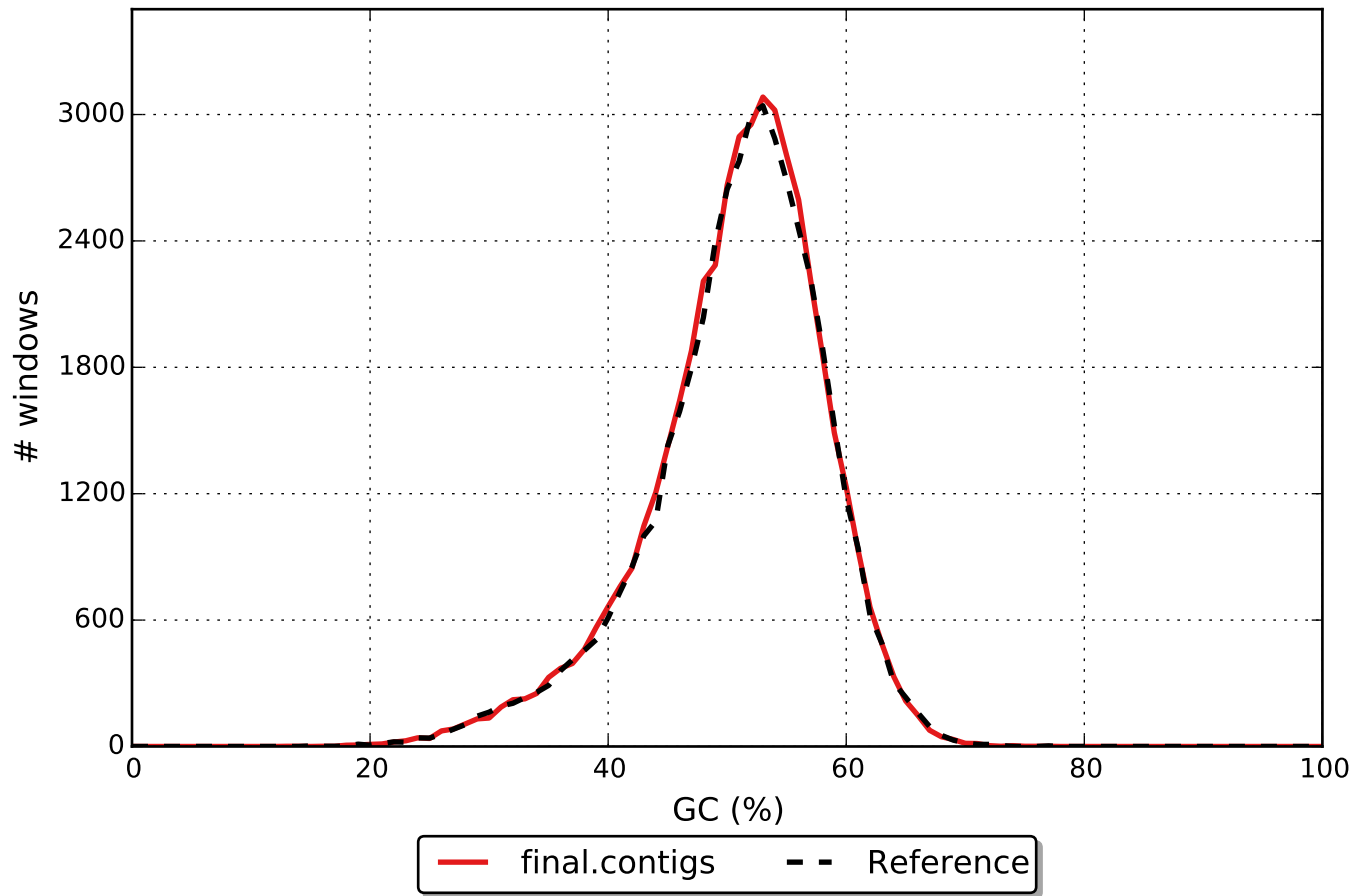
	final.contigs
# fully unaligned contigs	555
Fully unaligned length	377919
# partially unaligned contigs	20
# with misassembly	0
# both parts are significant	20
Partially unaligned length	10116
# N's	0



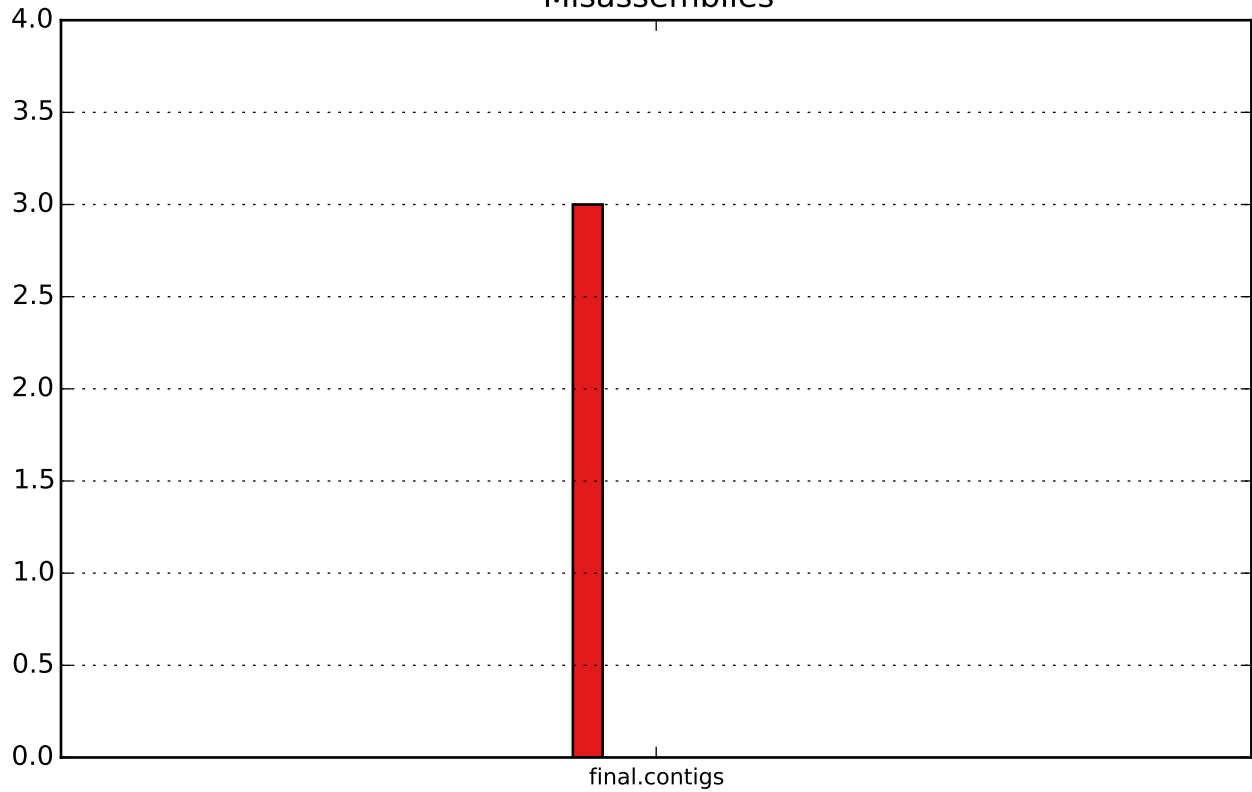




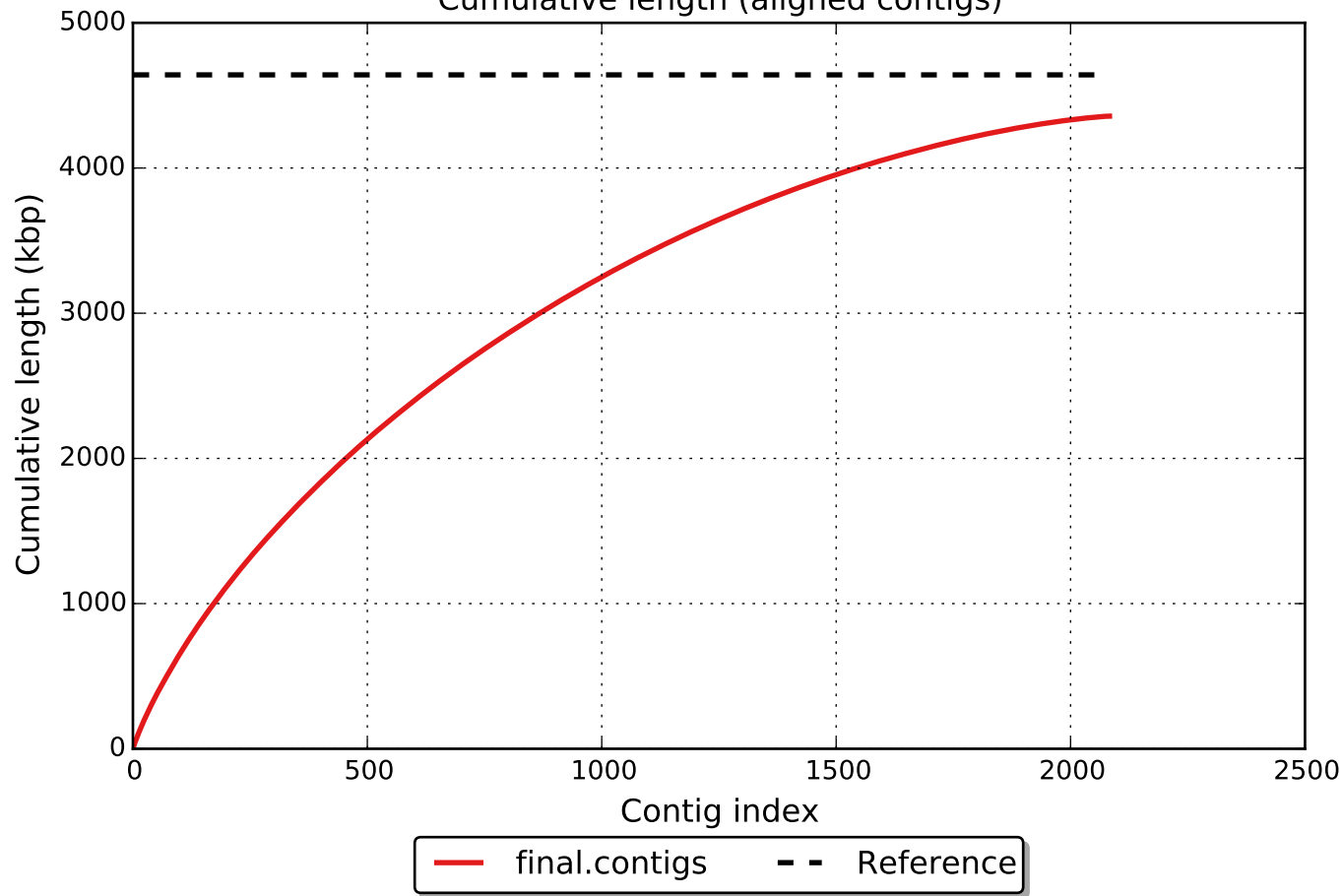
GC content

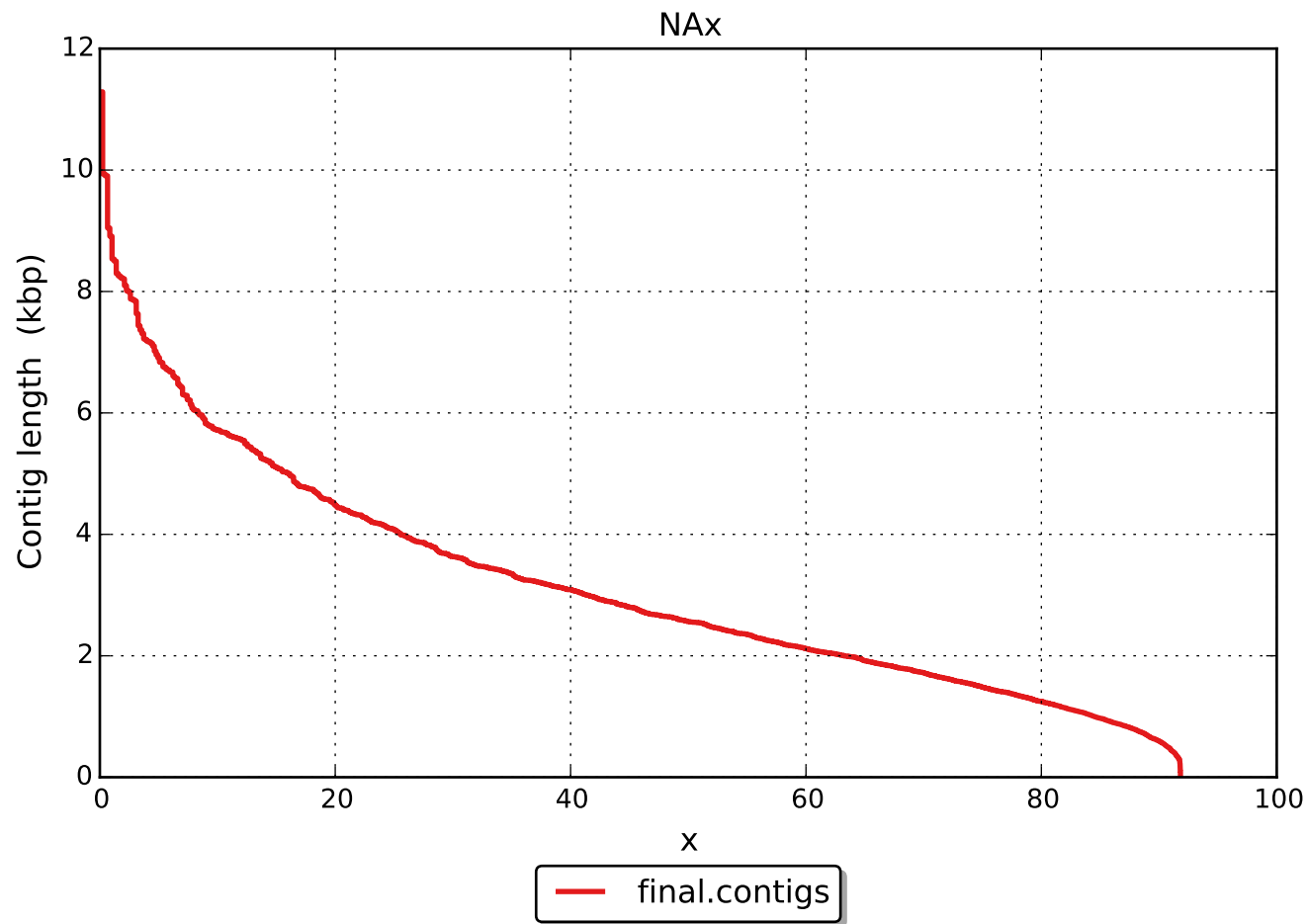


Misassemblies



Cumulative length (aligned contigs)





NGAx

