

# Report

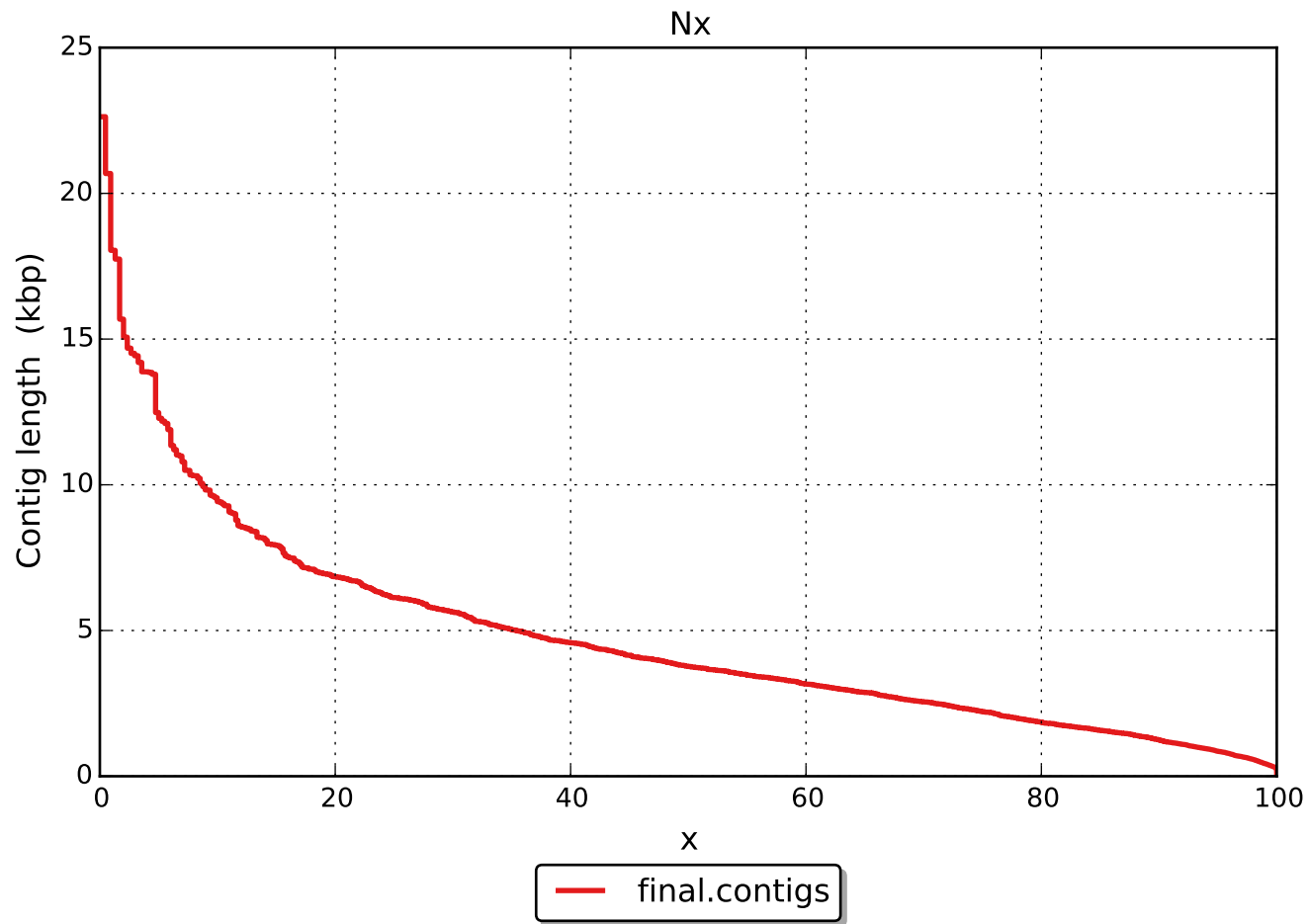
	final.contigs
# contigs (>= 0 bp)	1852
# contigs (>= 1000 bp)	1334
# contigs (>= 5000 bp)	221
# contigs (>= 10000 bp)	31
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4710811
Total length (>= 1000 bp)	4390205
Total length (>= 5000 bp)	1665674
Total length (>= 10000 bp)	411577
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1852
Largest contig	22629
Total length	4710811
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	3767
NG50	3814
N75	2214
NG75	2300
L50	381
LG50	372
L75	780
LG75	757
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	31226
# local misassemblies	4
# unaligned contigs	215 + 15 part
Unaligned length	129331
Genome fraction (%)	96.010
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	242.23
# indels per 100 kbp	0.02
Largest alignment	22627
NA50	3749
NGA50	3804
NA75	2211
NGA75	2285
LA50	382
LGA50	373
LA75	783
LGA75	760

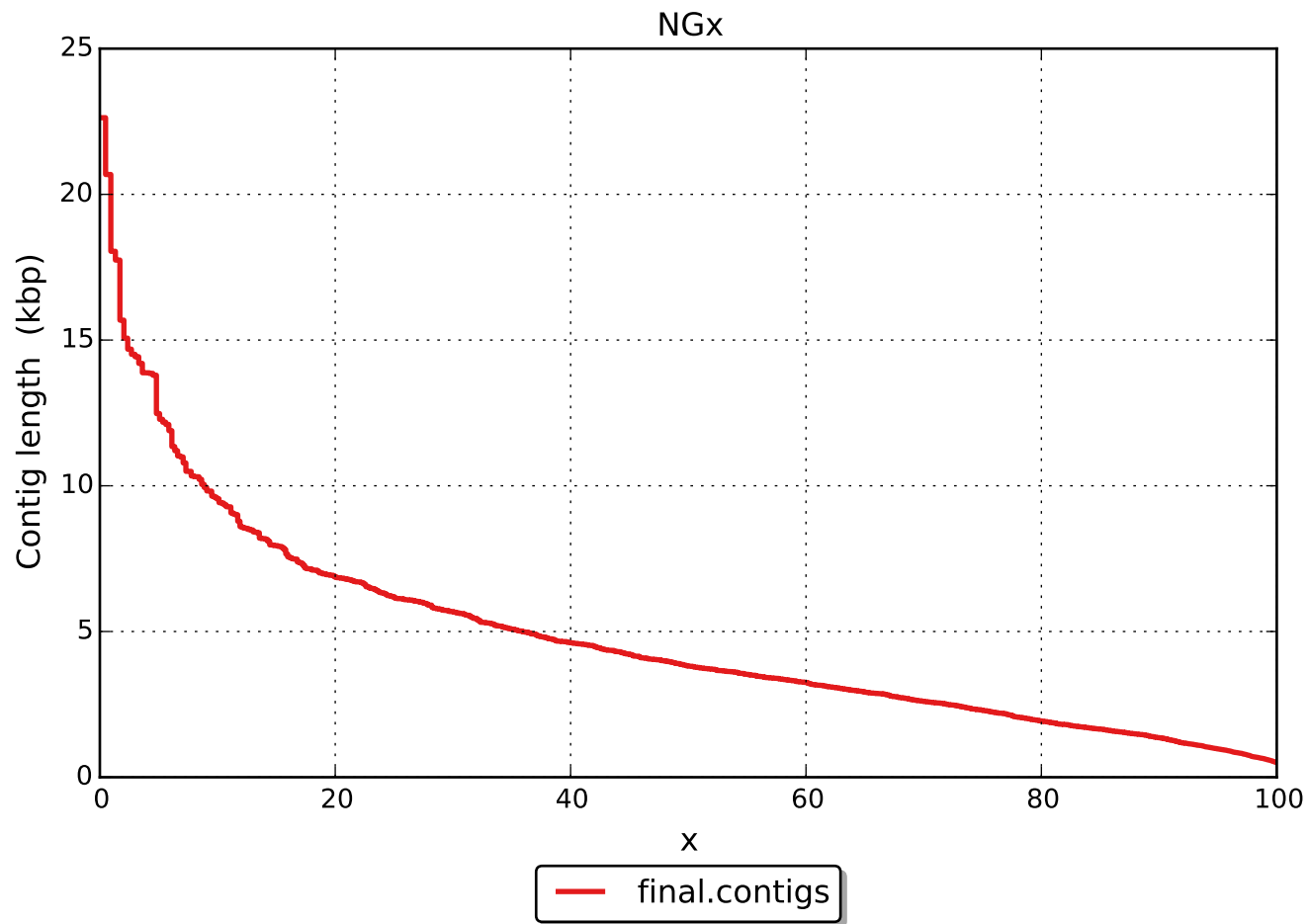
## Misassemblies report

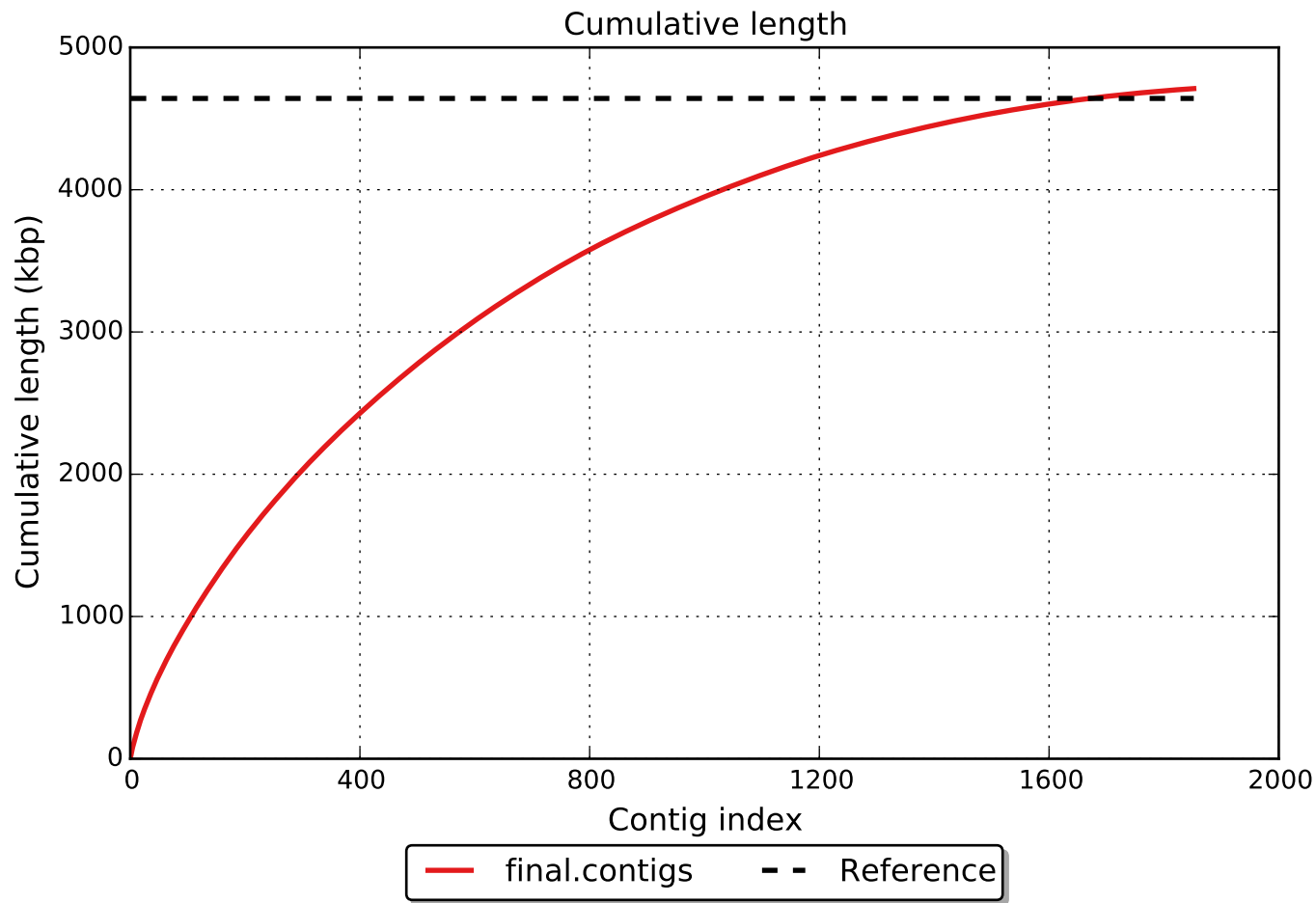
	final.contigs
# misassemblies	5
# relocations	5
# translocations	0
# inversions	0
# misassembled contigs	5
Misassembled contigs length	31226
# local misassemblies	4
# mismatches	10795
# indels	1
# short indels	0
# long indels	1
Indels length	24

## Unaligned report

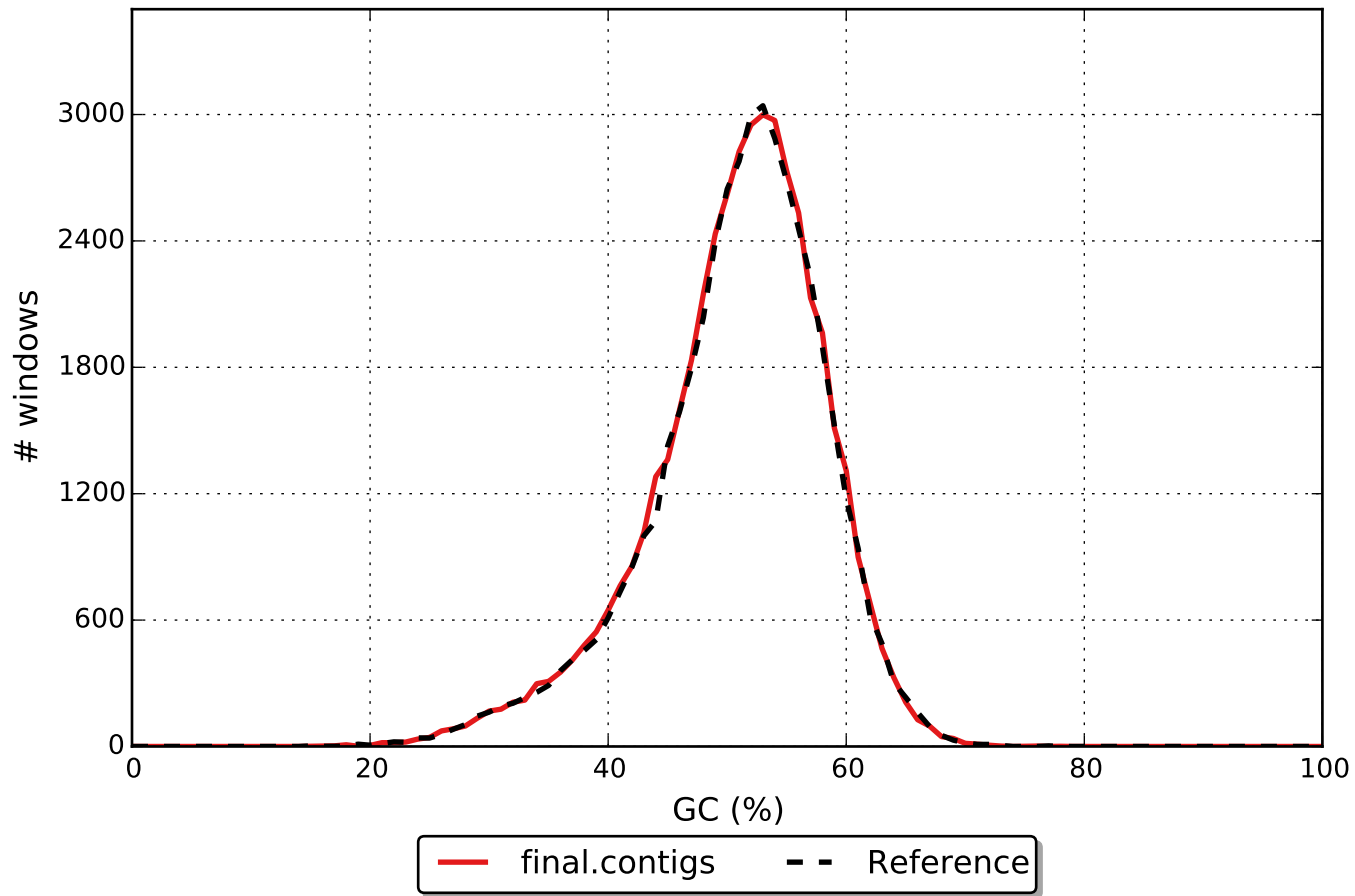
	final.contigs
# fully unaligned contigs	215
Fully unaligned length	124764
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	15
Partially unaligned length	4567
# N's	0

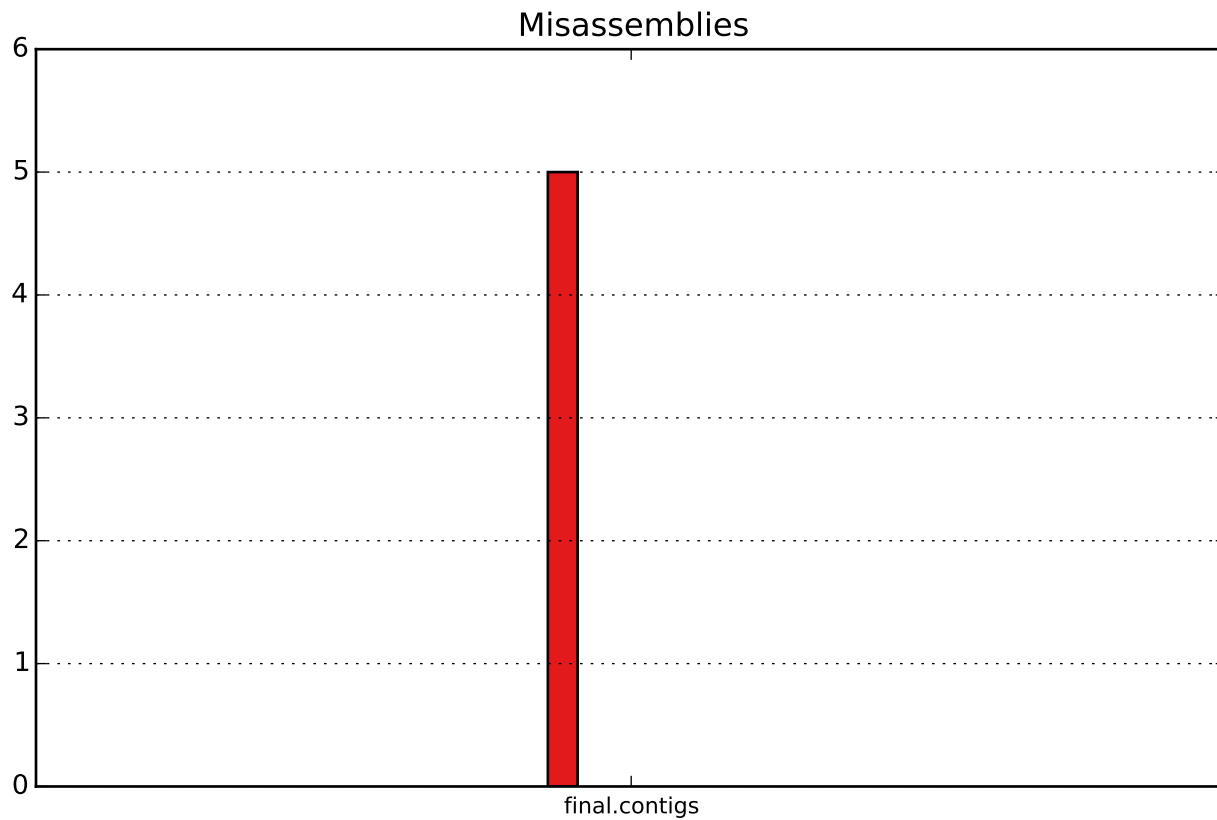






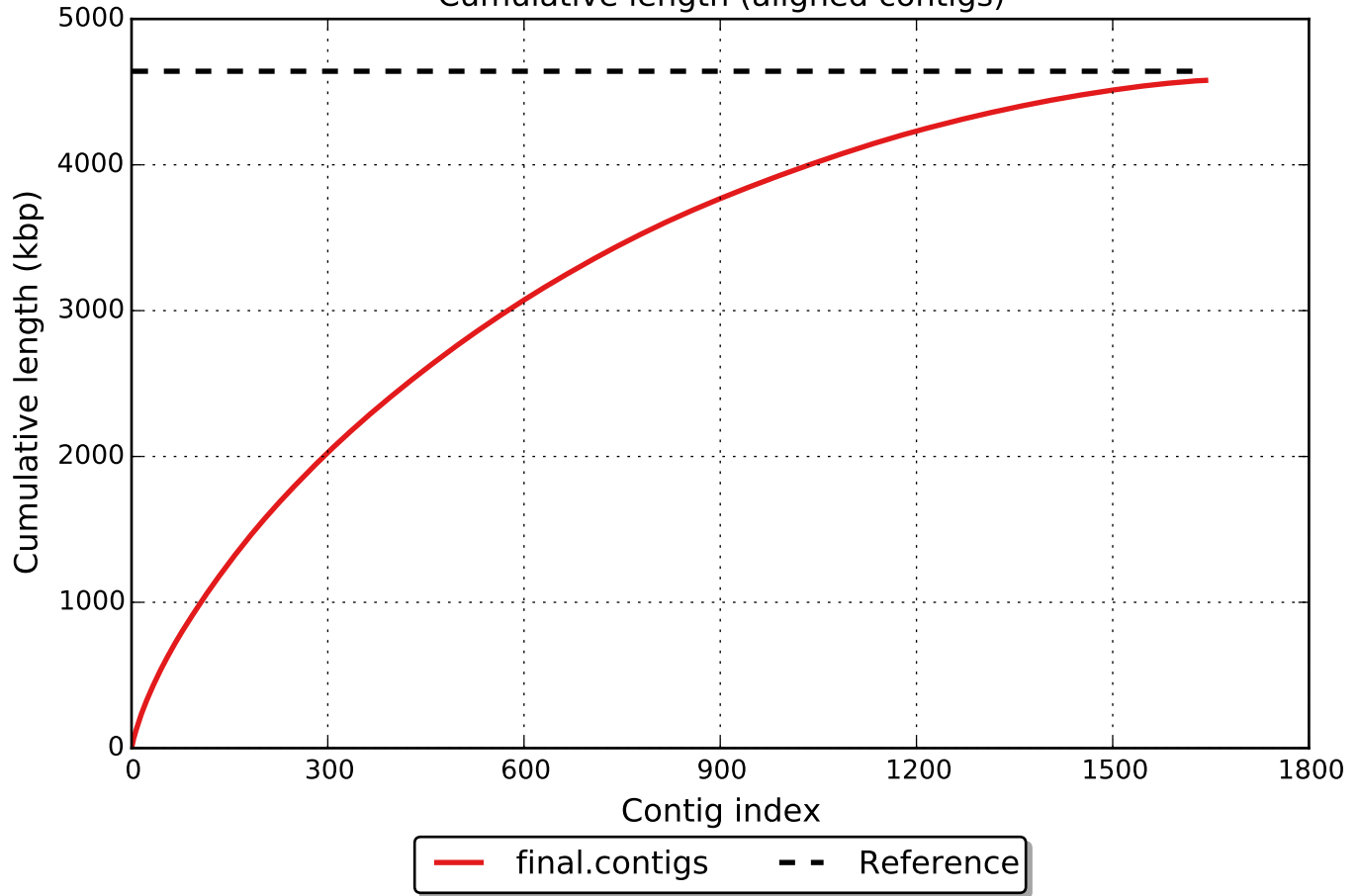
GC content

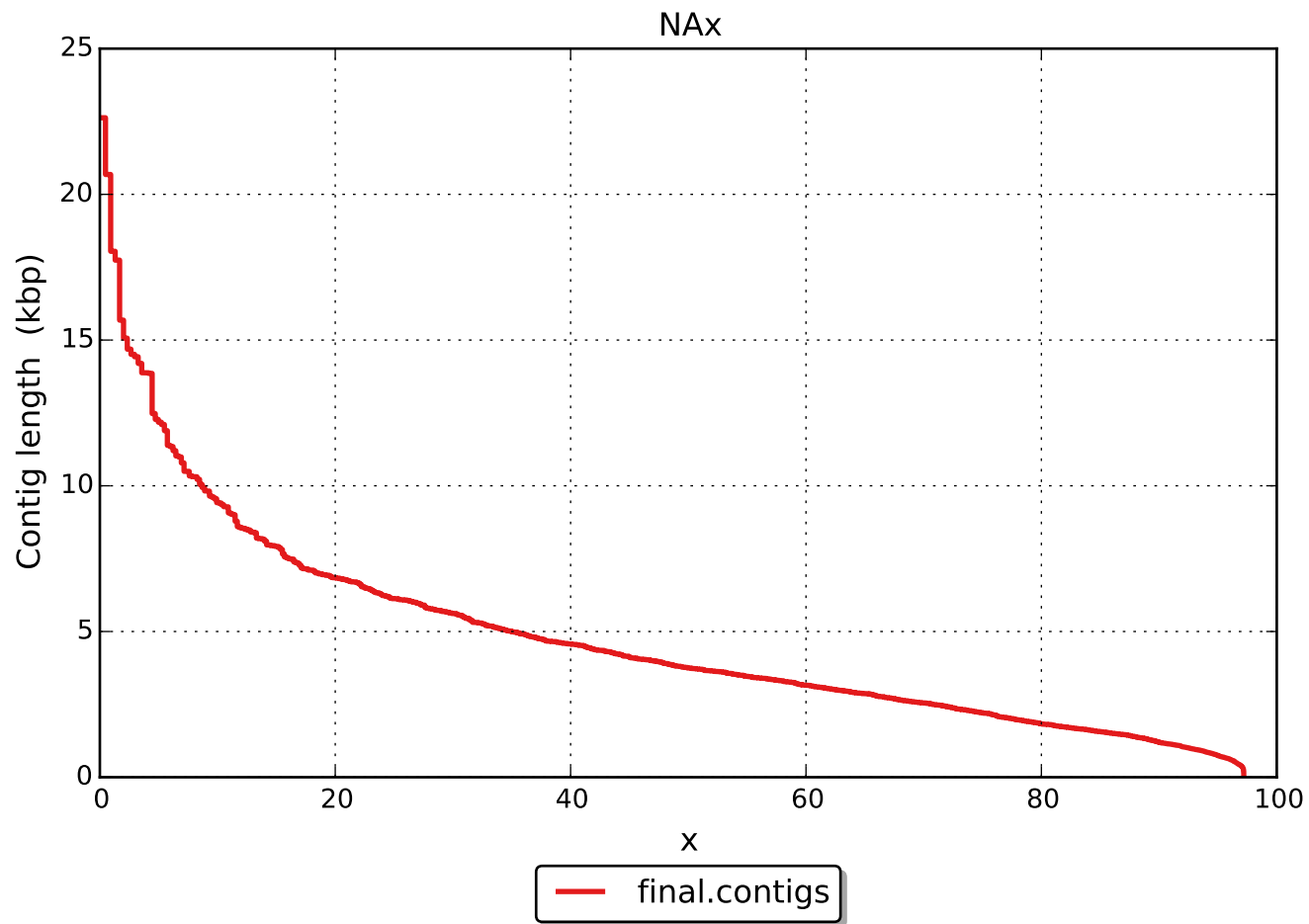






Cumulative length (aligned contigs)





NGAx

