

Report

	nd.asm
# contigs (>= 0 bp)	82
# contigs (>= 1000 bp)	82
# contigs (>= 5000 bp)	82
# contigs (>= 10000 bp)	82
# contigs (>= 25000 bp)	82
# contigs (>= 50000 bp)	82
Total length (>= 0 bp)	2898224197
Total length (>= 1000 bp)	2898224197
Total length (>= 5000 bp)	2898224197
Total length (>= 10000 bp)	2898224197
Total length (>= 25000 bp)	2898224197
Total length (>= 50000 bp)	2898224197
# contigs	82
Largest contig	237405279
Total length	2898224197
Reference length	2938464690
GC (%)	40.92
Reference GC (%)	40.88
N50	106090521
NG50	106090521
N75	63899818
NG75	63899818
L50	10
LG50	10
L75	19
LG75	19
# misassemblies	1227
# misassembled contigs	61
Misassembled contigs length	2740877545
# local misassemblies	433
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	42
# unaligned mis. contigs	11
# unaligned contigs	0 + 64 part
Unaligned length	22021119
Genome fraction (%)	97.421
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.43
# indels per 100 kbp	170.98
Largest alignment	111497488
Total aligned length	2865321418
NA50	57779597
NGA50	57779597
NA75	31402254
NGA75	29439947
LA50	18
LGA50	18
LA75	35
LGA75	36

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	nd.asm
# misassemblies	1227
# contig misassemblies	1227
# c. relocations	570
# c. translocations	654
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	61
Misassembled contigs length	2740877545
# local misassemblies	433
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	5
# possible TEs	42
# unaligned mis. contigs	11
# mismatches	840411
# indels	4882423
# indels (<= 5 bp)	4823730
# indels (> 5 bp)	58693
Indels length	8272677

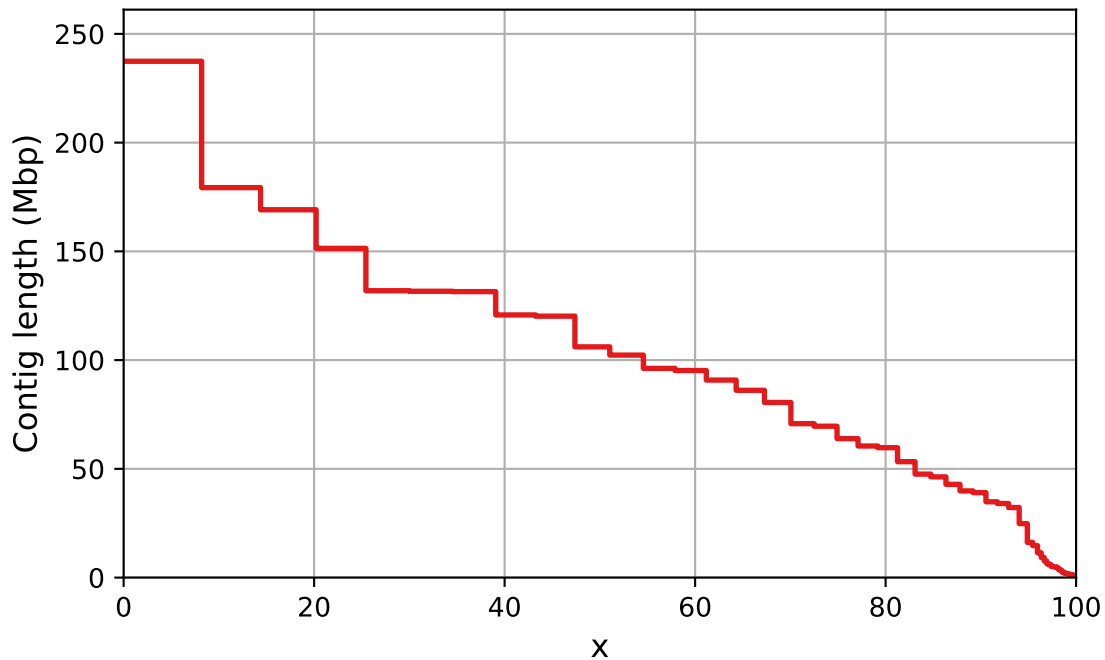
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	nd.asm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	64
Partially unaligned length	22021119
# N's	0

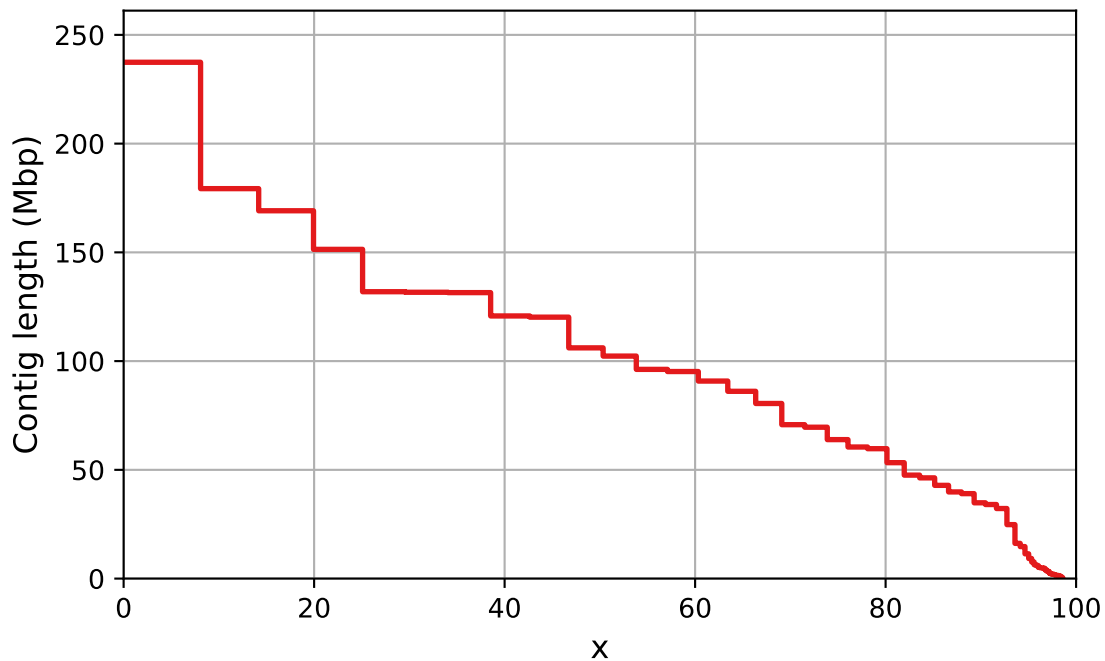
All statistics are based on contigs of size ≥ 3000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



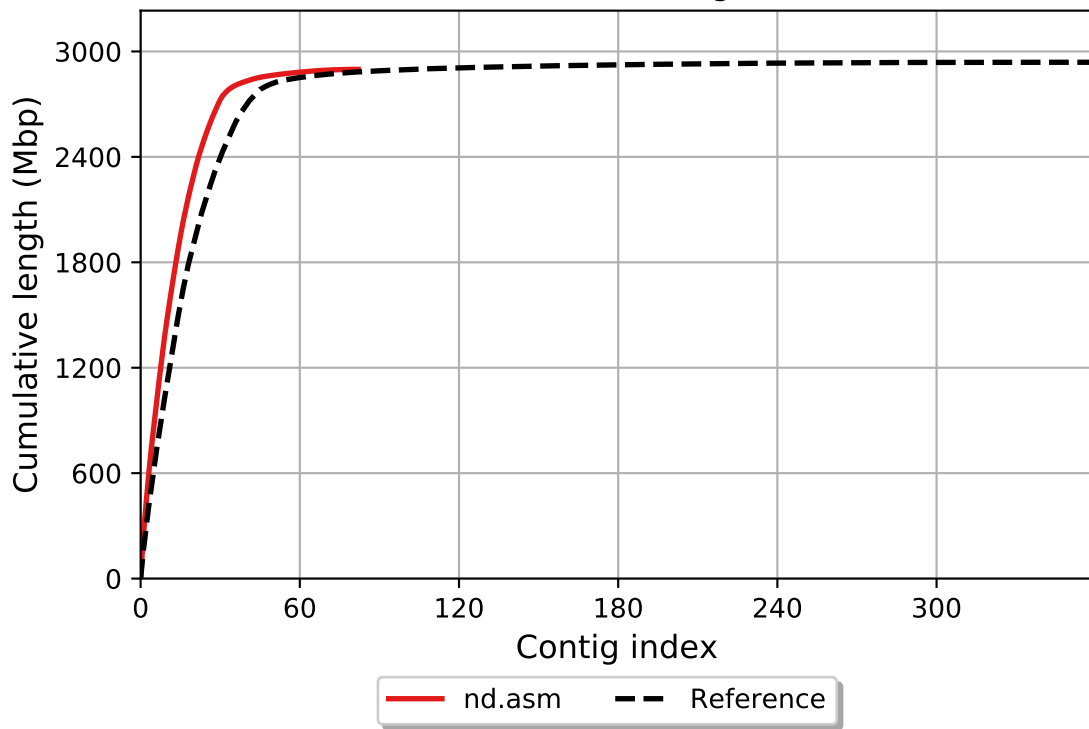
nd.asm

NGx

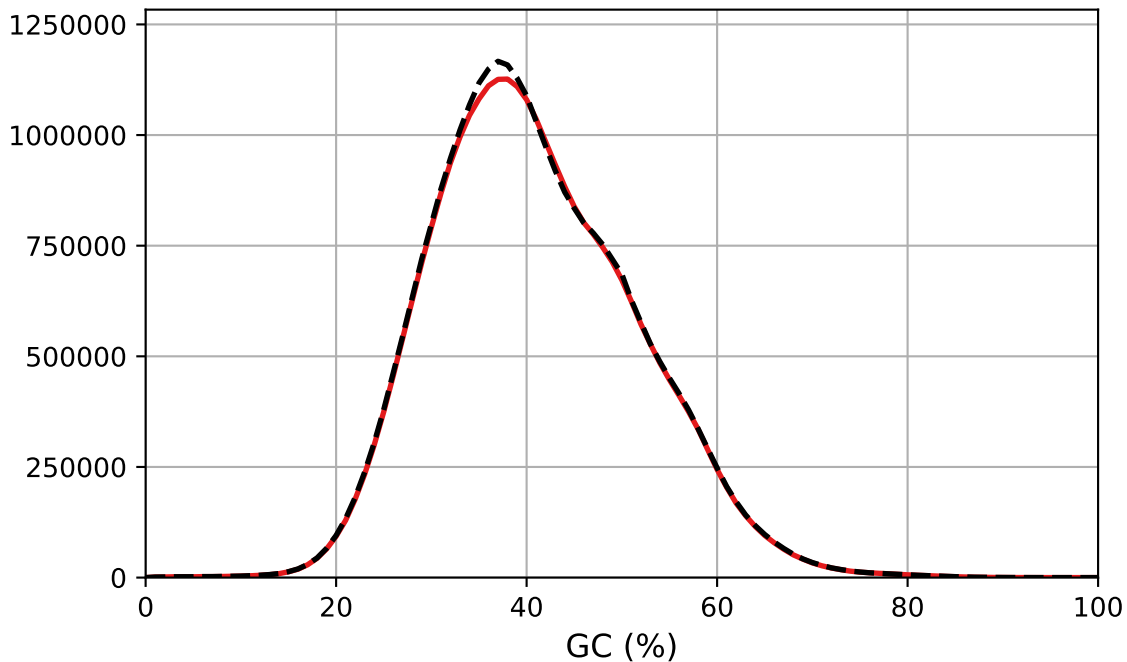


— nd.asm

Cumulative length

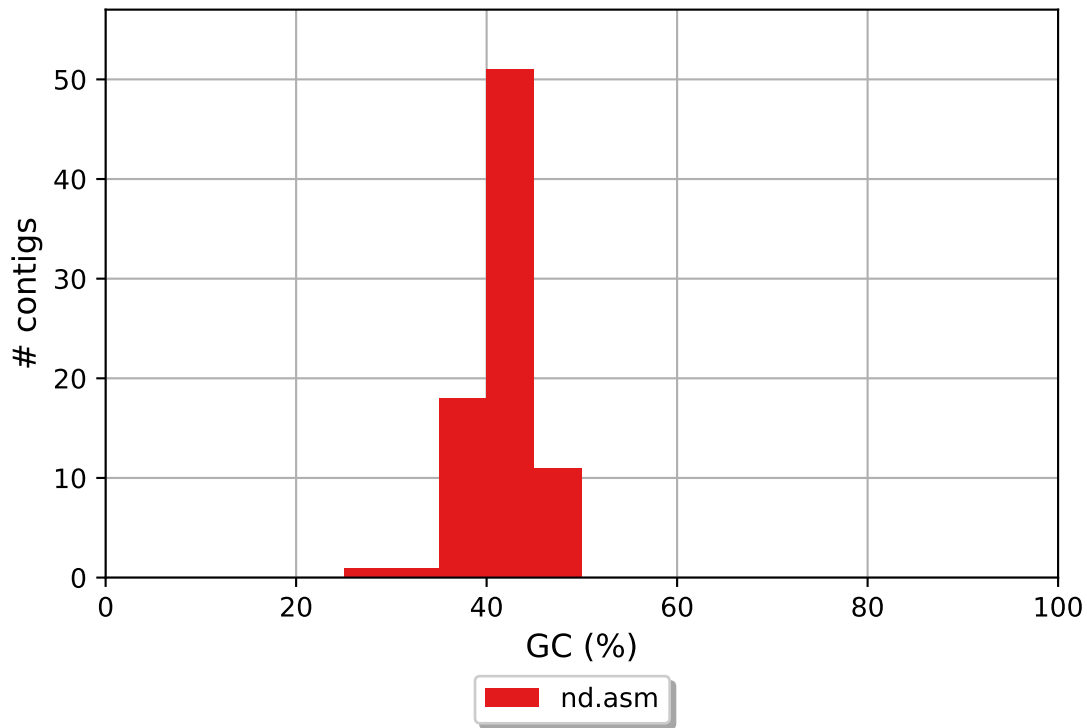


GC content

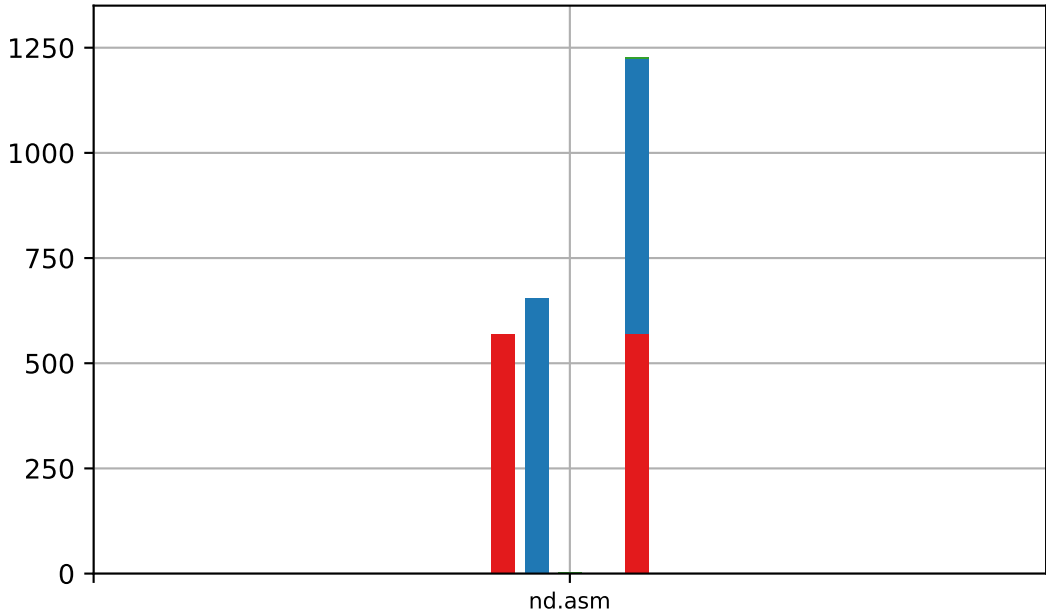


— nd.asm - - Reference

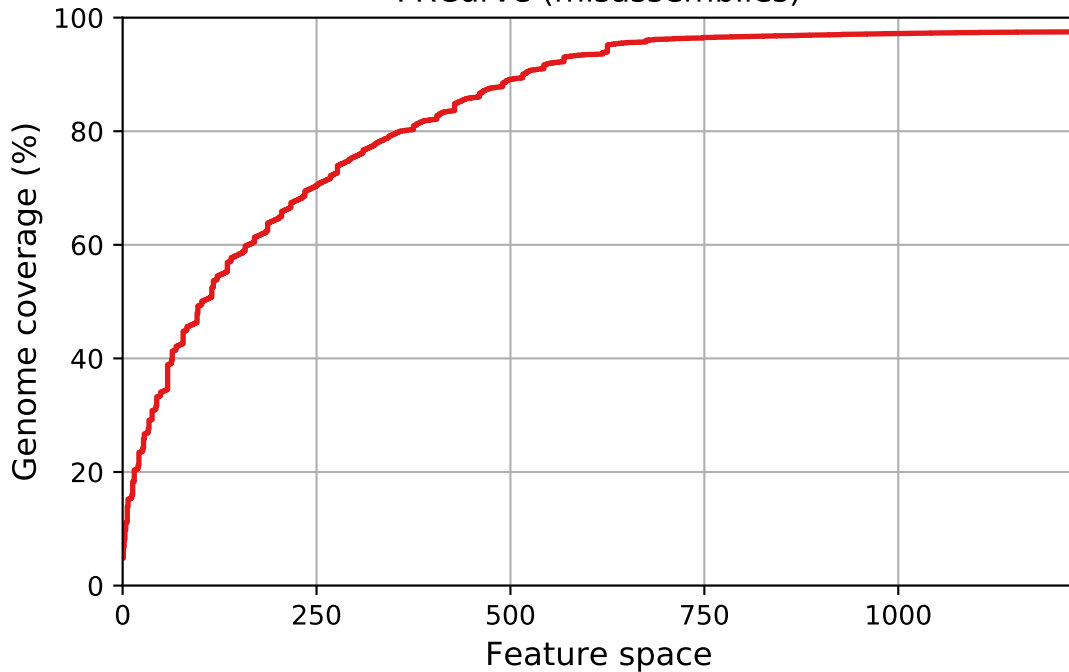
nd.asm GC content



Misassemblies

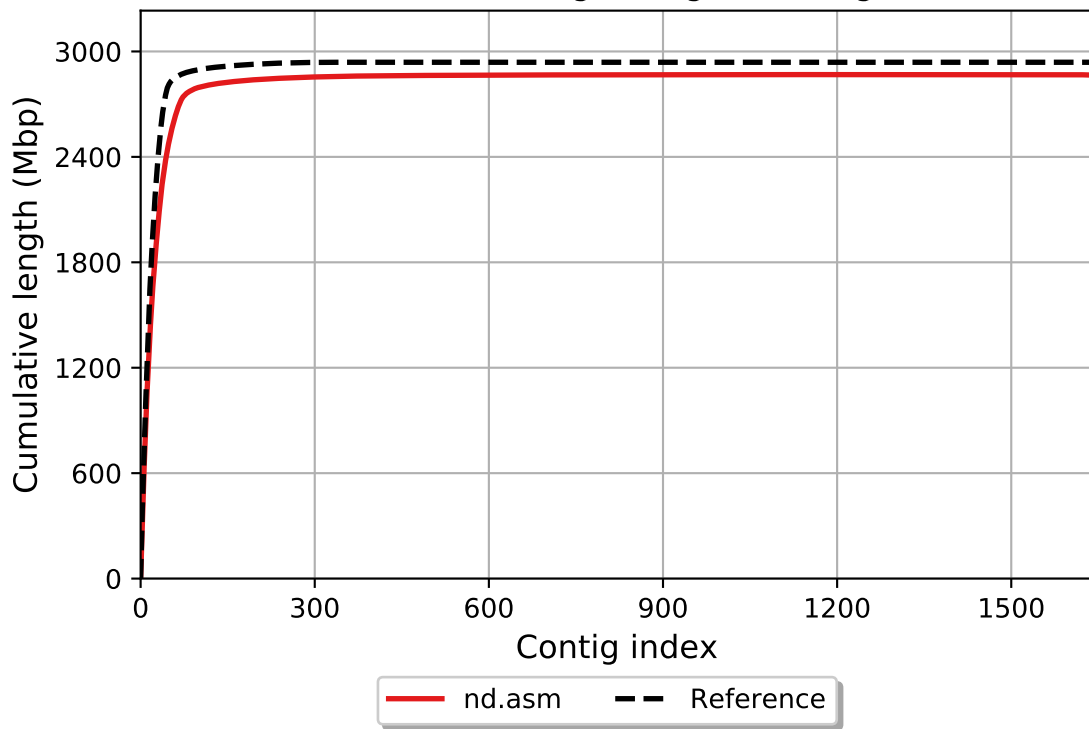


FRCurve (misassemblies)

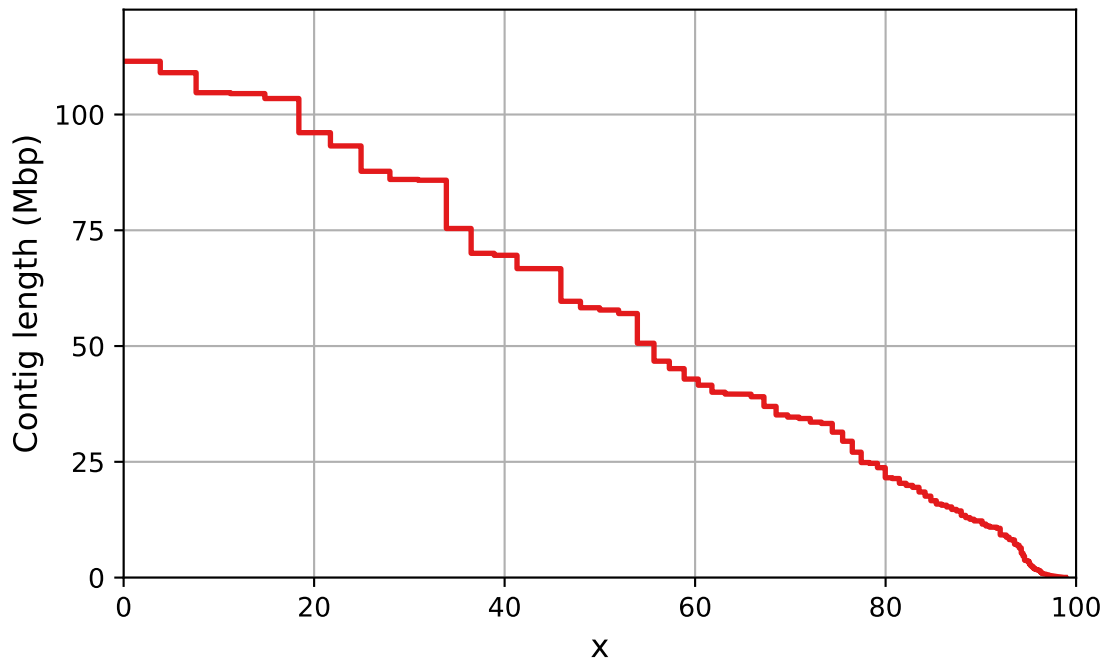


— nd.asm

Cumulative length (aligned contigs)

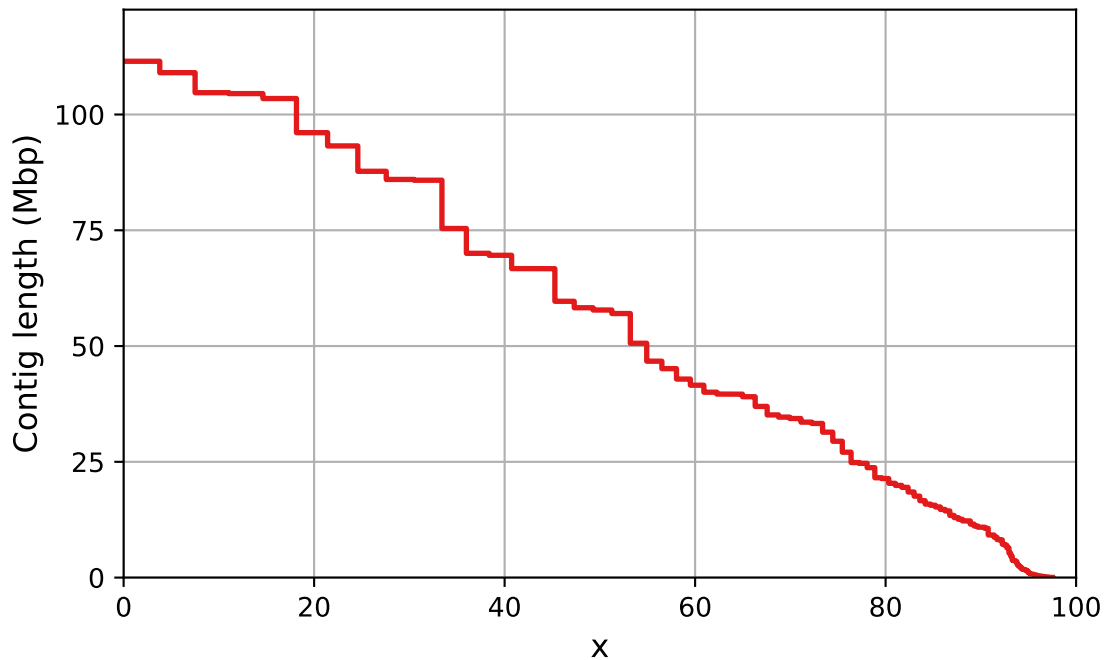


NAX



— nd.asm

NGAx



— nd.asm