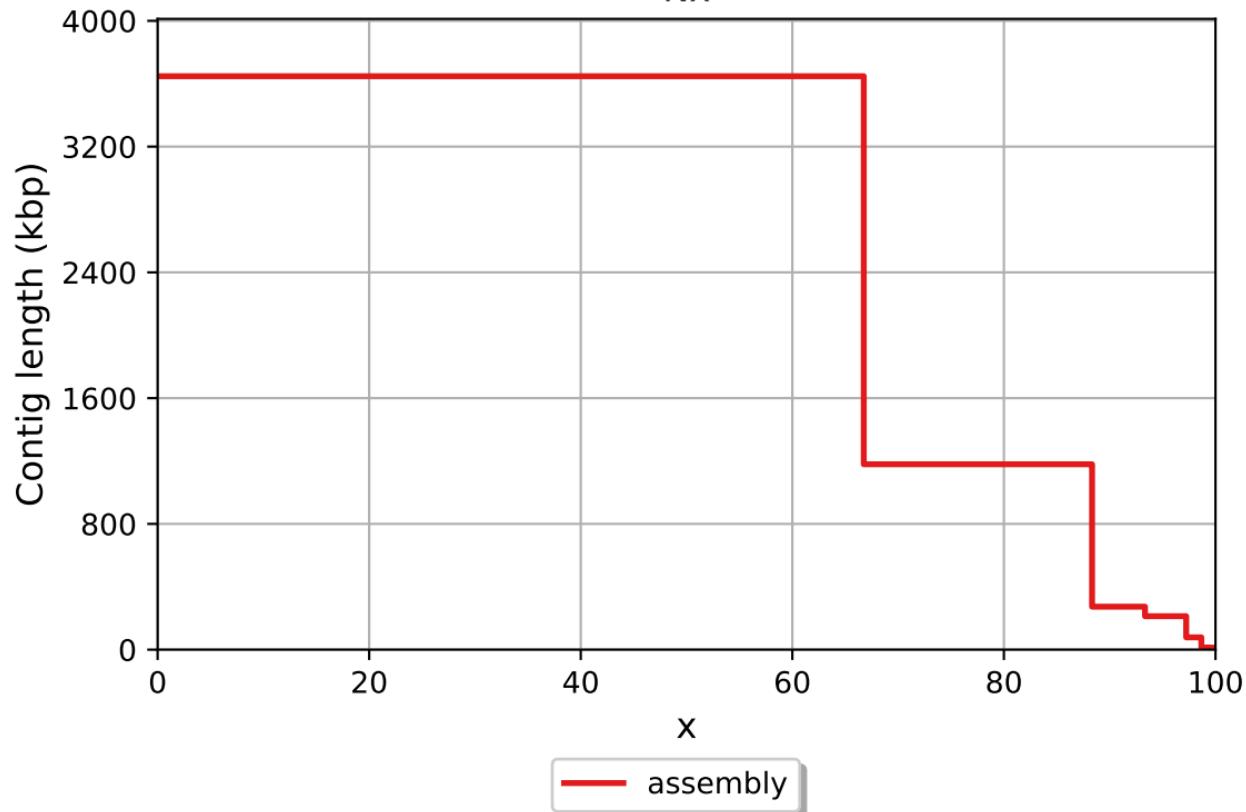


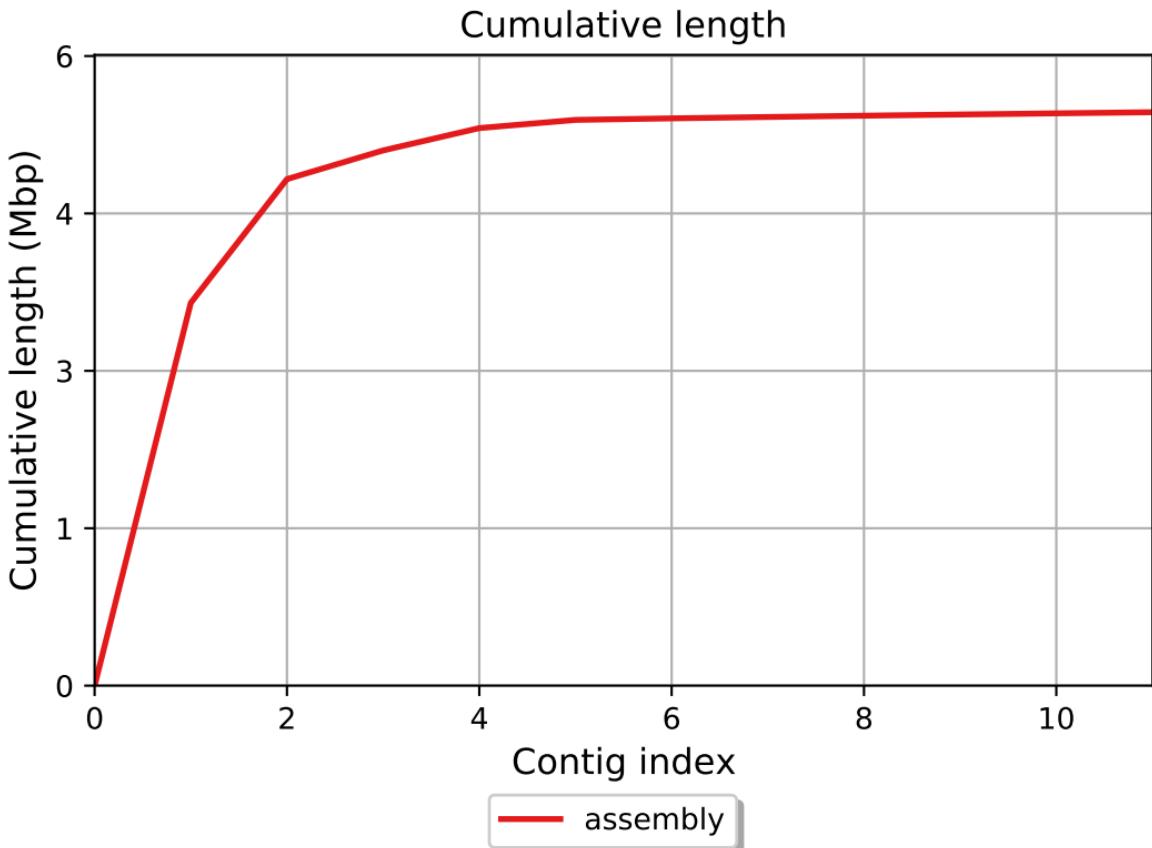
# Report

	assembly
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	5464622
Total length (>= 1000 bp)	5464622
Total length (>= 5000 bp)	5464622
Total length (>= 10000 bp)	5464622
Total length (>= 25000 bp)	5391563
Total length (>= 50000 bp)	5391563
# contigs	11
Largest contig	3647742
Total length	5464622
GC (%)	43.24
N50	3647742
N75	1179317
L50	1
L75	2
# N's per 100 kbp	0.00
# predicted genes (unique)	3884
# predicted genes (>= 0 bp)	3886 + 0 part
# predicted genes (>= 300 bp)	3323 + 0 part
# predicted genes (>= 1500 bp)	438 + 0 part
# predicted genes (>= 3000 bp)	52 + 0 part
# predicted rRNA genes	18 + 0 part

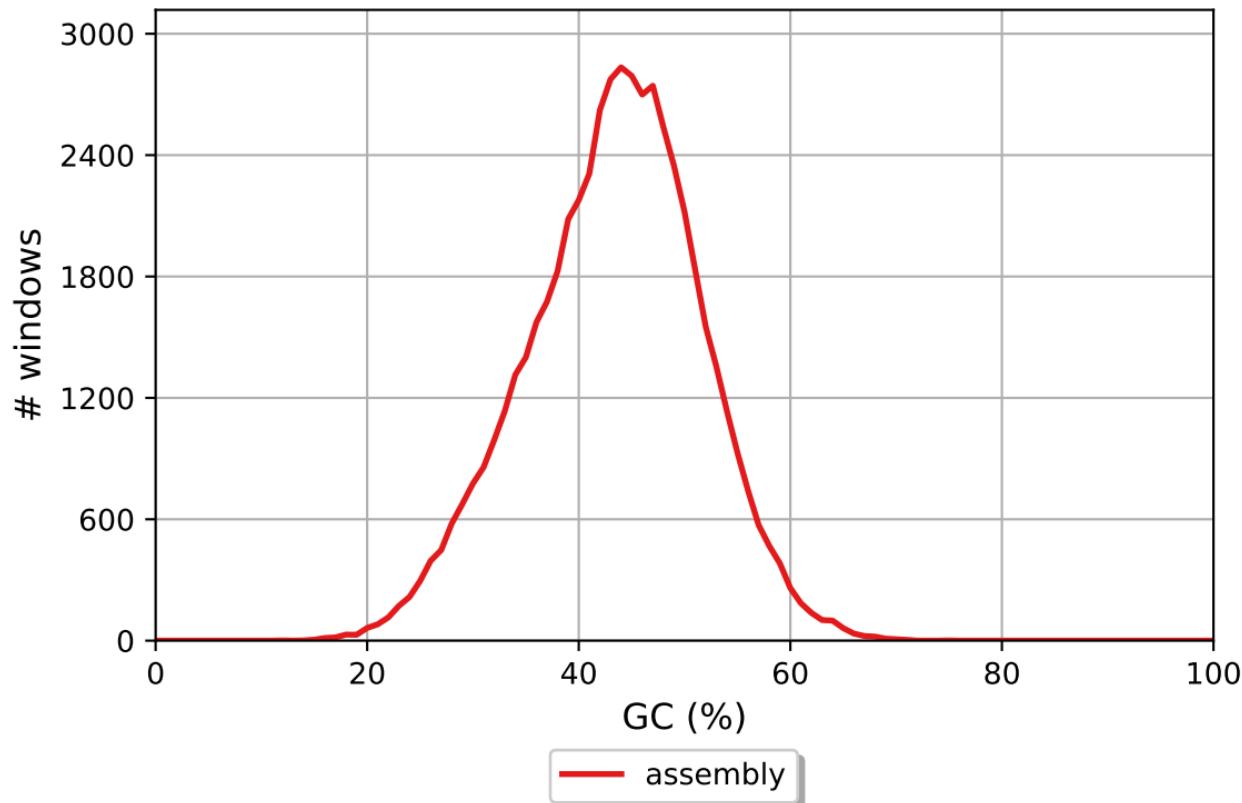
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx





## GC content



assembly GC content

