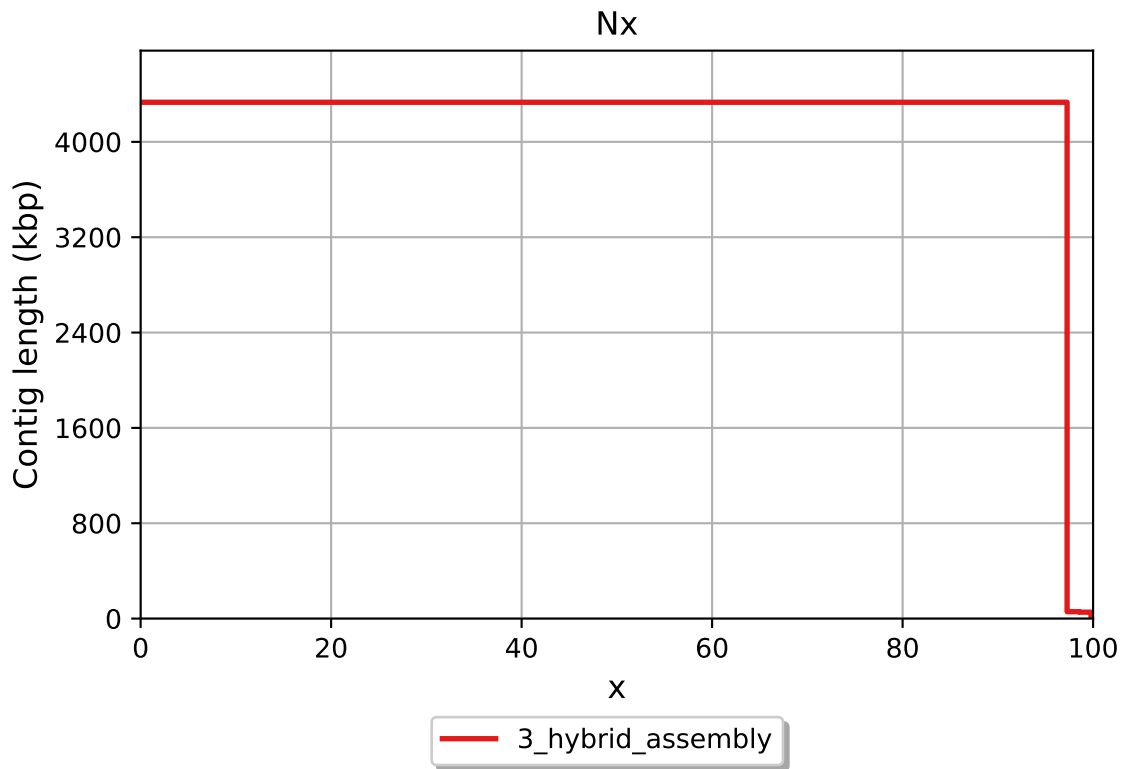
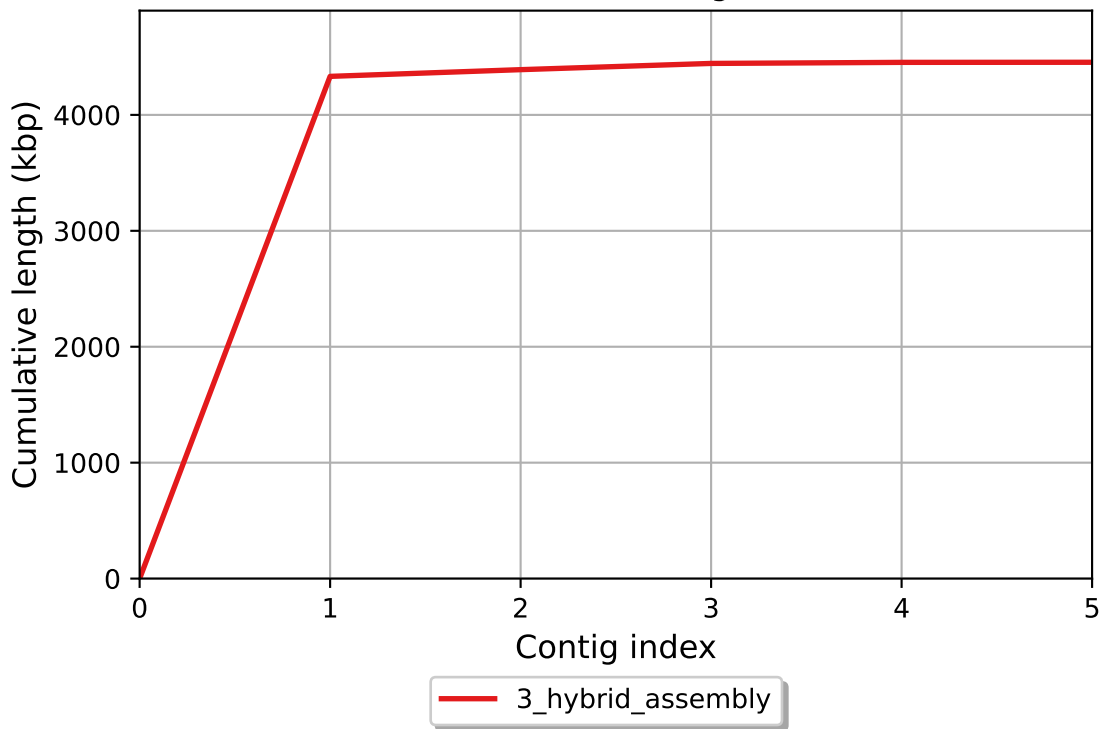


Report		3_hybrid_assembly
# contigs (>= 0 bp)		7
# contigs (>= 1000 bp)		4
# contigs (>= 5000 bp)		4
# contigs (>= 10000 bp)		3
# contigs (>= 25000 bp)		3
# contigs (>= 50000 bp)		3
Total length (>= 0 bp)		4454332
Total length (>= 1000 bp)		4453091
Total length (>= 5000 bp)		4453091
Total length (>= 10000 bp)		4443965
Total length (>= 25000 bp)		4443965
Total length (>= 50000 bp)		4443965
# contigs		5
Largest contig		4332314
Total length		4453949
Reference length		-
Estimated reference length		-
GC (%)		45.71
Reference GC (%)		-
N50		4332314
NG50		-
N90		4332314
NG90		-
auN		4215421.0
auNG		-
L50		1
LG50		-
L90		1
LG90		-
# total reads		-
# left		-
# right		-
Mapped (%)		-
Reference mapped (%)		-
Properly paired (%)		-
Reference properly paired (%)		-
Avg. coverage depth		-
Reference avg. coverage depth		-
Coverage >= 1x (%)		-
Reference coverage >= 1x (%)		-
# large blocks misassemblies		-
# misassemblies		-
# misassembled contigs		-
Misassembled contigs length		-
# local misassemblies		-
# scaffold gap ext. mis.		-
# scaffold gap loc. mis.		-
# structural variations		-
# possible TEs		-
# unaligned mis. contigs		-
# unaligned contigs		-
Unaligned length		-
Genome fraction (%)		-
Duplication ratio		-
Avg contig read support		-
# N's per 100 kbp		0.00
# mismatches per 100 kbp		-
# indels per 100 kbp		-
# genomic features		-
# operons		-
Complete BUSCO (%)		-
Partial BUSCO (%)		-
# predicted genes (unique)		2495
# predicted genes (>= 0 bp)		2520 + 0 part
# predicted genes (>= 300 bp)		2445 + 0 part
# predicted genes (>= 1500 bp)		816 + 0 part
# predicted genes (>= 3000 bp)		216 + 0 part
# predicted rRNA genes		15 + 0 part
Largest alignment		-
Total aligned length		-
NA50		-
NGA50		-
NA90		-
NGA90		-
auNA		-
auNGA		-
LA50		-
LGA50		-
LA90		-
LGA90		-
K-mer-based compl. (%)		-
K-mer-based cor. length (%)		-
K-mer-based mis. length (%)		-

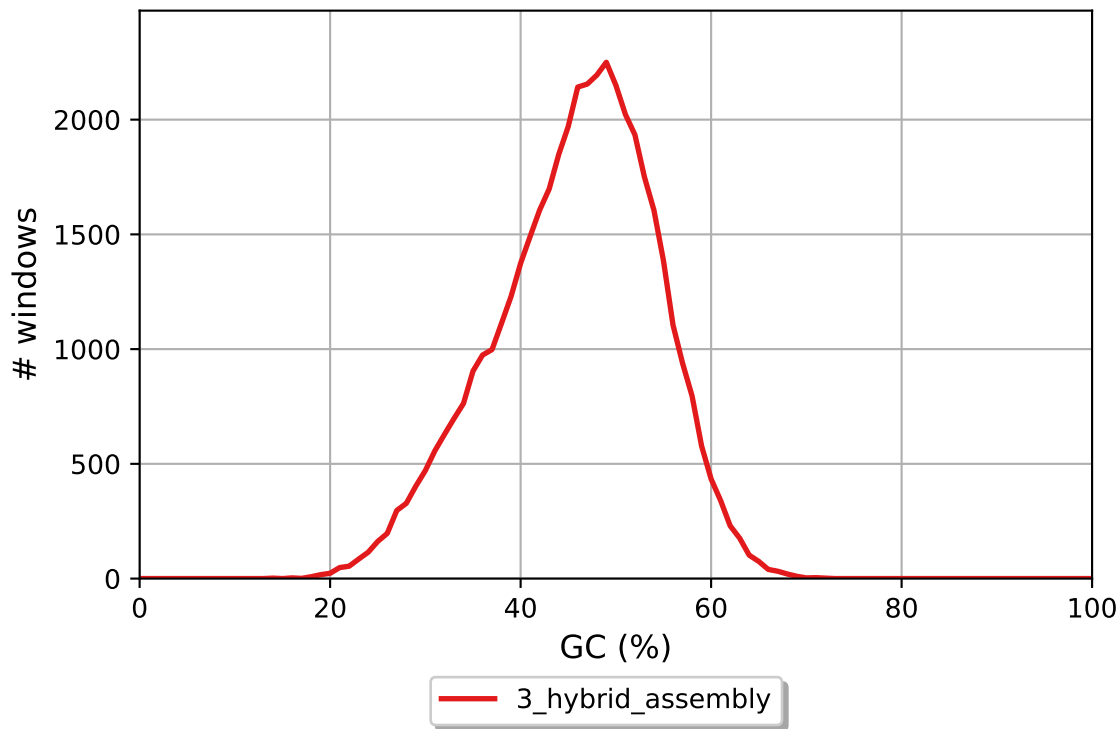
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



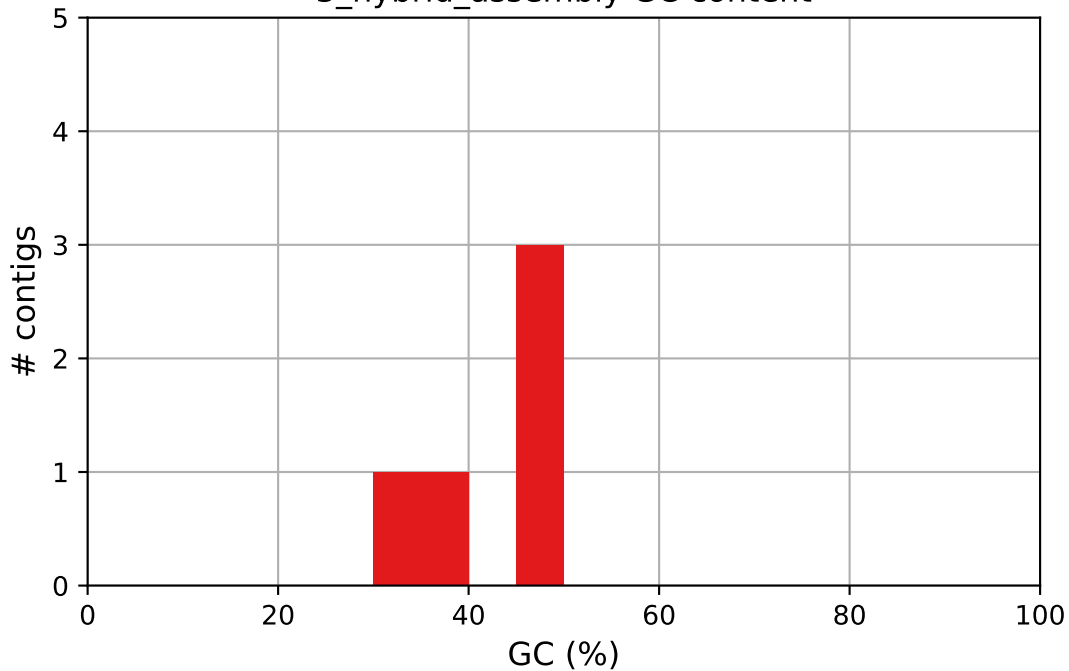
Cumulative length



GC content



3_hybrid_assembly GC content



3_hybrid_assembly