

Report

	spades
# contigs (>= 0 bp)	15269
# contigs (>= 1000 bp)	2357
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	9480477
Total length (>= 1000 bp)	3815843
Total length (>= 5000 bp)	133432
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	15134
Largest contig	9825
Total length	9459172
GC (%)	56.06
N50	801
N75	452
L50	3376
L75	7317
# total reads	68205781
# left	34082806
# right	34082806
Mapped (%)	99.49
Properly paired (%)	80.31
Avg. coverage depth	1067
Coverage >= 1x (%)	99.98
# N's per 100 kbp	0.00
Complete BUSCO (%)	54.73
Partial BUSCO (%)	16.22
# predicted genes (unique)	11813
# predicted genes (>= 0 bp)	8618 + 3198 part
# predicted genes (>= 300 bp)	6085 + 2406 part
# predicted genes (>= 1500 bp)	118 + 28 part
# predicted genes (>= 3000 bp)	7 + 0 part
# predicted rRNA genes	11 + 3 part

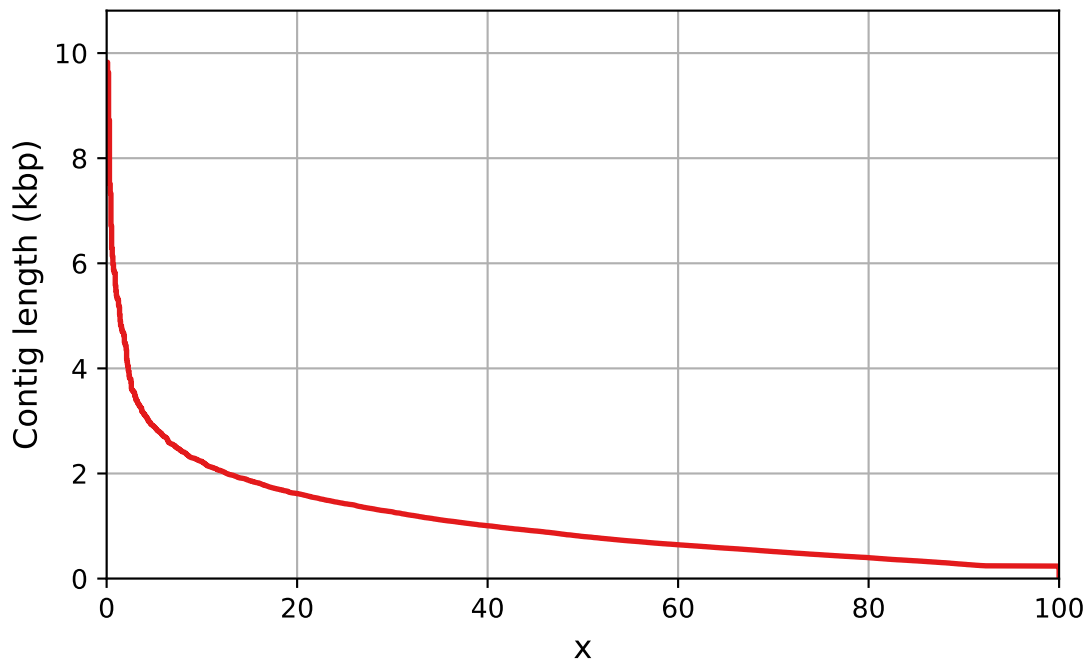
All statistics are based on contigs of size >= 200 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Reads report

	spades
# total reads	68205781
# left	34082806
# right	34082806
# mapped	67860537
Mapped (%)	99.49
# properly paired	54774378
Properly paired (%)	80.31
# singletons	158246
Singletons (%)	0.23
# misjoint mates	12866048
Misjoint mates (%)	18.86
Avg. coverage depth	1067
Coverage $\geq 1x$ (%)	99.98
Coverage $\geq 5x$ (%)	99.78
Coverage $\geq 10x$ (%)	99.41

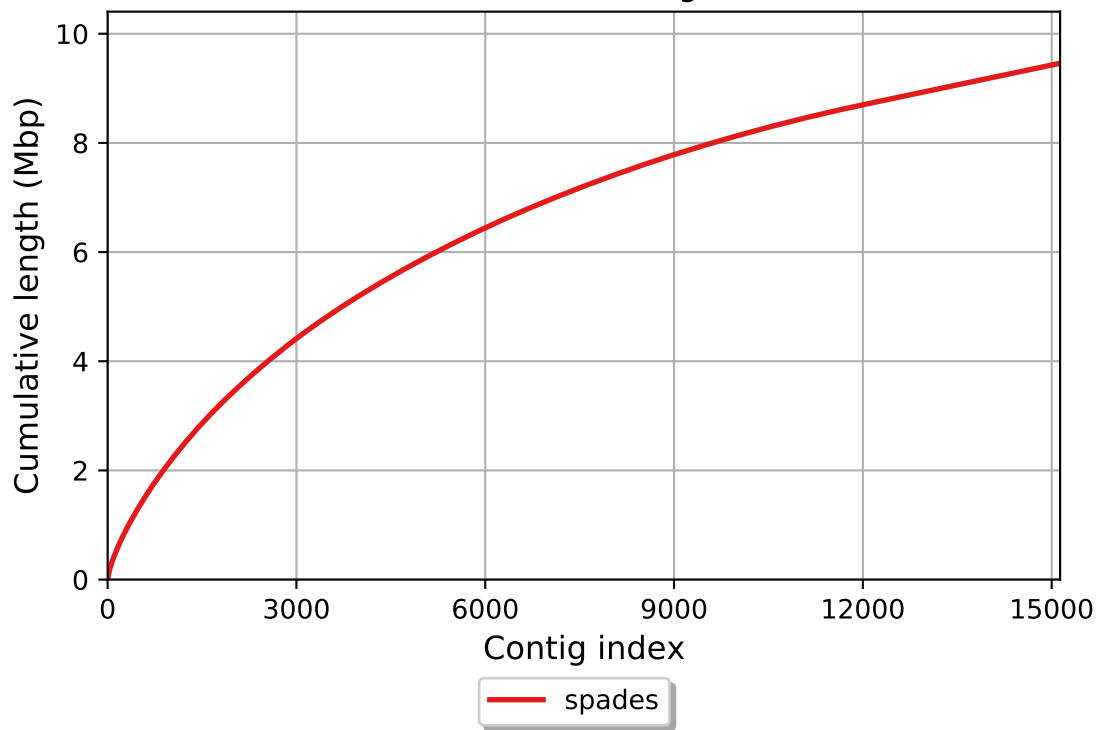
All statistics are based on contigs of size ≥ 200 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

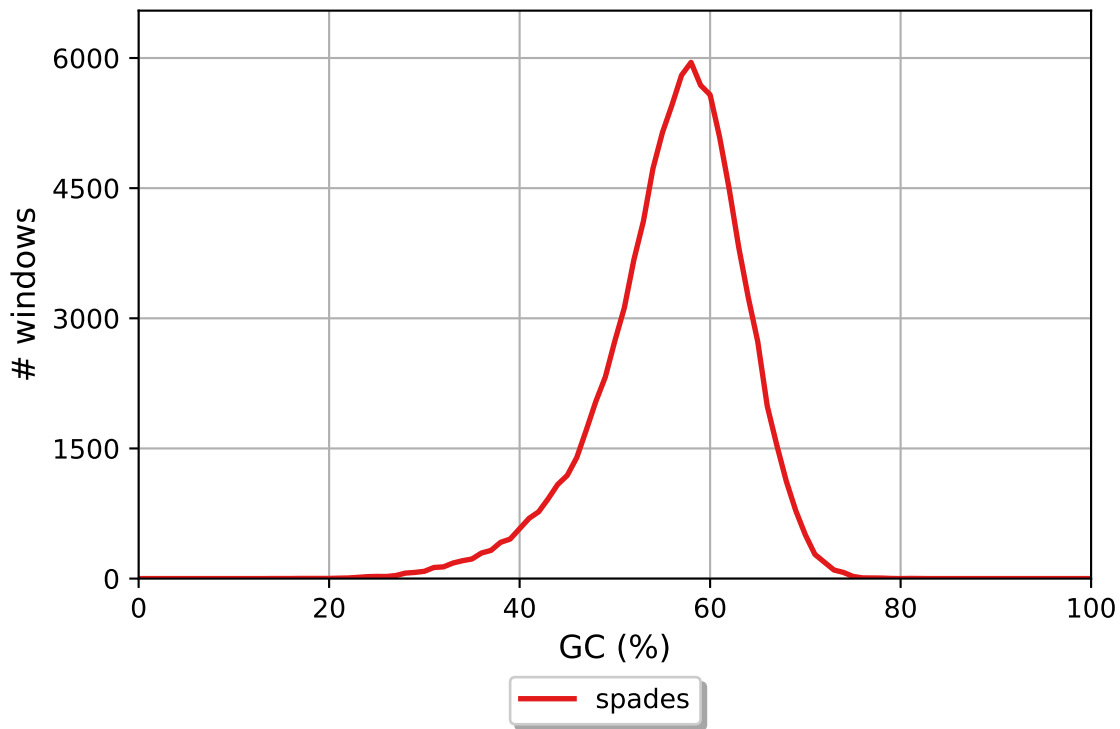


spades

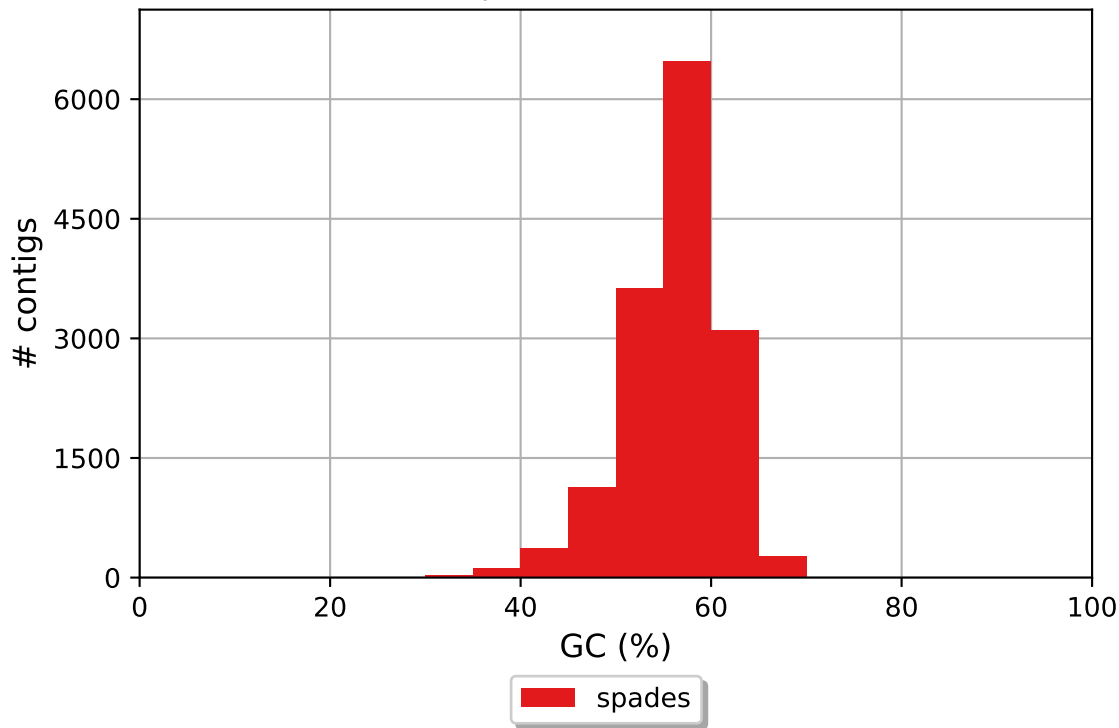
Cumulative length



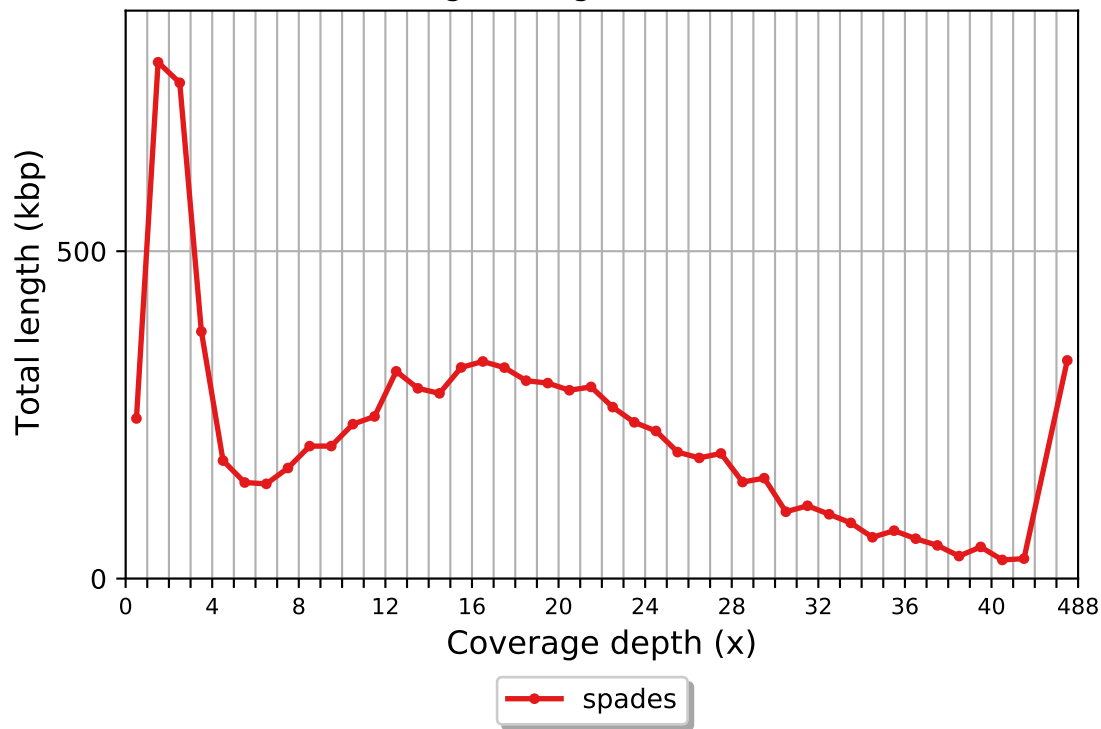
GC content



spades GC content



Coverage histogram (bin size: 1x)



spades coverage histogram (bin size: 1x)

