

Report

	SPAdes-default
# contigs (>= 0 bp)	1483
# contigs (>= 1000 bp)	182
# contigs (>= 5000 bp)	95
# contigs (>= 10000 bp)	69
# contigs (>= 25000 bp)	43
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	5614218
Total length (>= 1000 bp)	5306059
Total length (>= 5000 bp)	5111847
Total length (>= 10000 bp)	4916102
Total length (>= 25000 bp)	4536140
Total length (>= 50000 bp)	4043208
# contigs	256
Largest contig	313048
Total length	5356818
Reference length	4641652
GC (%)	50.59
Reference GC (%)	50.79
N50	130187
NG50	158316
N75	53593
NG75	72478
L50	13
LG50	11
L75	30
LG75	22
# misassemblies	125
# misassembled contigs	41
Misassembled contigs length	4363302
# local misassemblies	172
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# unaligned contigs	162 + 66 part
Unaligned length	1355064
Genome fraction (%)	85.937
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2317.46
# indels per 100 kbp	28.80
# genomic features	7687 + 397 part
Largest alignment	160579
Total aligned length	3995045
NA50	29024
NGA50	33470
NGA75	14167
LA50	51
LGA50	39
LGA75	90

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).

Misassemblies report

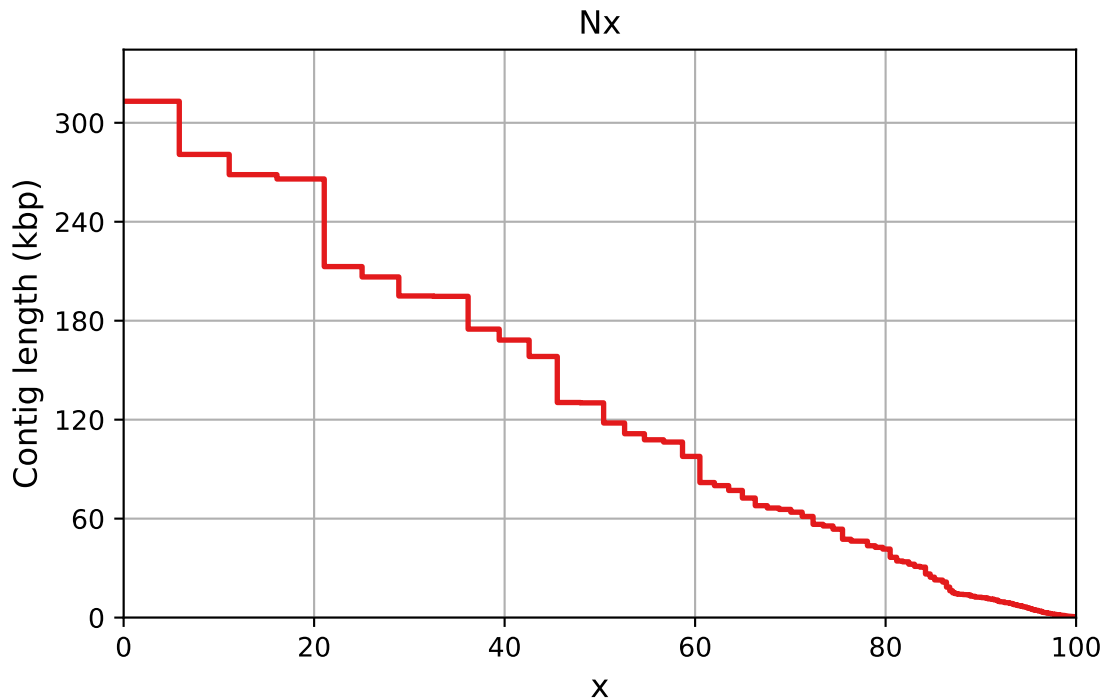
	SPAdes-default
# misassemblies	125
# contig misassemblies	125
# c. relocations	125
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	41
Misassembled contigs length	4363302
# local misassemblies	172
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	92441
# indels	1149
# indels (<= 5 bp)	1009
# indels (> 5 bp)	140
Indels length	4671

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).

Unaligned report

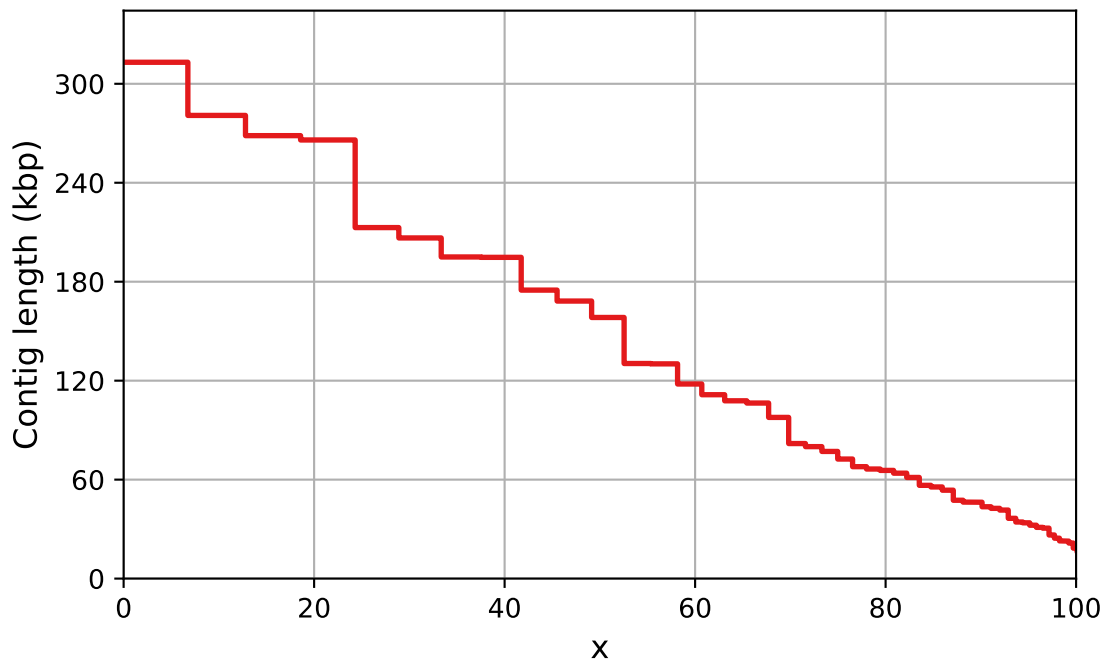
	SPAdes-default
# fully unaligned contigs	162
Fully unaligned length	550541
# partially unaligned contigs	66
Partially unaligned length	804523
# N's	0

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).



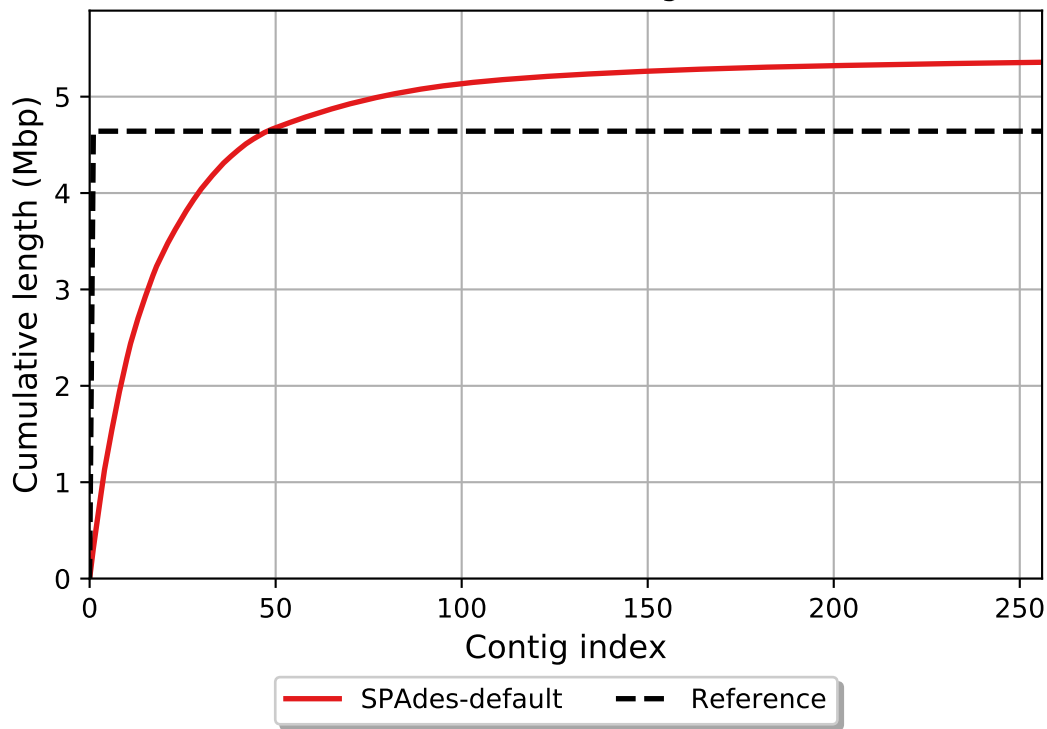
— SPAdes-default

NGx

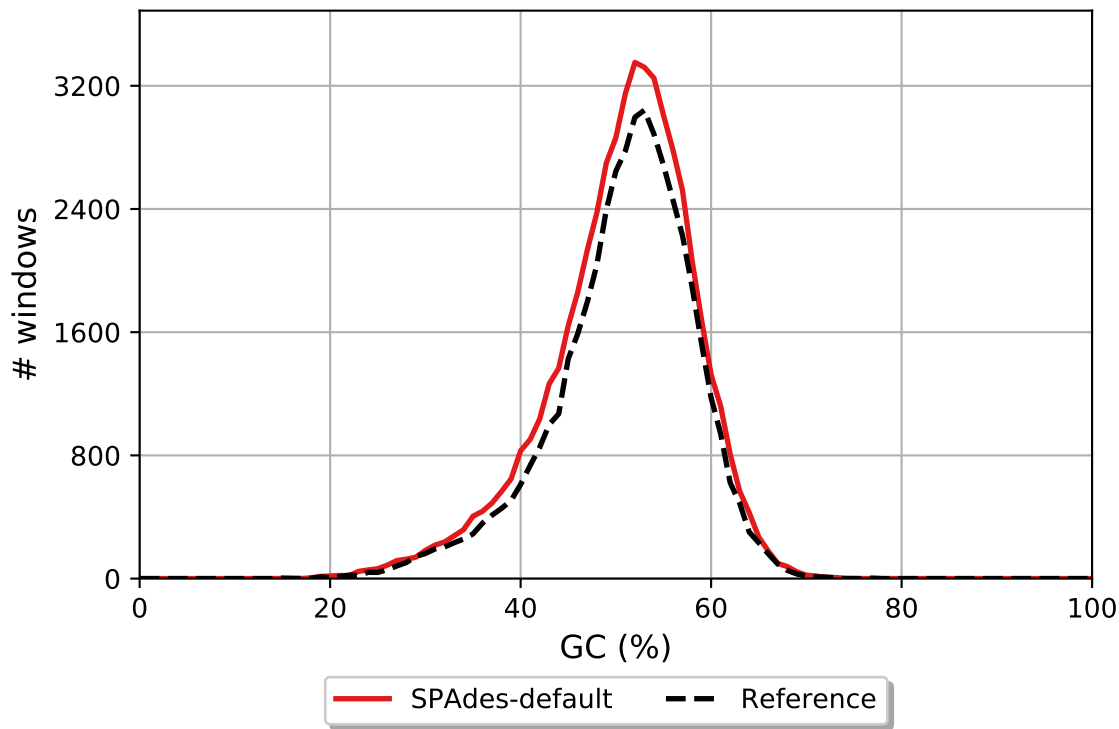


— SPAdes-default

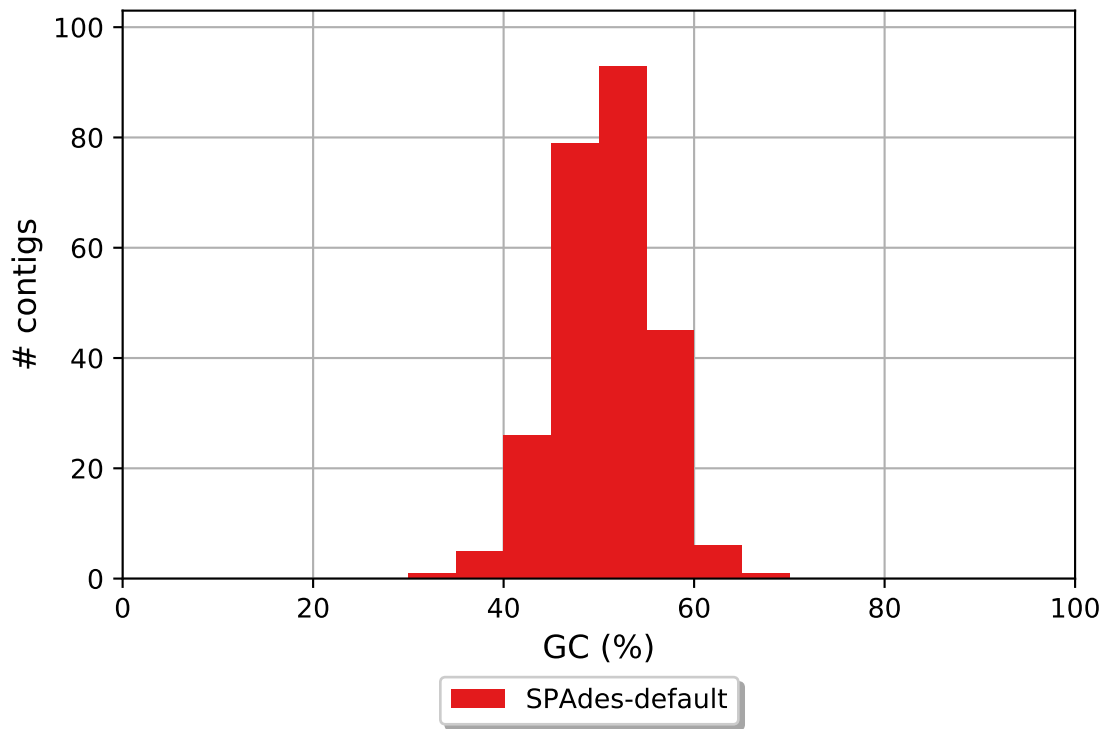
Cumulative length



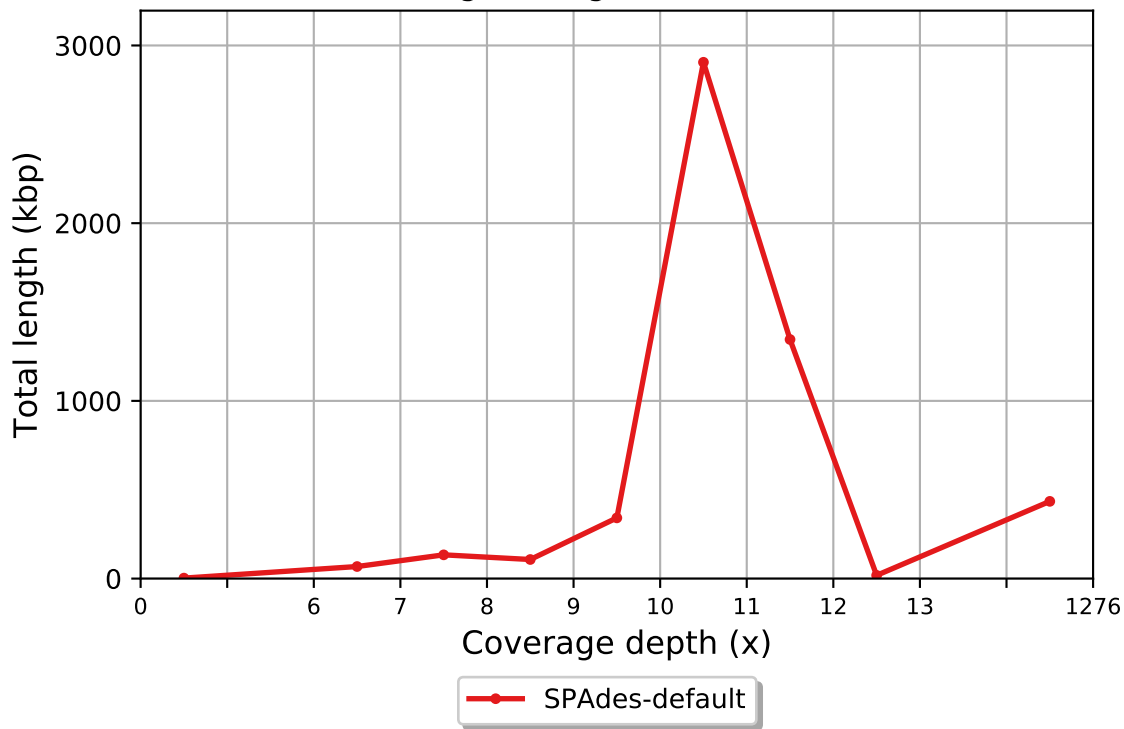
GC content



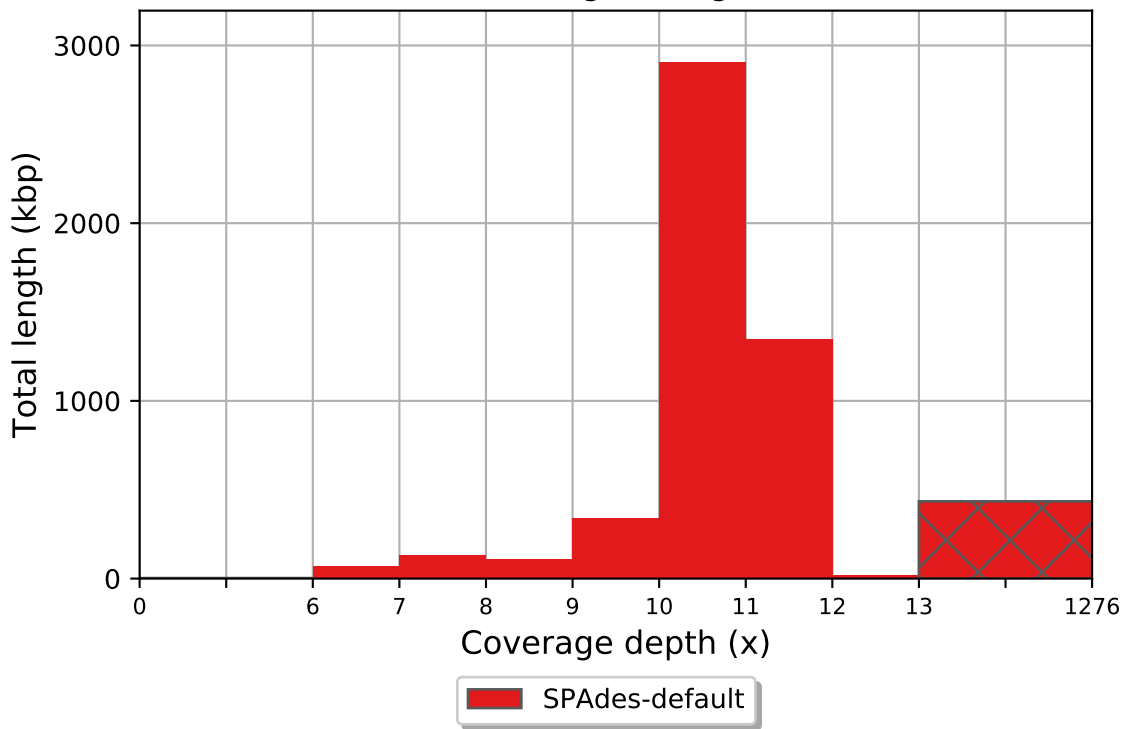
SPAdes-default GC content



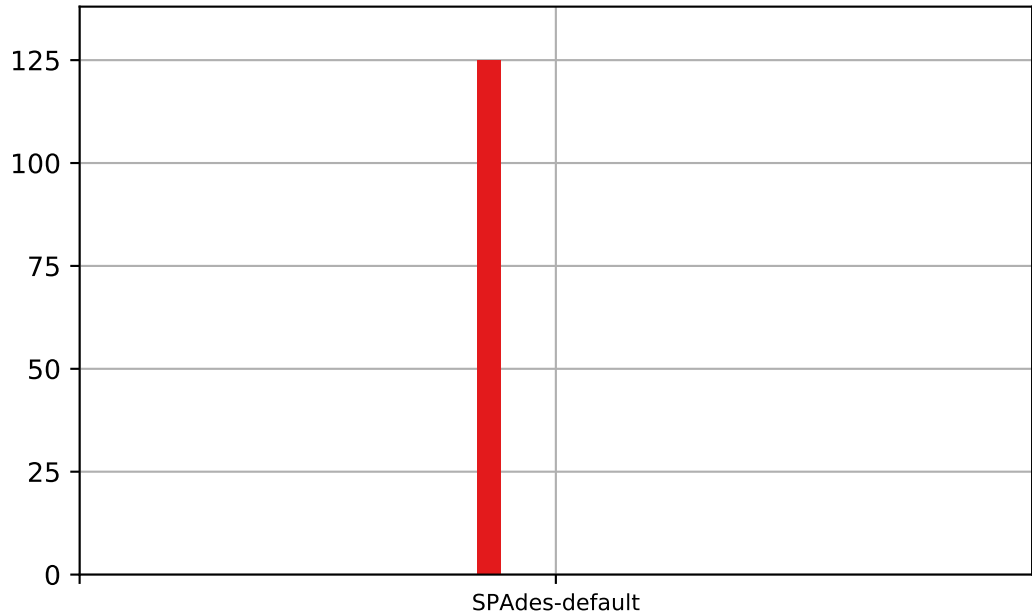
Coverage histogram (bin size: 1x)



SPAdes-default coverage histogram (bin size: 1x)

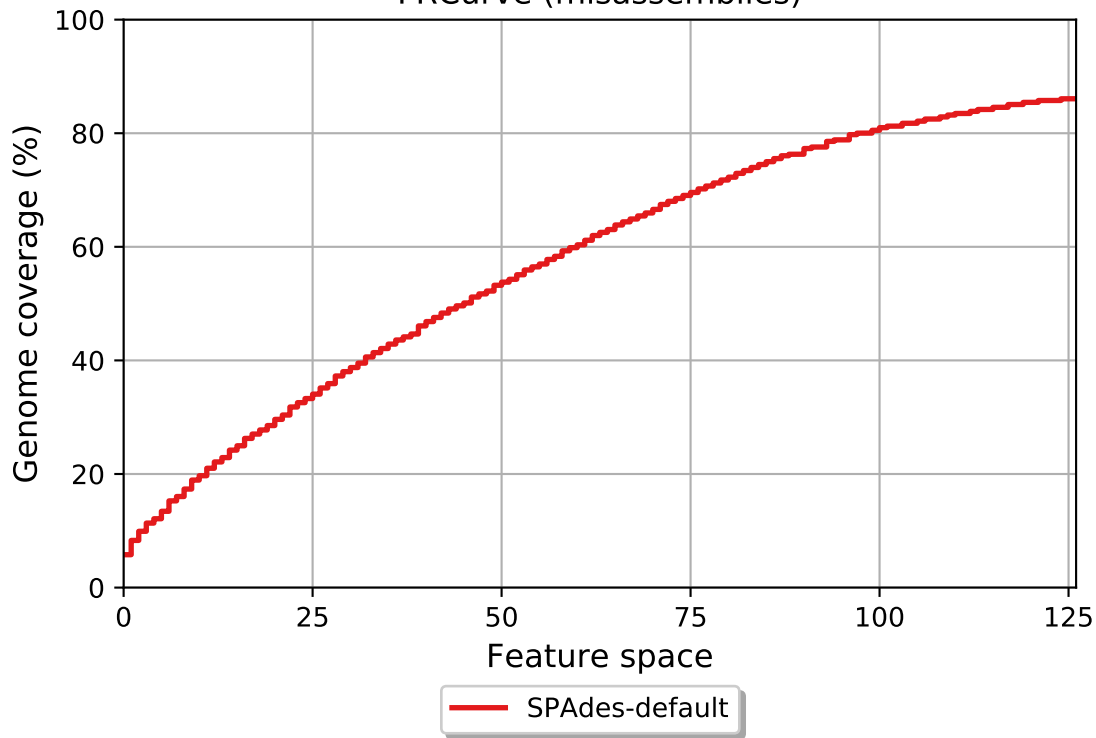


Misassemblies

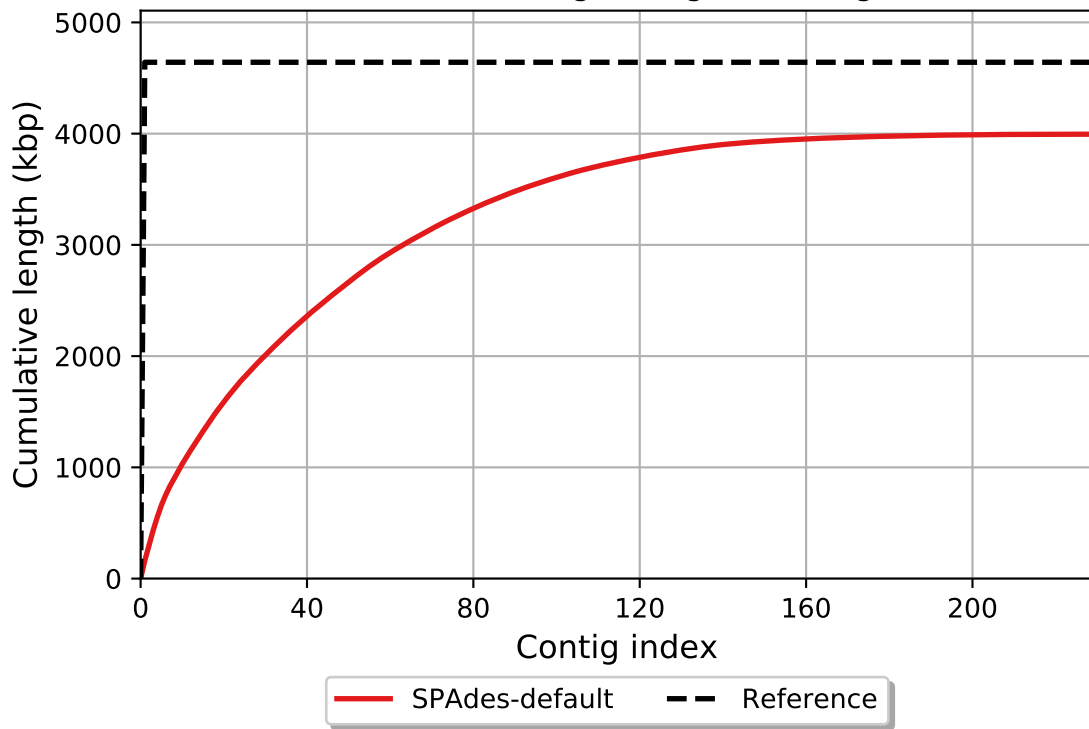


 # relocations

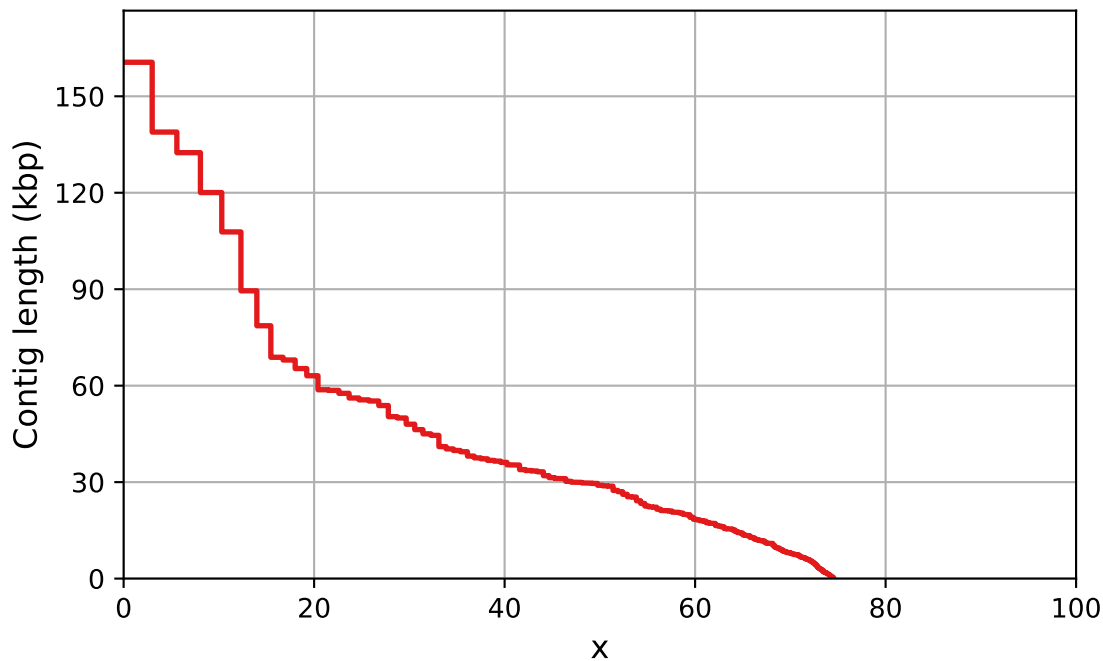
FRCurve (misassemblies)



Cumulative length (aligned contigs)

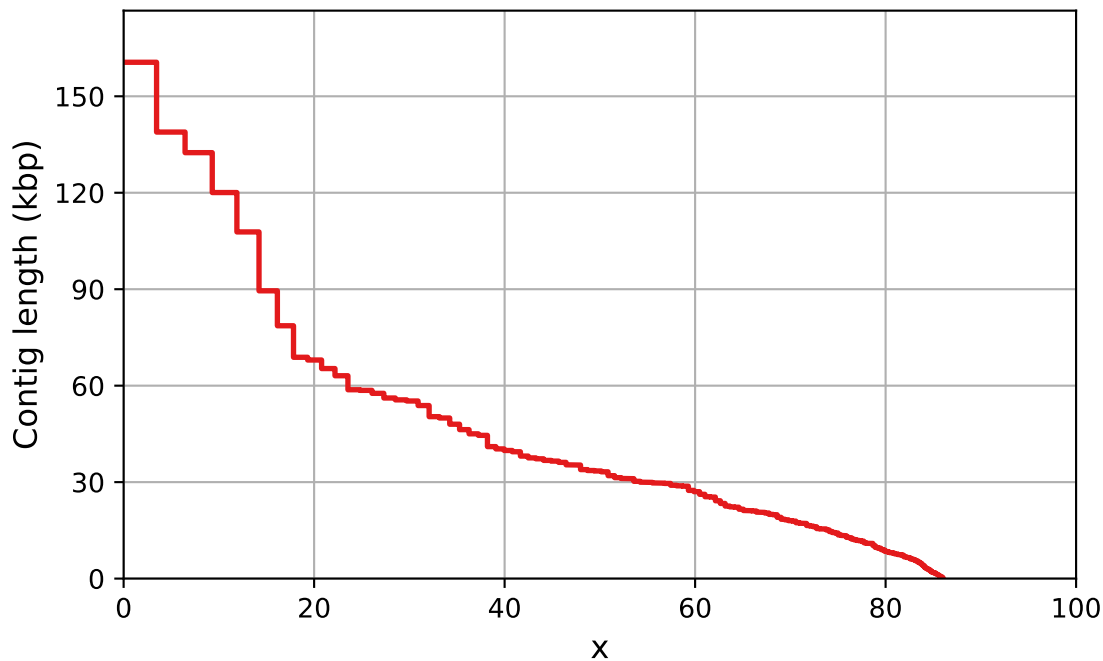


NAx



— SPAdes-default

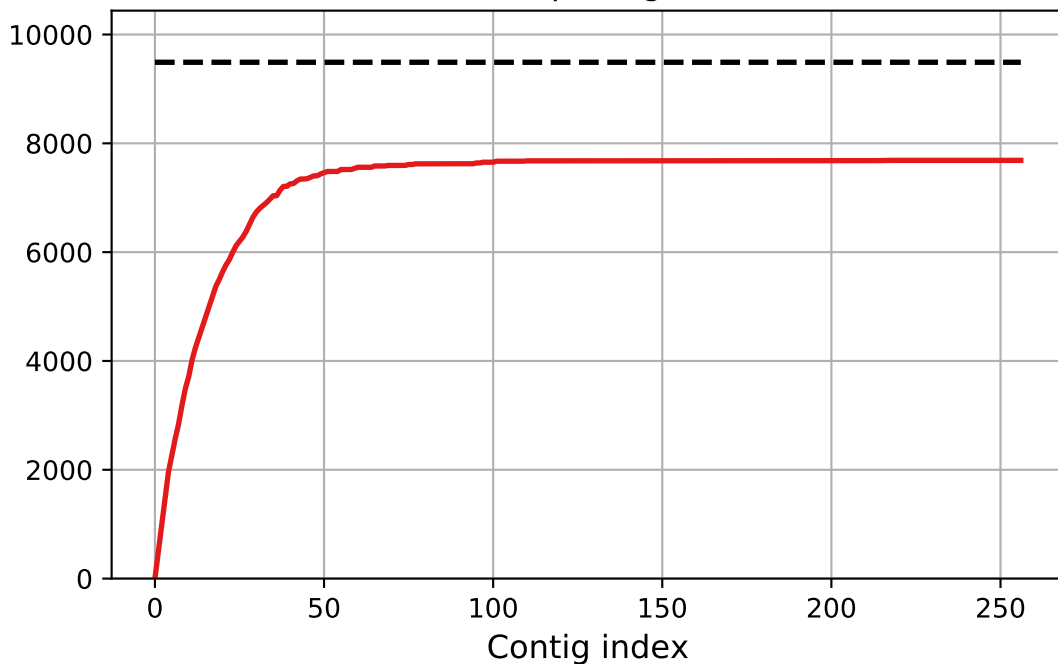
NGAx



— SPAdes-default

Cumulative # complete genomic features

Cumulative # complete genomic features



— SPAdes-default - - - Reference

FRCurve (genomic features)

