

Report

	final_assembly_canu_and_spades_node3_120419
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	3164587
Total length (>= 1000 bp)	3164587
Total length (>= 5000 bp)	3164587
Total length (>= 10000 bp)	3136755
Total length (>= 25000 bp)	3125355
Total length (>= 50000 bp)	3057031
# contigs	9
Largest contig	2773702
Total length	3164587
Reference length	3168410
GC (%)	37.72
Reference GC (%)	37.70
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	3052405
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.935
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.22
# indels per 100 kbp	5.10
Largest alignment	2195416
Total aligned length	3164587
NA50	2195416
NGA50	2195416
NA75	578286
NGA75	578286
LA50	1
LGA50	1
LA75	2
LGA75	2

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

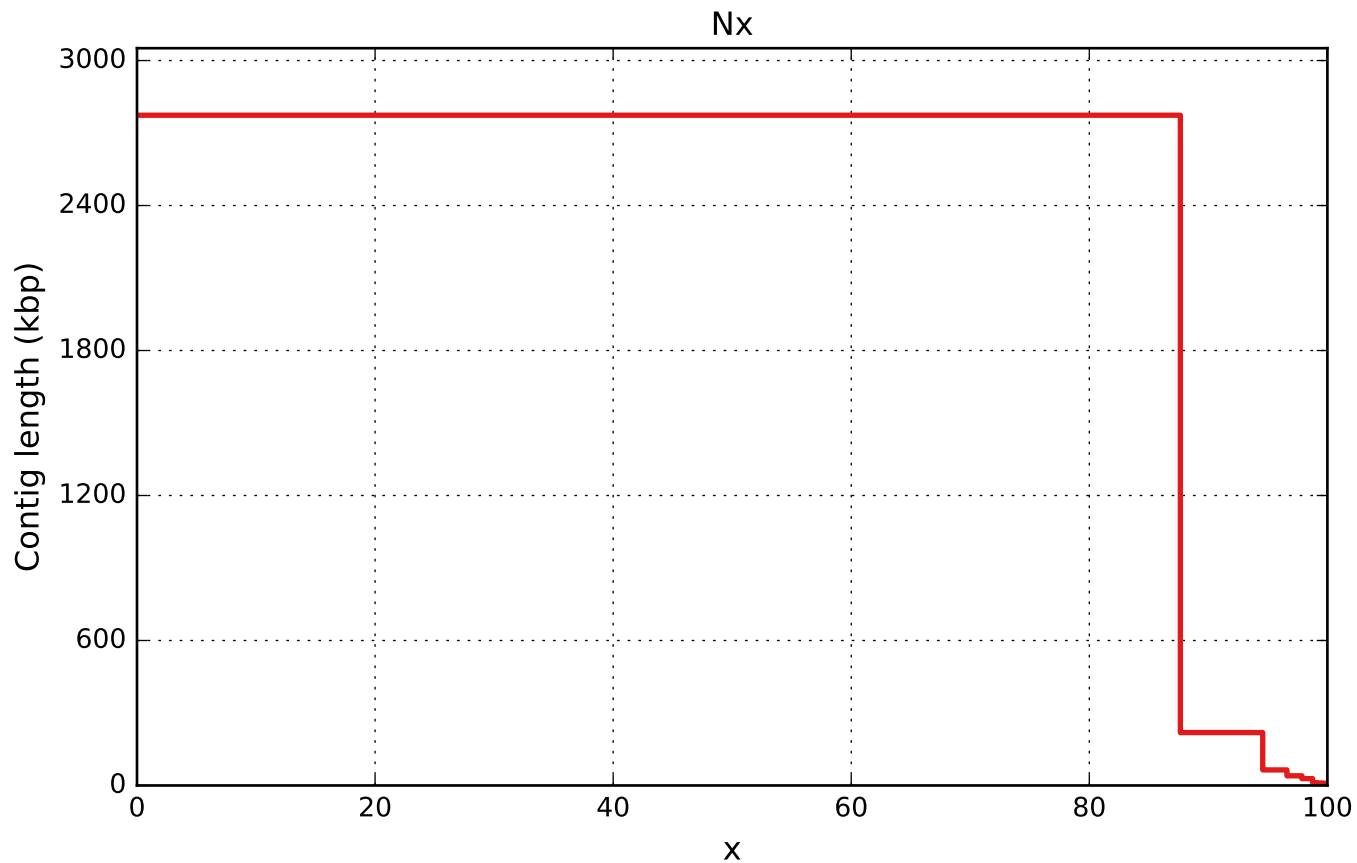
	final_assembly_canu_and_spades_node3_120419
# misassemblies	7
# relocations	5
# translocations	2
# inversions	0
# misassembled contigs	5
Misassembled contigs length	3052405
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	195
# indels	160
# indels (≤ 5 bp)	152
# indels (> 5 bp)	8
Indels length	287

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).

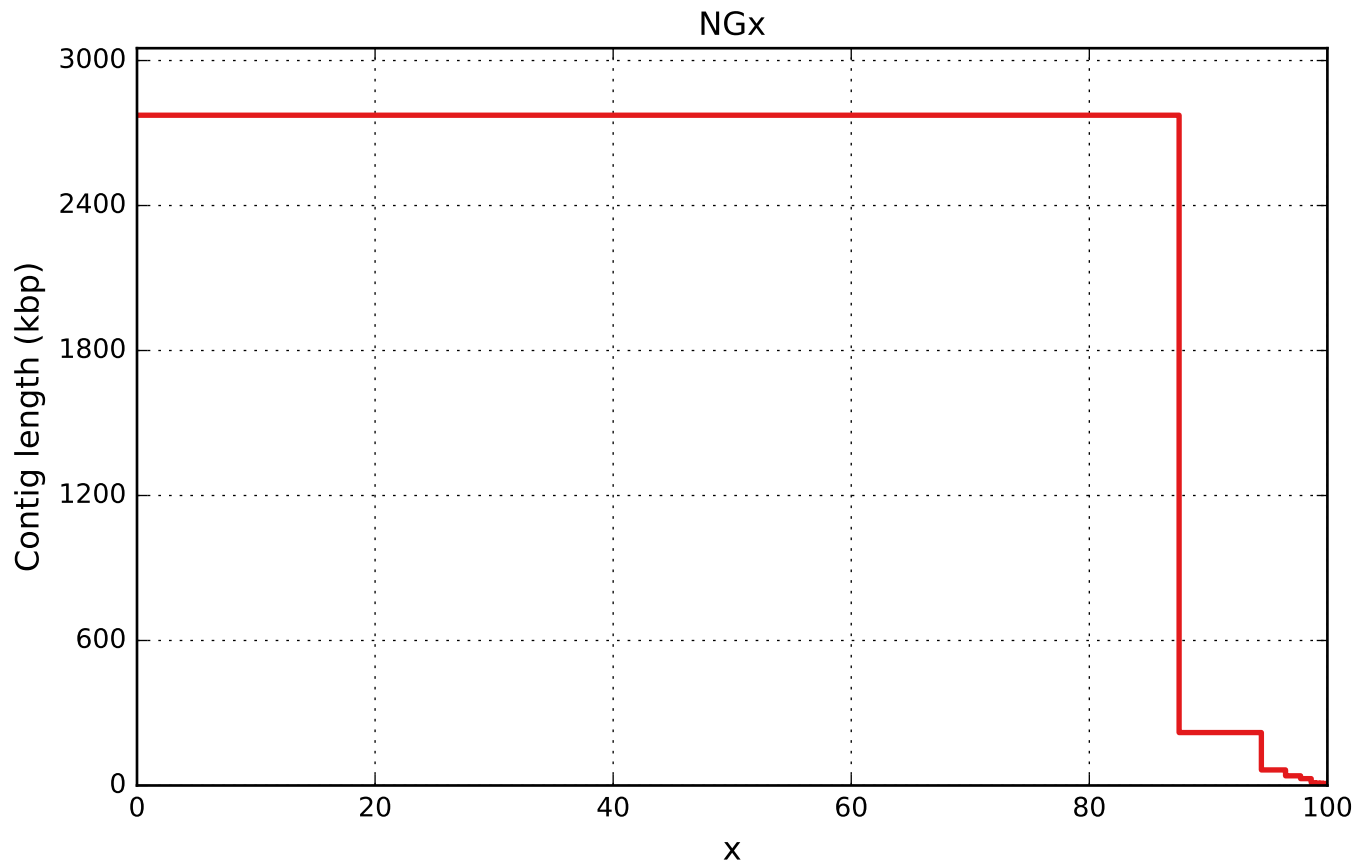
Unaligned report

	final_assembly_canu_and_spades_node3_120419
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

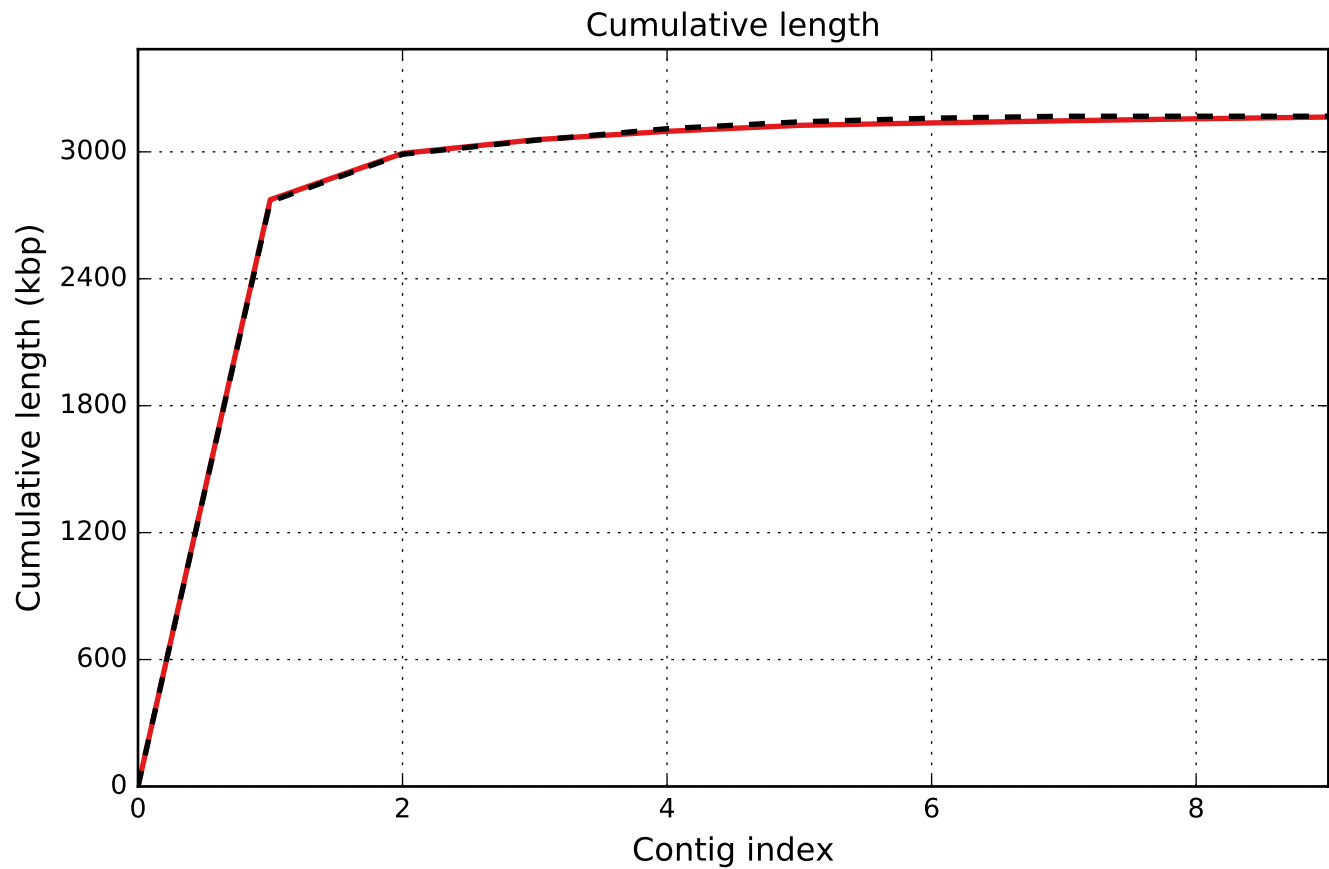
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



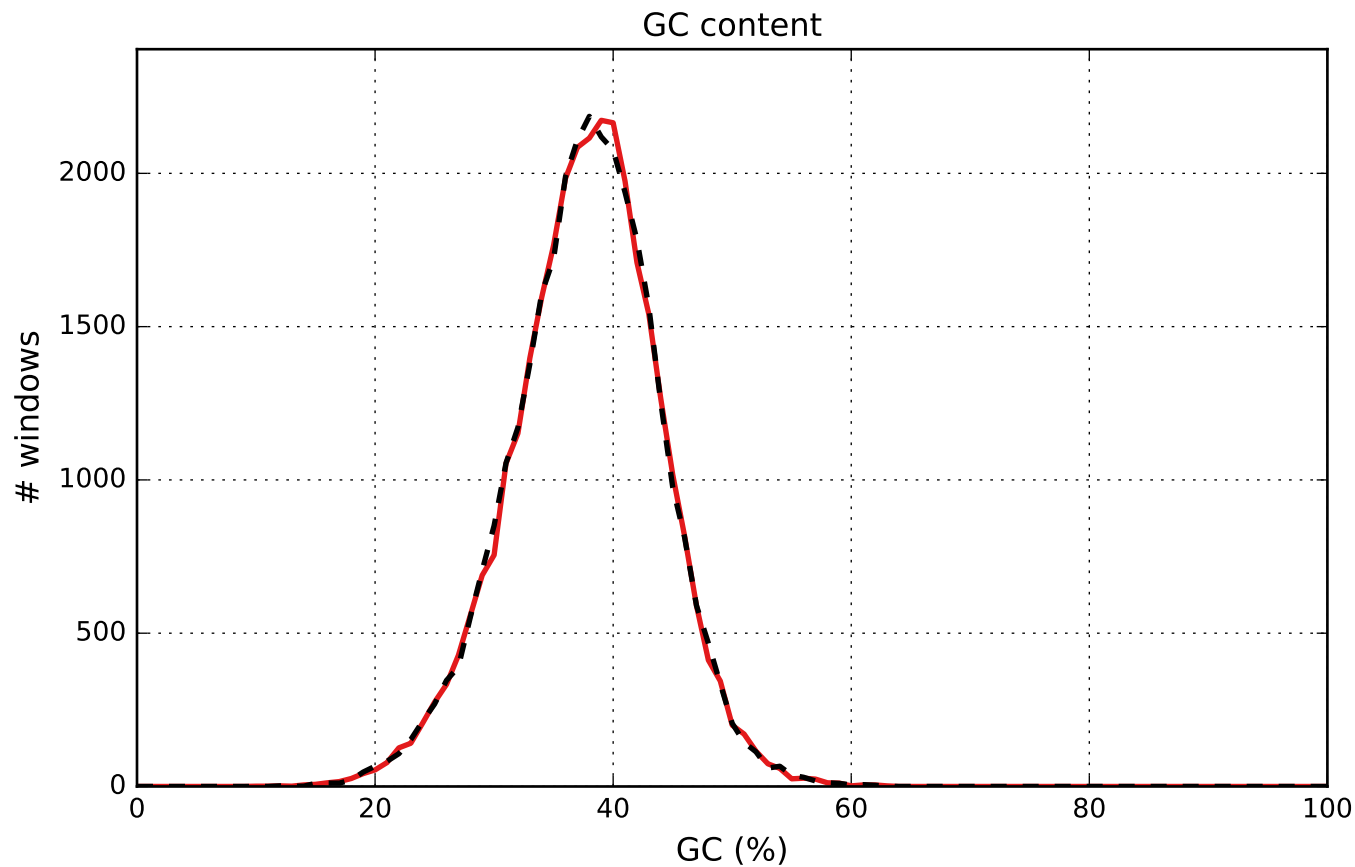
— final_assembly_canu_and_spades_node3_120419



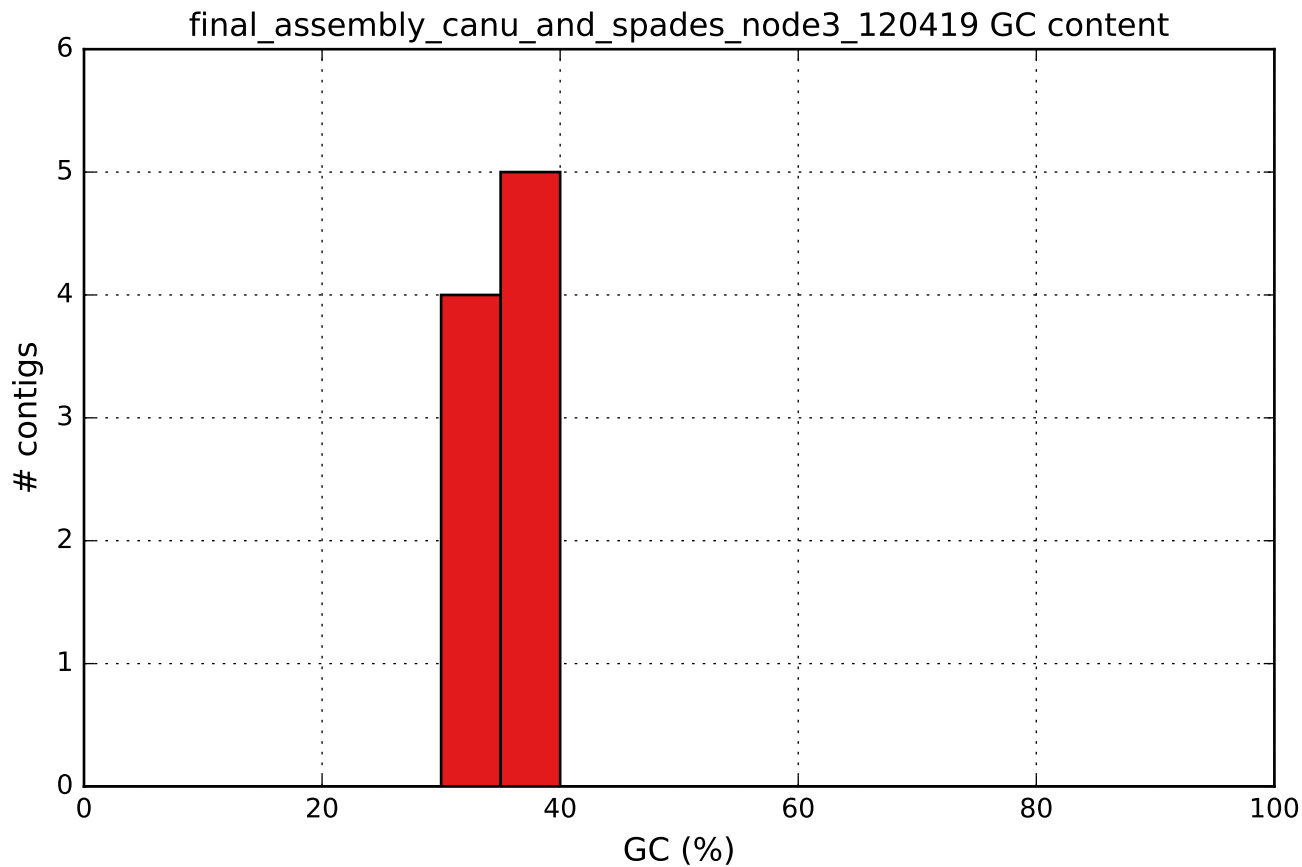
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— final_assembly_canu_and_spades_node3_120419 - - Reference

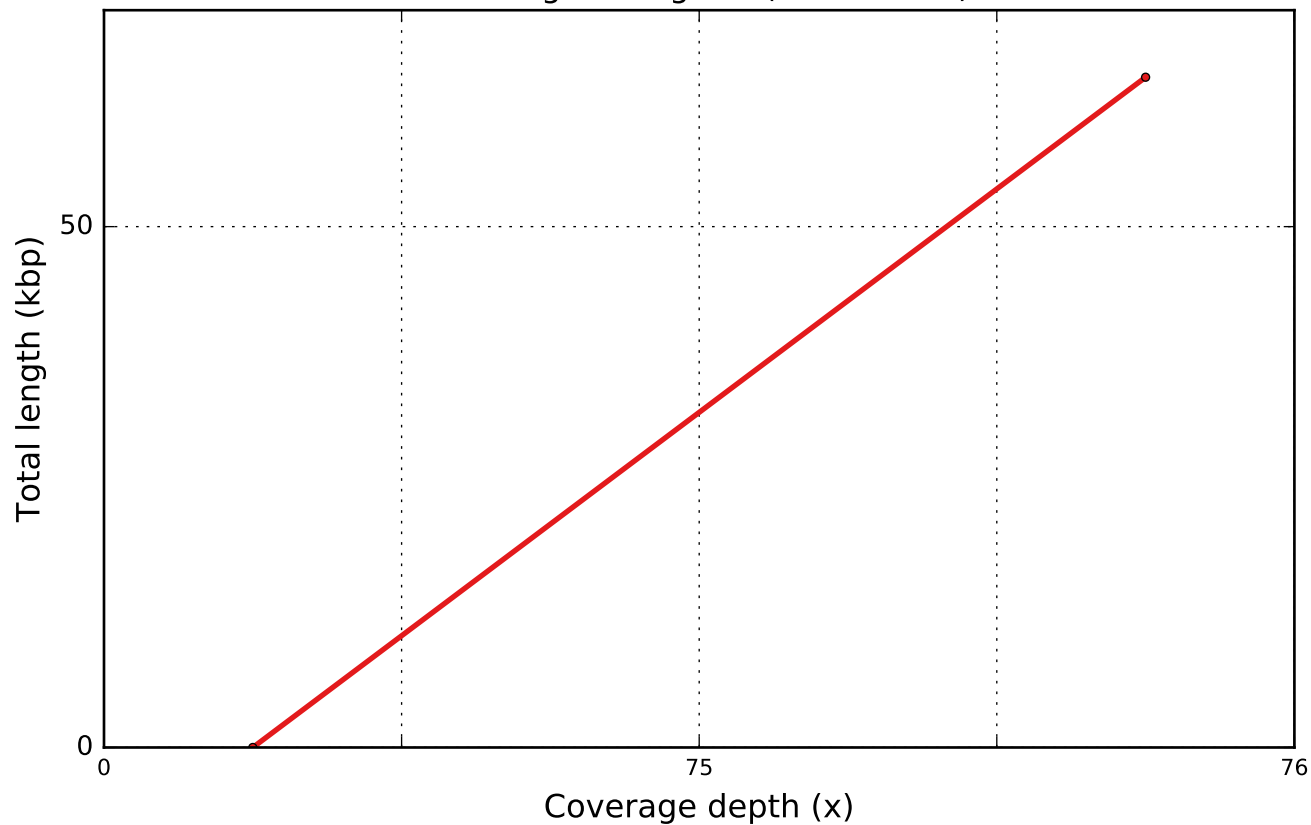


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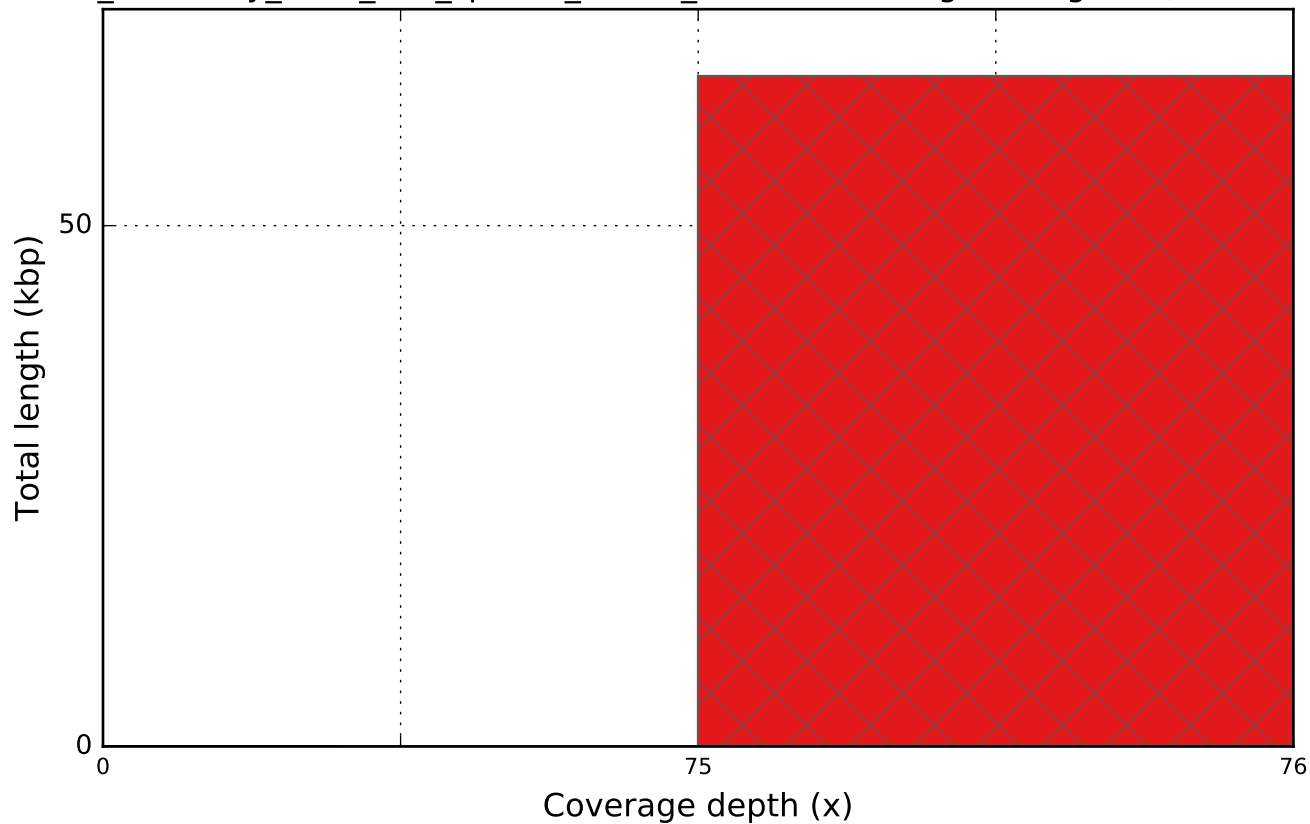
final_assembly_canu_and_spades_node3_120419

Coverage histogram (bin size: 1x)

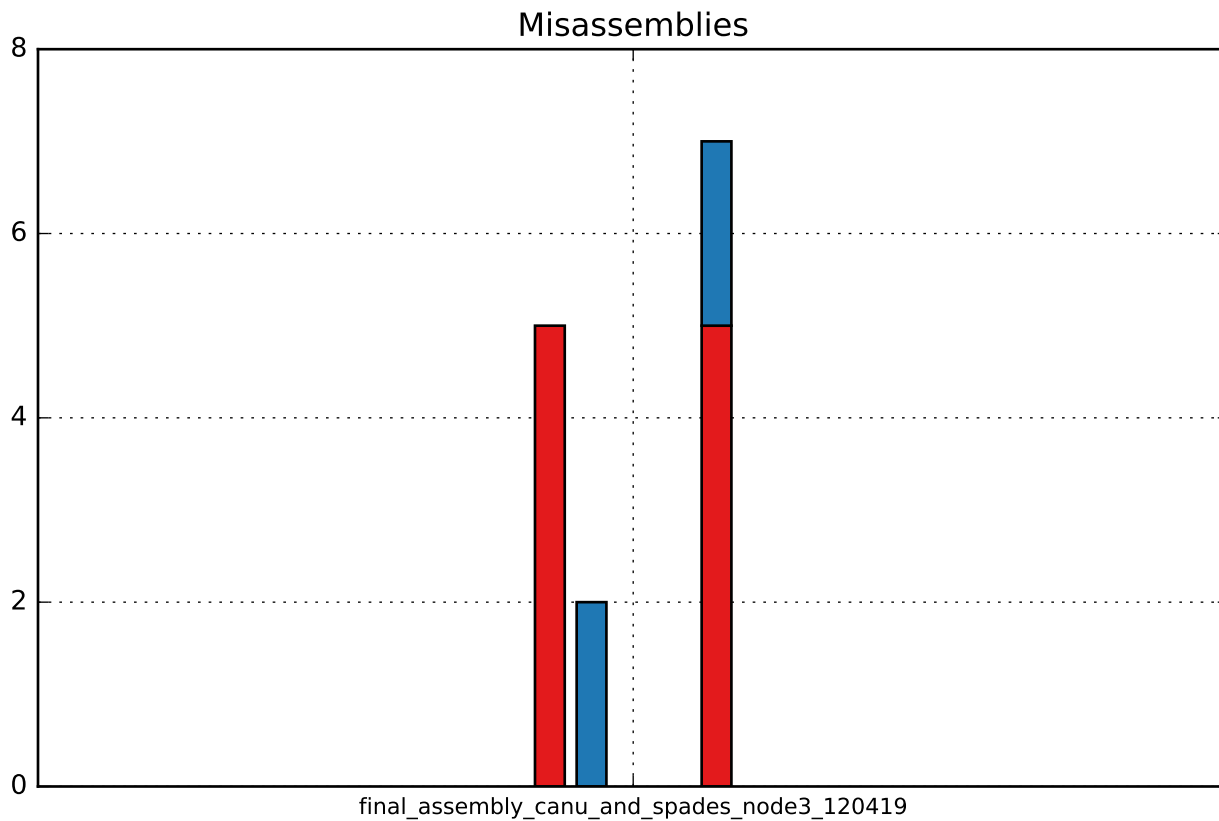


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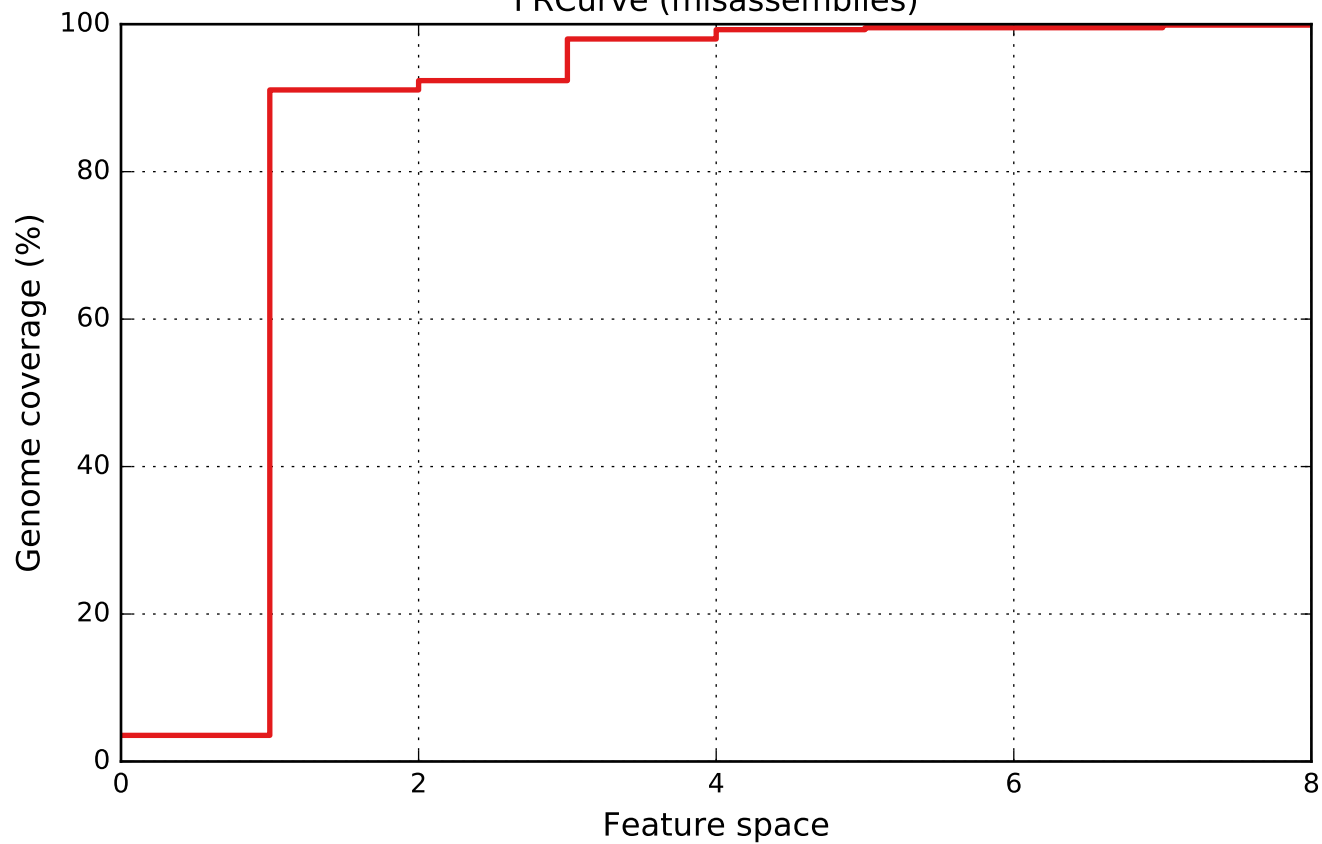
final_assembly_canu_and_spades_node3_120419 coverage histogram (bin size: 1x)



final_assembly_canu_and_spades_node3_120419

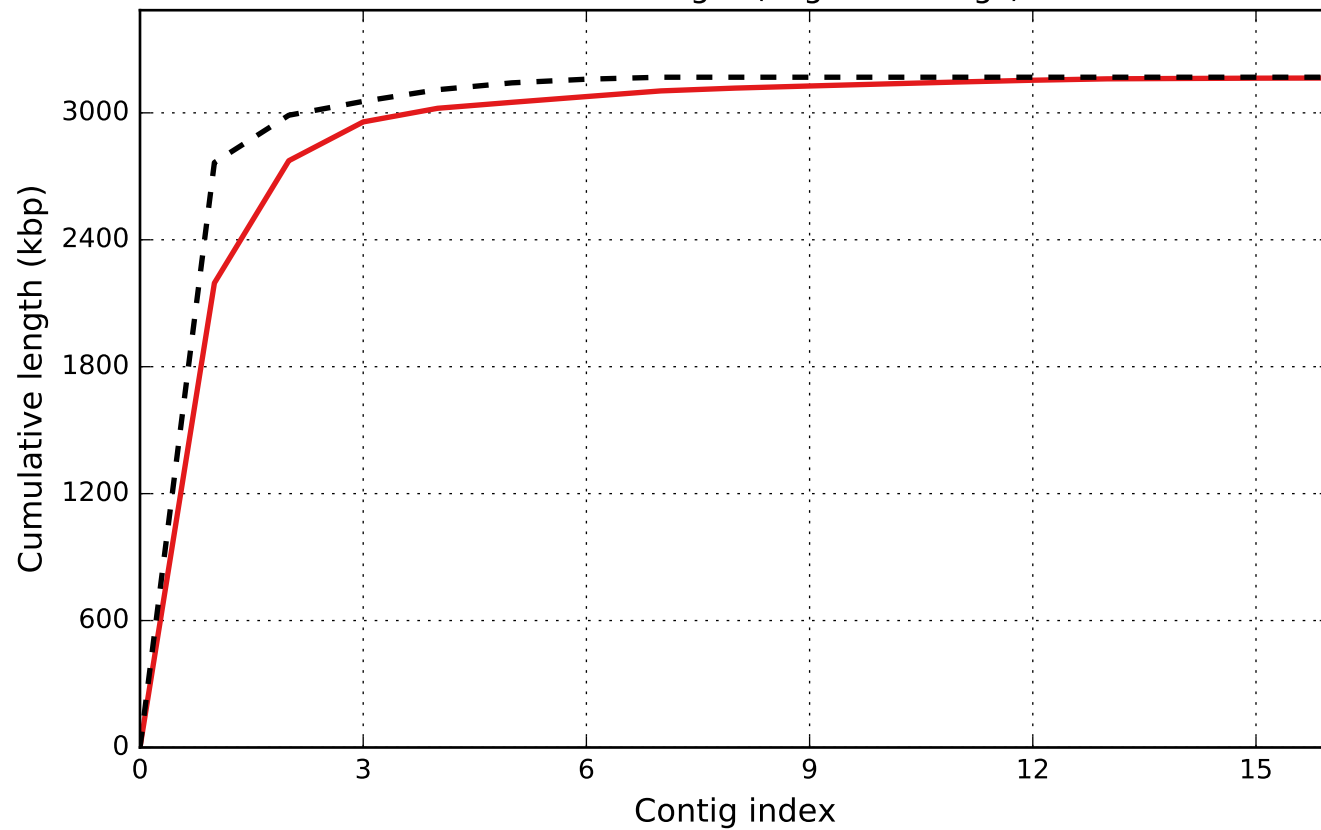


FRCurve (misassemblies)

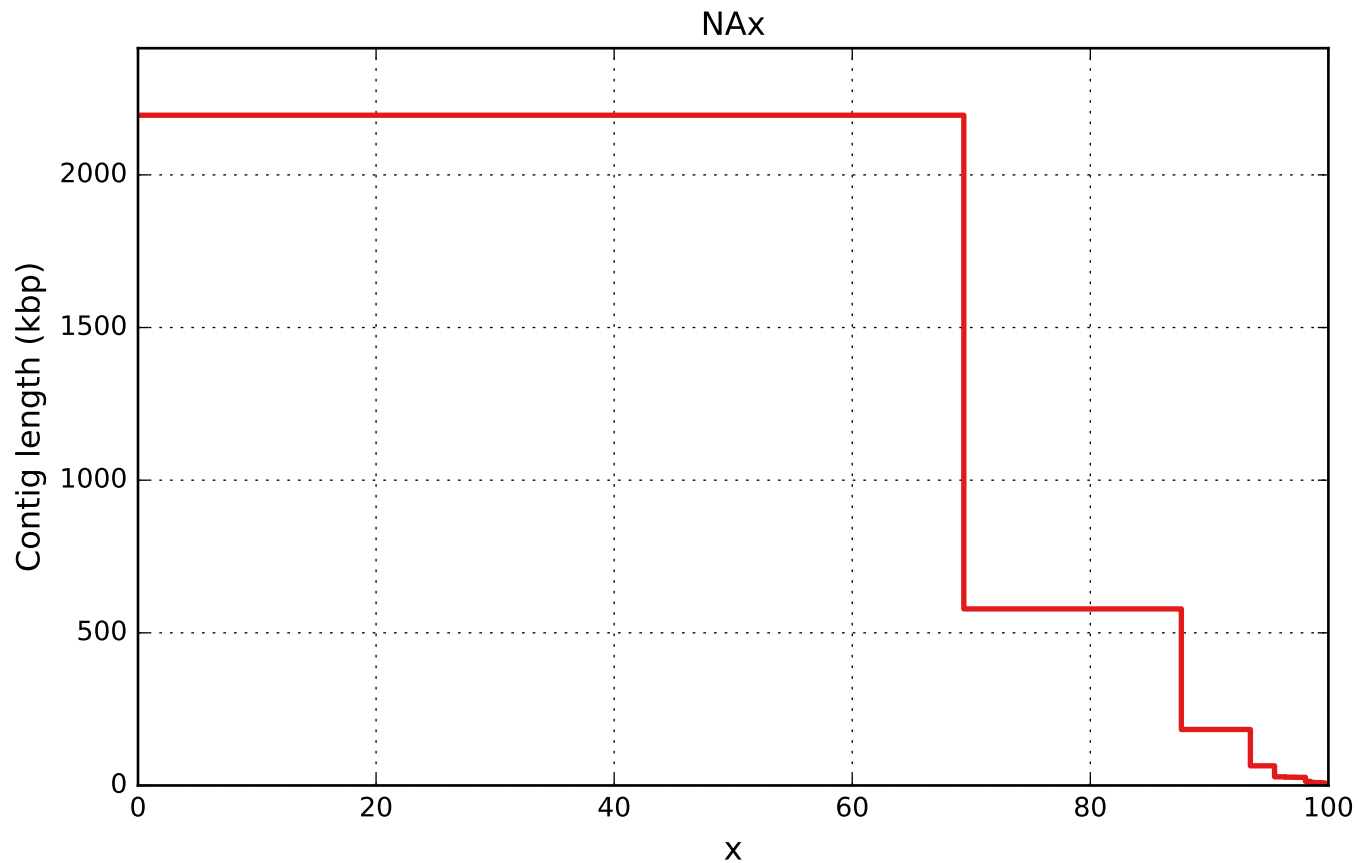


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Cumulative length (aligned contigs)

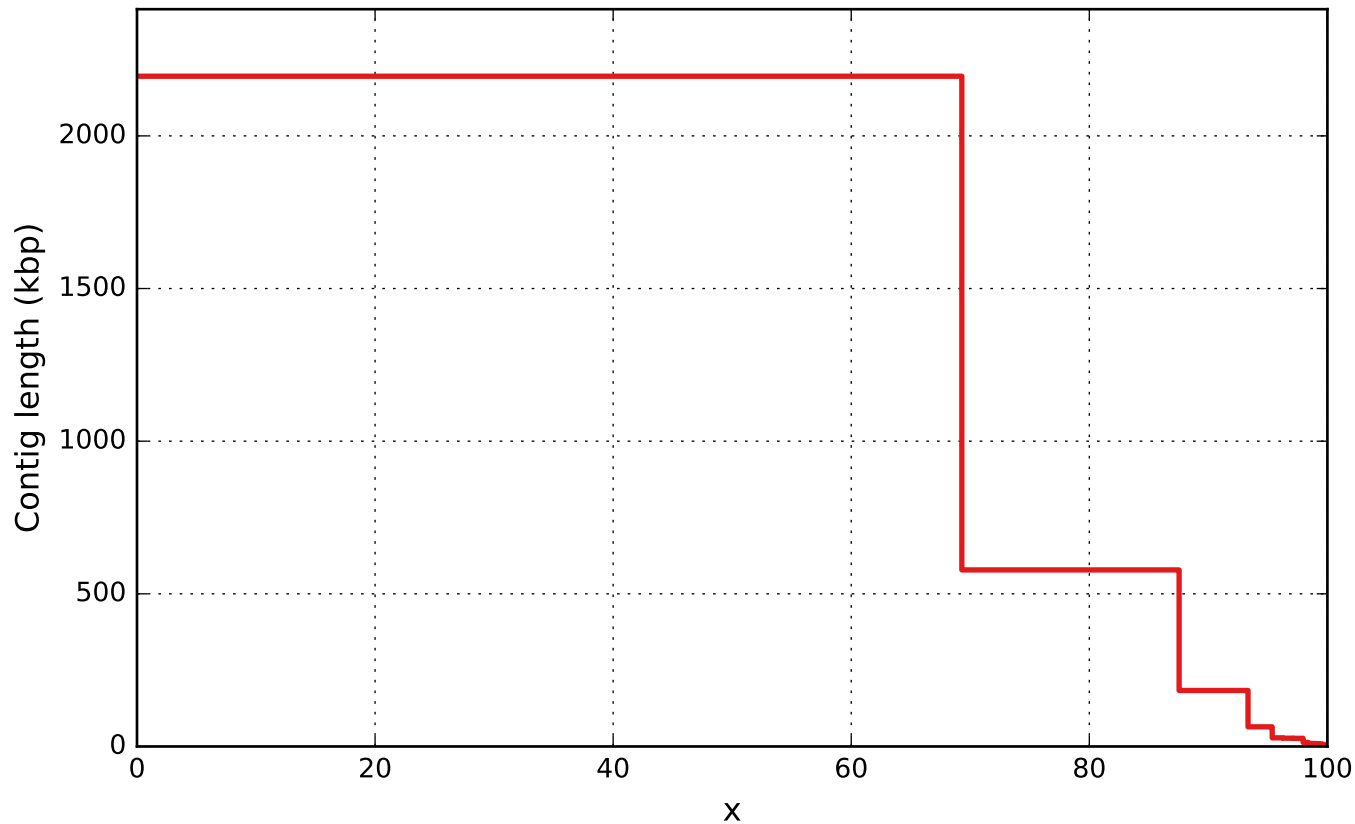


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— final_assembly_canu_and_spades_node3_120419

NGAx



— final_assembly_canu_and_spades_node3_120419