

Report

	contigs_spades
# contigs (>= 0 bp)	43
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	3151876
Total length (>= 1000 bp)	3145695
Total length (>= 5000 bp)	3124883
Total length (>= 10000 bp)	3094039
Total length (>= 25000 bp)	3094039
Total length (>= 50000 bp)	3094039
# contigs	16
Largest contig	2765031
Total length	3146525
Reference length	3168410
GC (%)	37.71
Reference GC (%)	37.70
N50	2765031
NG50	2765031
N75	2765031
NG75	2765031
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	2816937
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 1 part
Unaligned length	5848
Genome fraction (%)	98.892
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.97
# indels per 100 kbp	3.73
Largest alignment	1899903
Total aligned length	3128539
NA50	1899903
NGA50	1899903
NA75	858689
NGA75	858689
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

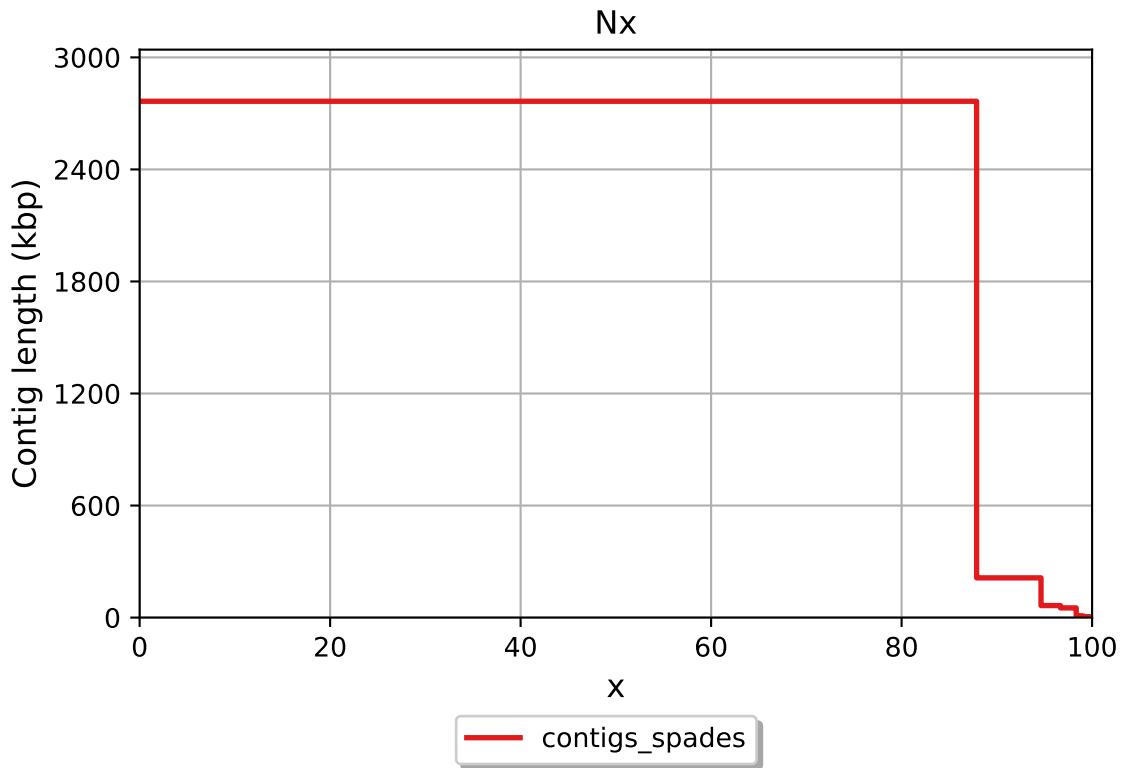
	contigs_spades
# misassemblies	3
# contig misassemblies	3
# c. relocations	0
# c. translocations	2
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	2816937
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	939
# indels	117
# indels (<= 5 bp)	108
# indels (> 5 bp)	9
Indels length	256

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).

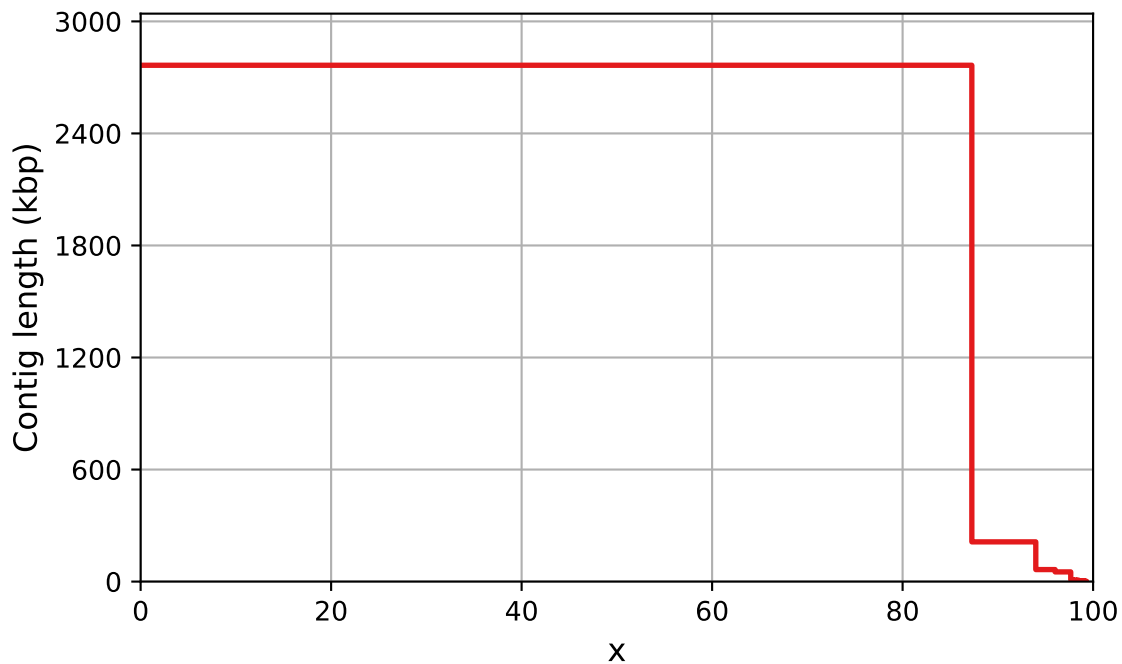
Unaligned report

	contigs_spades
# fully unaligned contigs	1
Fully unaligned length	3214
# partially unaligned contigs	1
Partially unaligned length	2634
# N's	0

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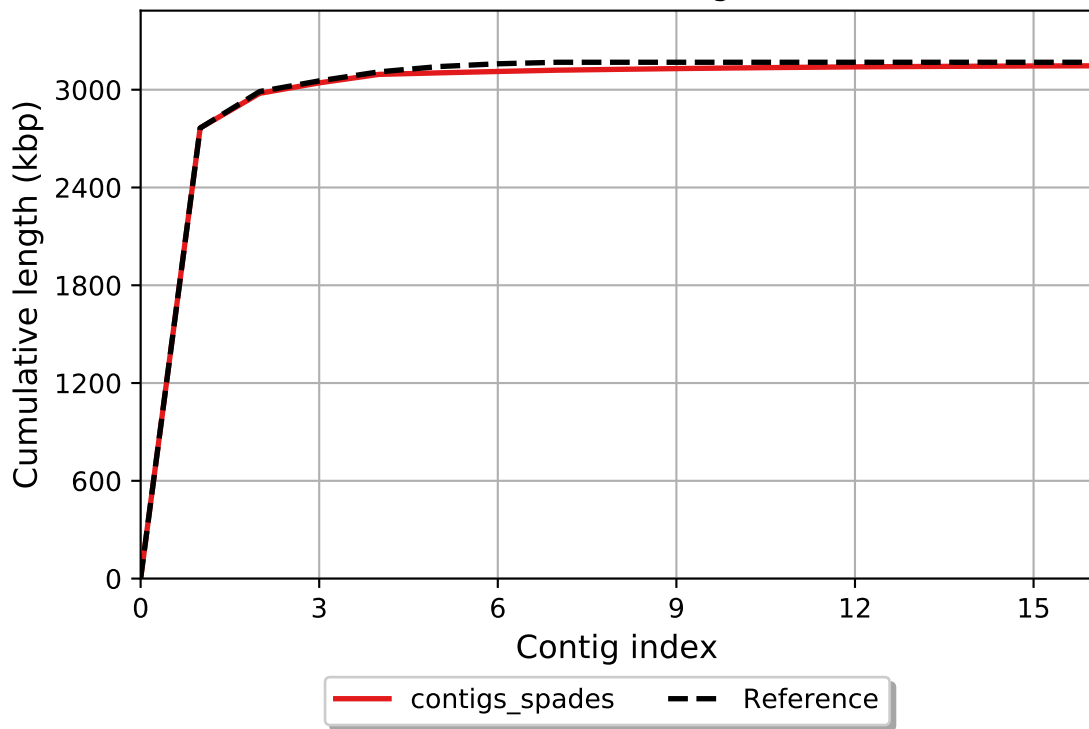


NGx

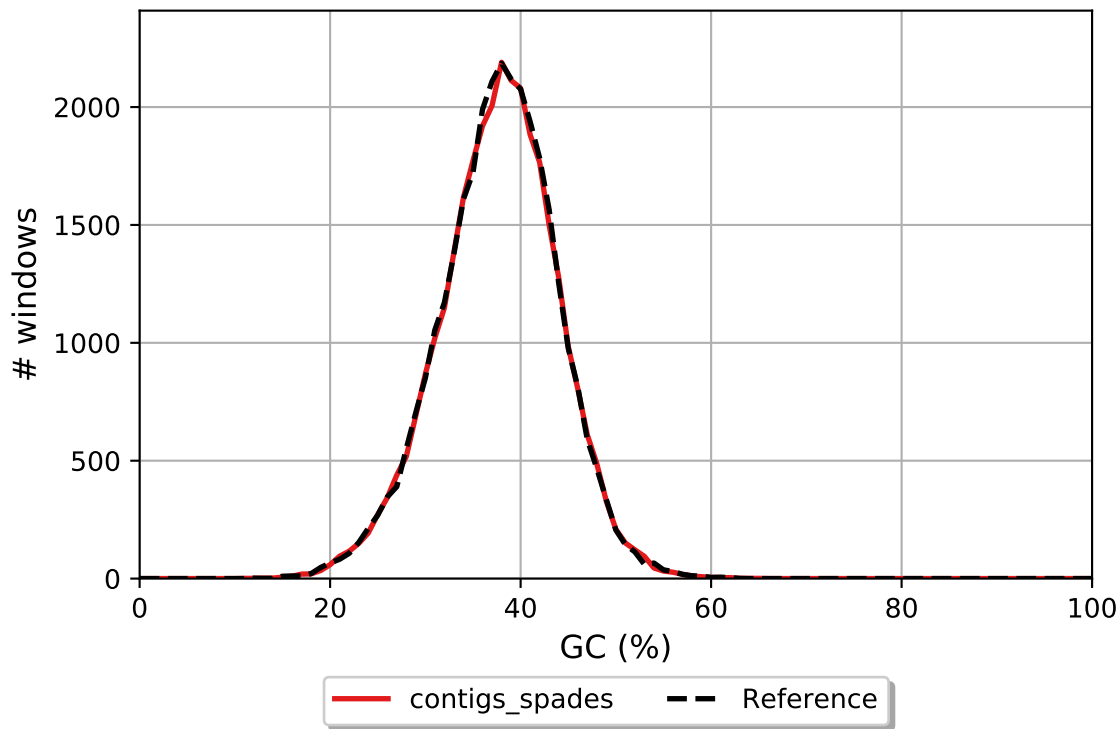


— contigs_spades

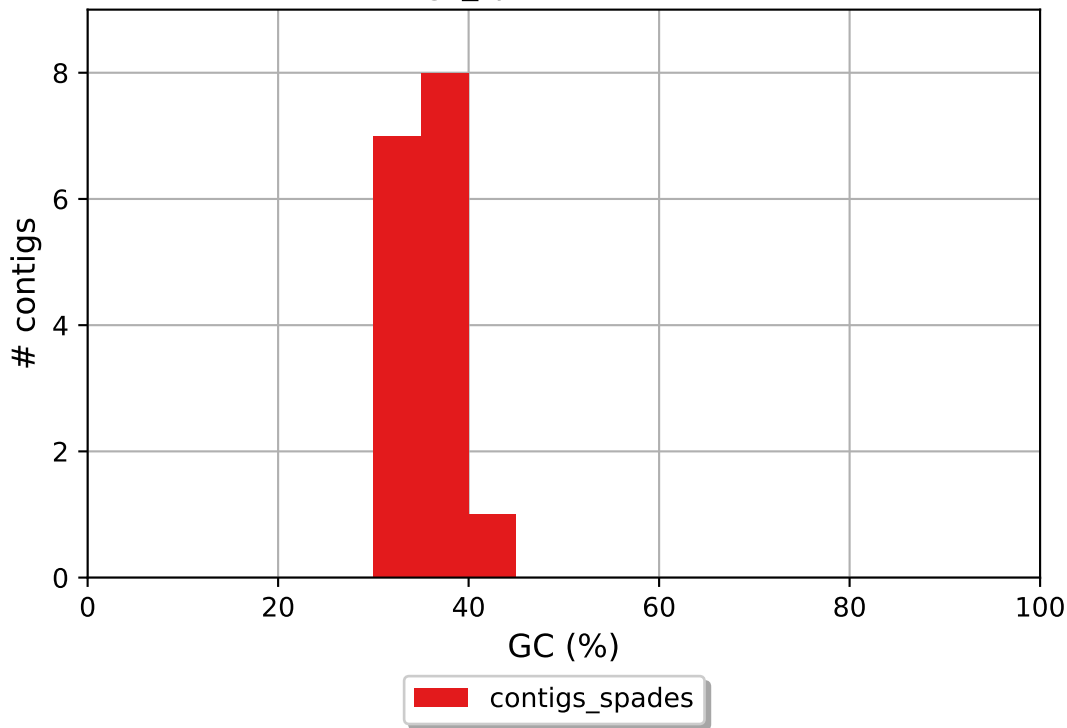
Cumulative length



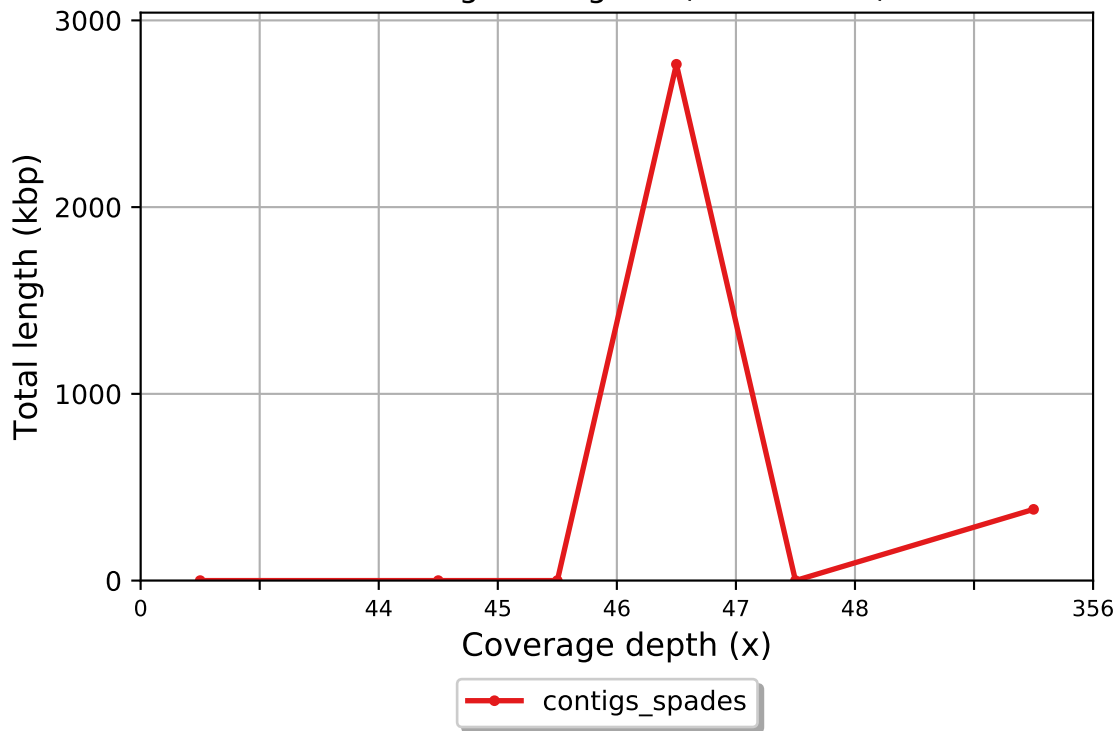
GC content



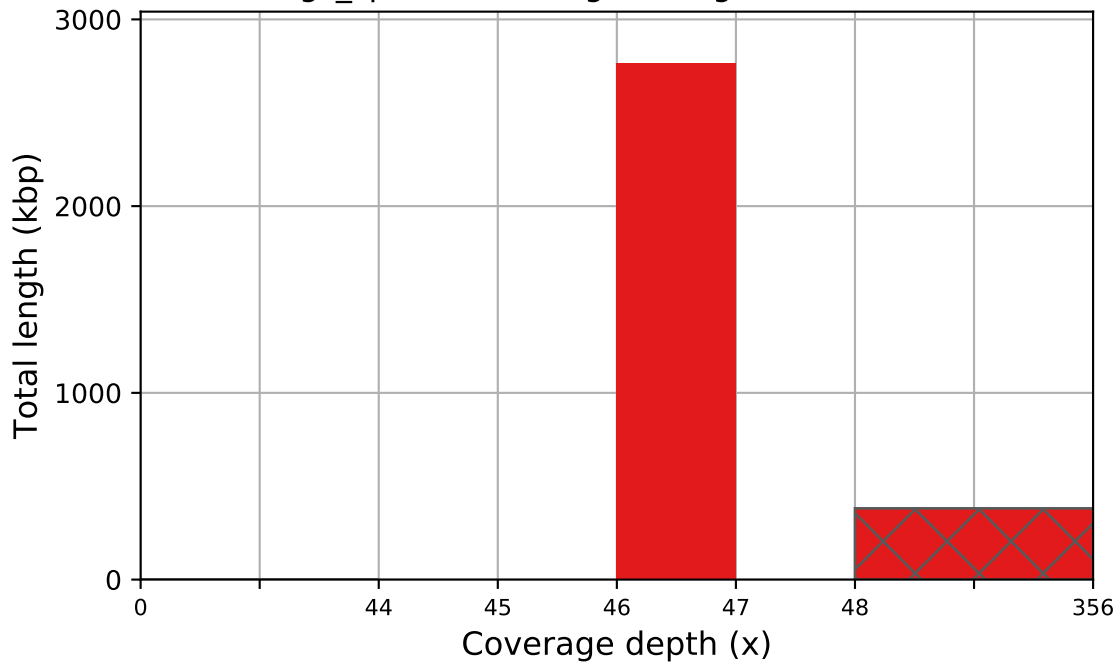
contigs_spades GC content



Coverage histogram (bin size: 1x)

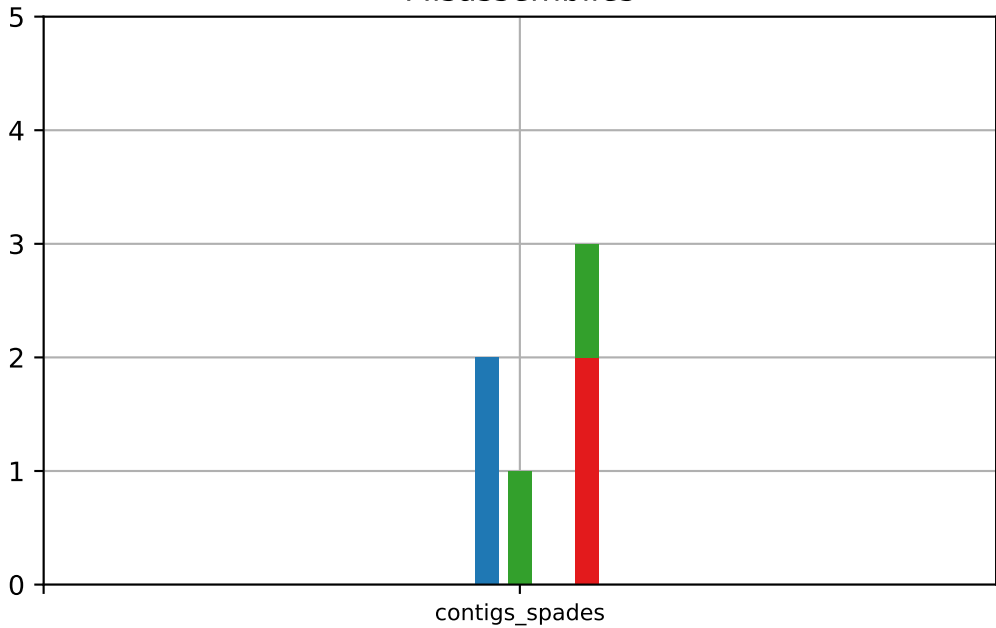


contigs_spades coverage histogram (bin size: 1x)



contigs_spades

Misassemblies

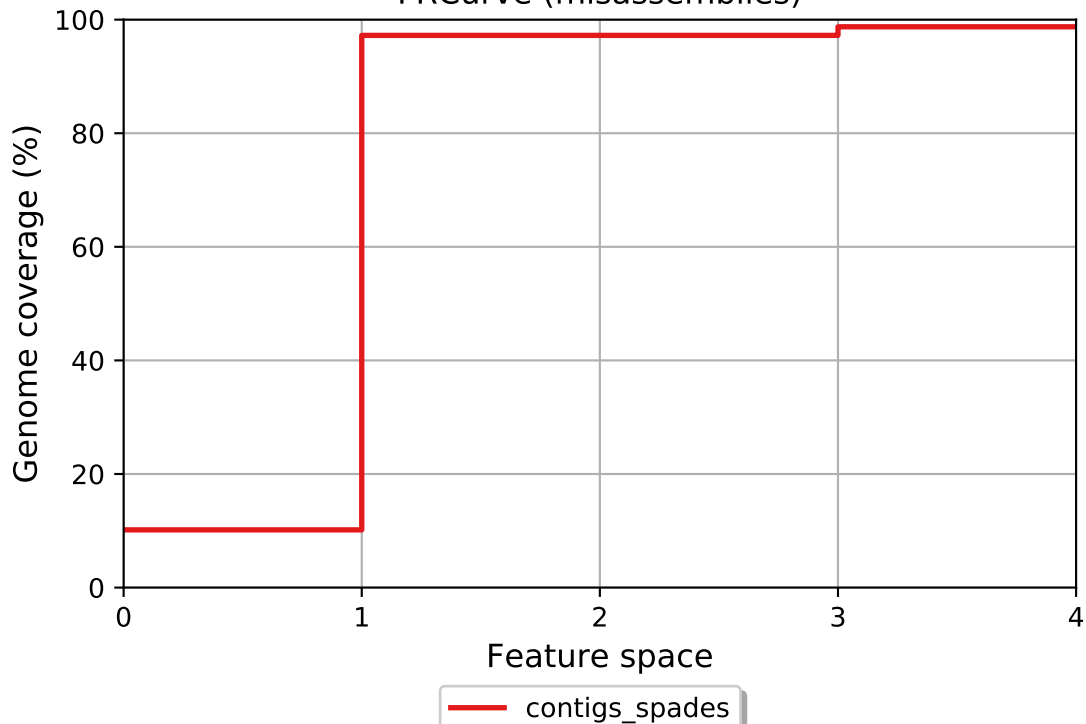


translocations

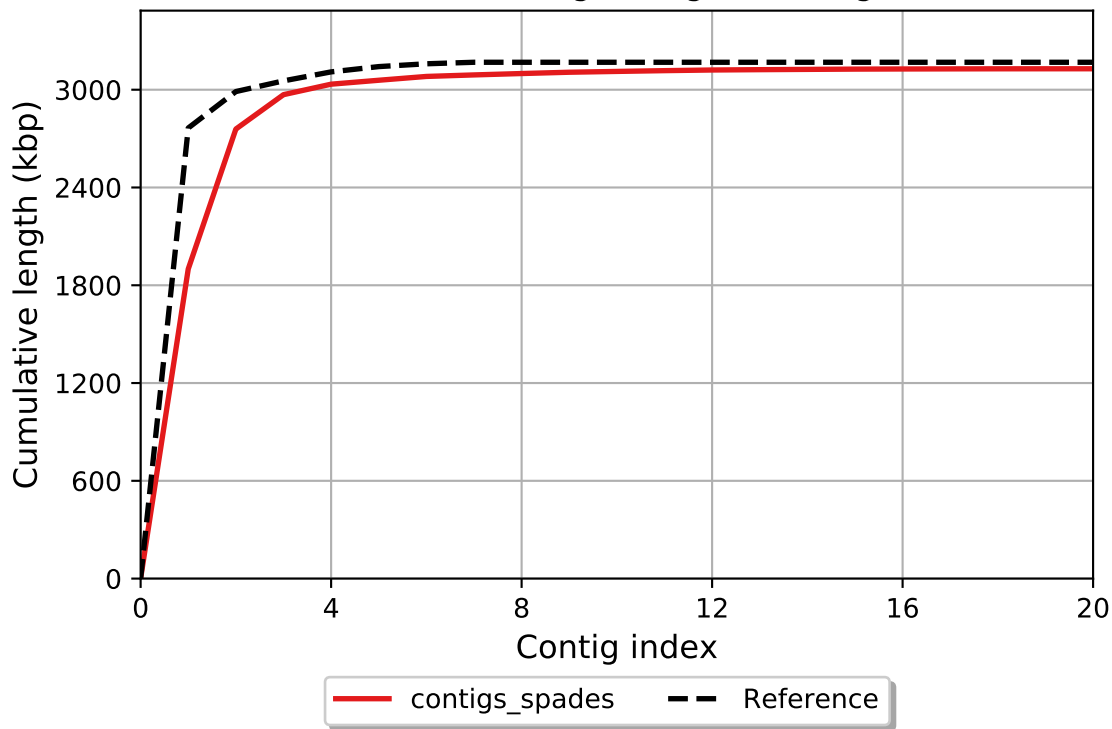


inversions

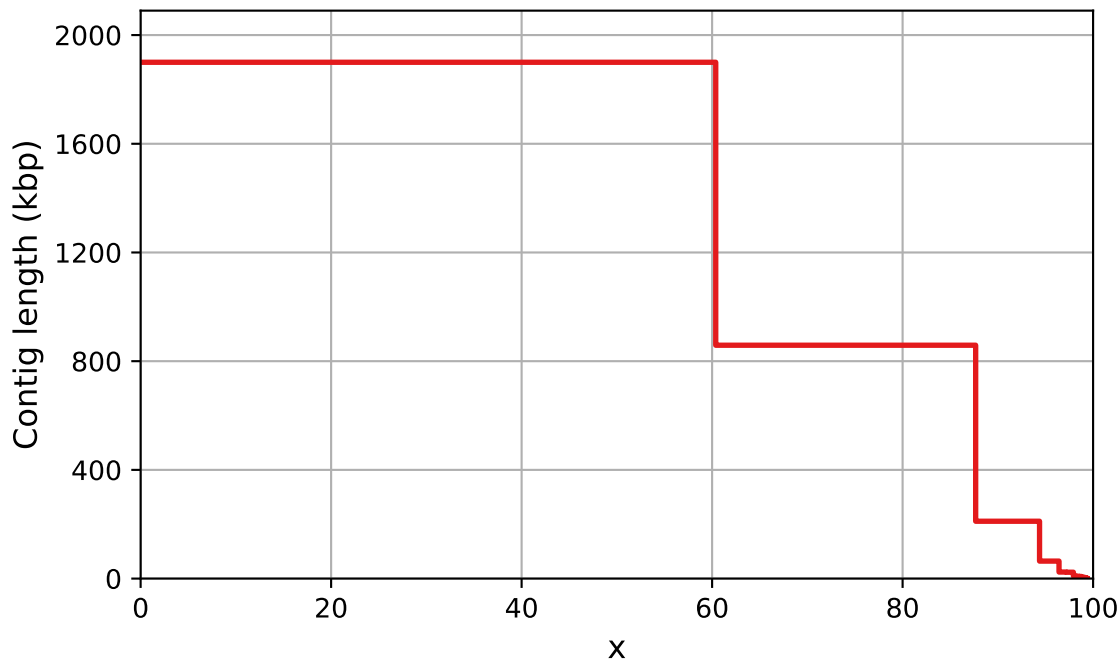
FRCurve (misassemblies)



Cumulative length (aligned contigs)

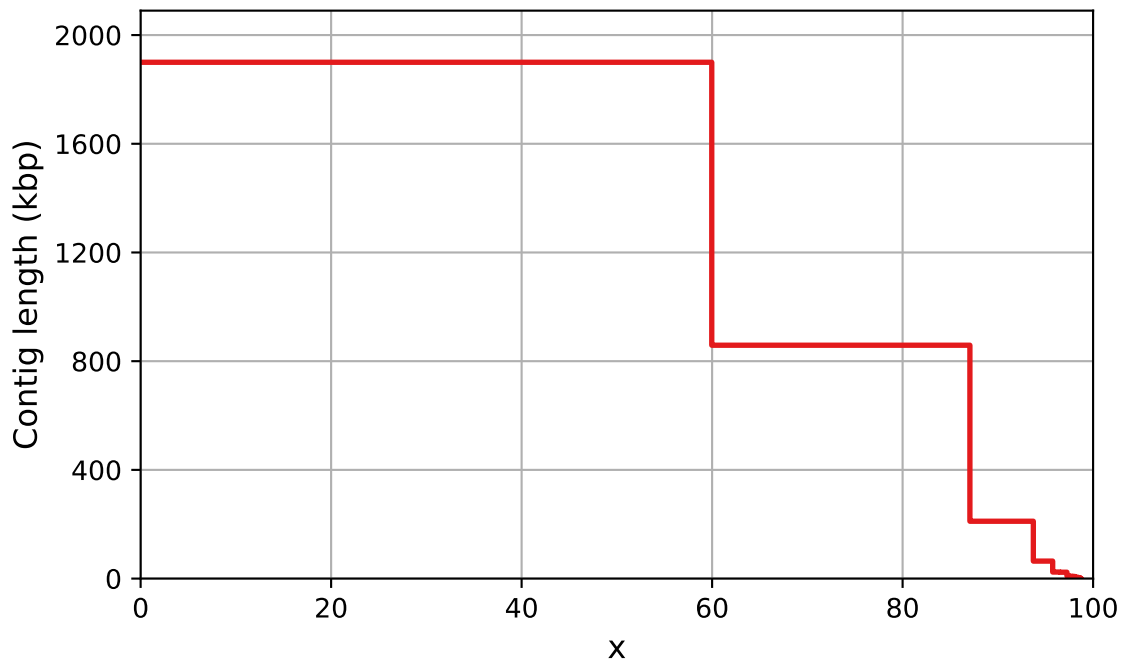


NAx



— contigs_spades

NGAx



— contigs_spades