

Report

	canu.contigs
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	7
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3143162
Total length (>= 1000 bp)	3143162
Total length (>= 5000 bp)	3138766
Total length (>= 10000 bp)	3138766
Total length (>= 25000 bp)	3110228
Total length (>= 50000 bp)	2999941
# contigs	8
Largest contig	2773593
Total length	3143162
Reference length	3168410
GC (%)	37.78
Reference GC (%)	37.70
N50	2773593
NG50	2773593
N75	2773593
NG75	2773593
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	6
# misassembled contigs	5
Misassembled contigs length	3068496
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.360
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.20
# indels per 100 kbp	13.96
Largest alignment	2195337
Total aligned length	3143158
NA50	2195337
NGA50	2195337
NA75	578256
NGA75	578256
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

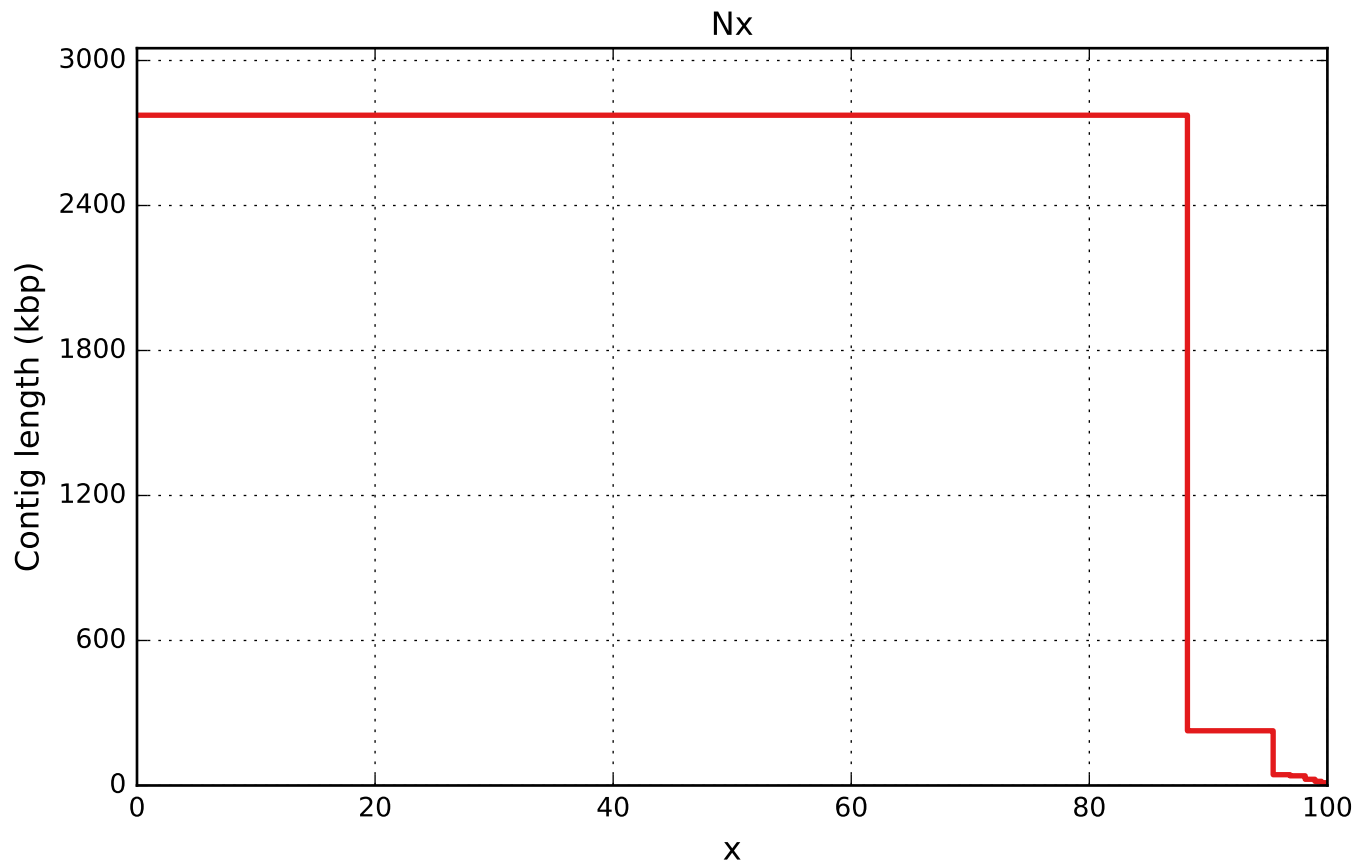
	canu.contigs
# misassemblies	6
# relocations	4
# translocations	2
# inversions	0
# misassembled contigs	5
Misassembled contigs length	3068496
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	162
# indels	435
# indels (≤ 5 bp)	426
# indels (> 5 bp)	9
Indels length	604

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).

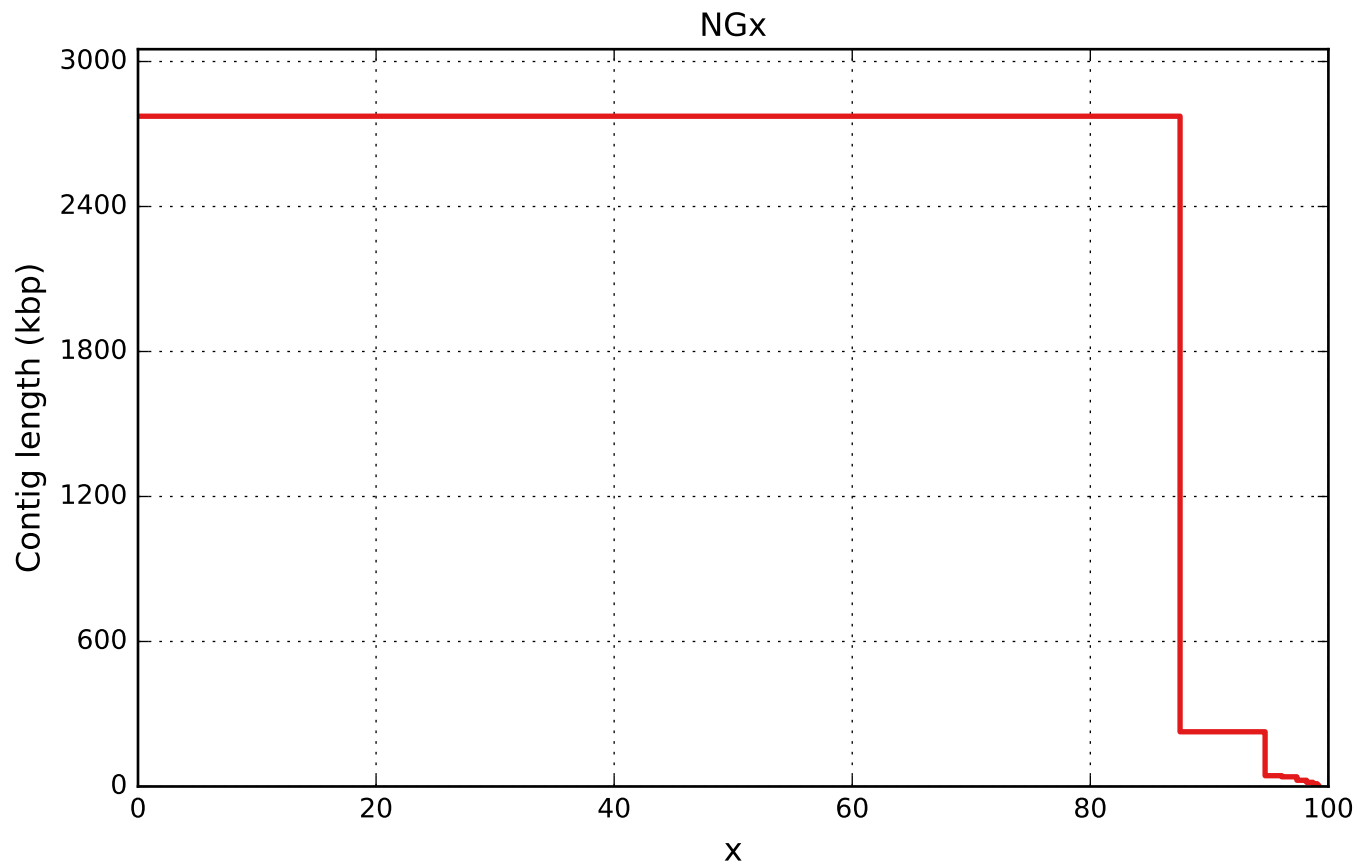
Unaligned report

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

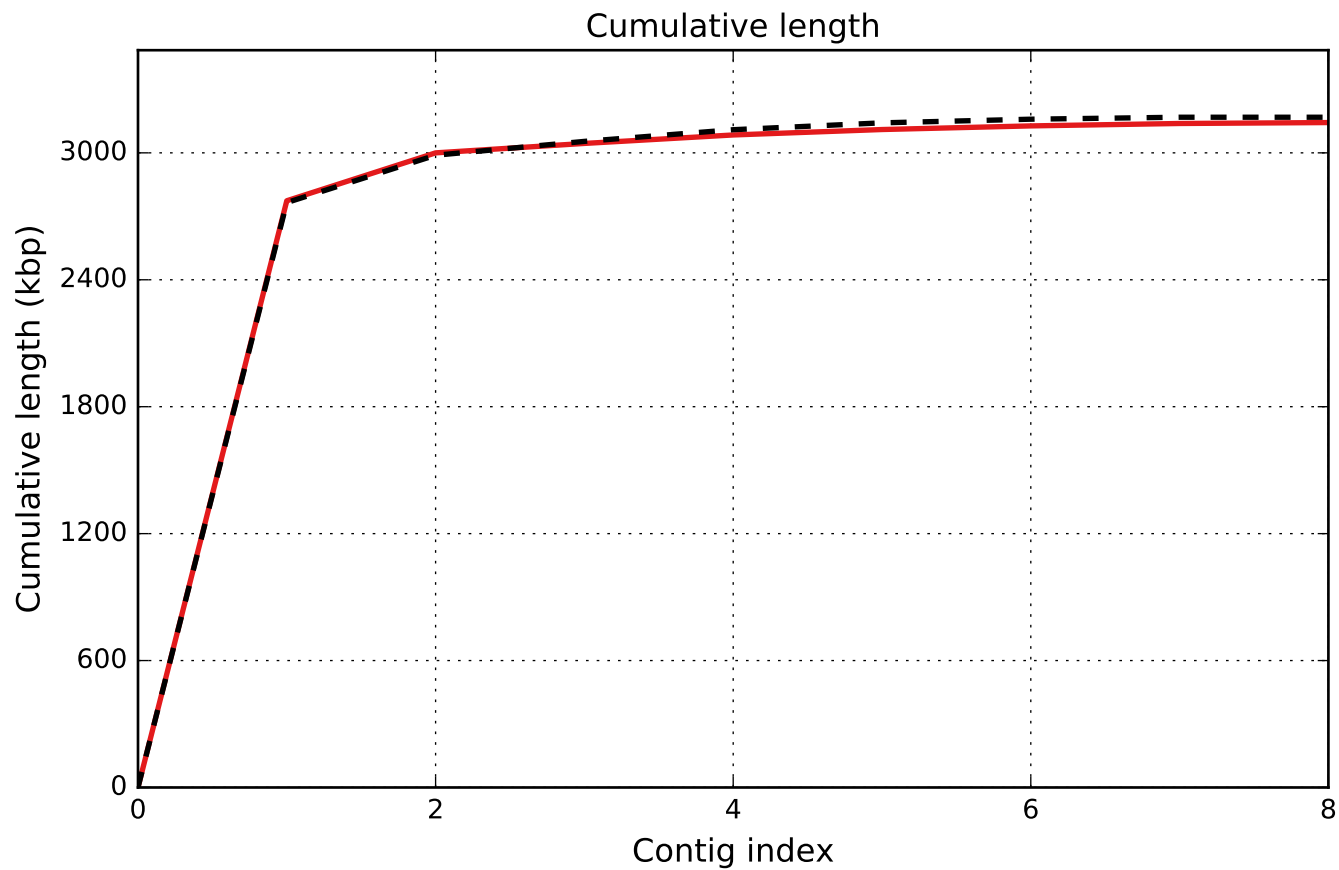
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

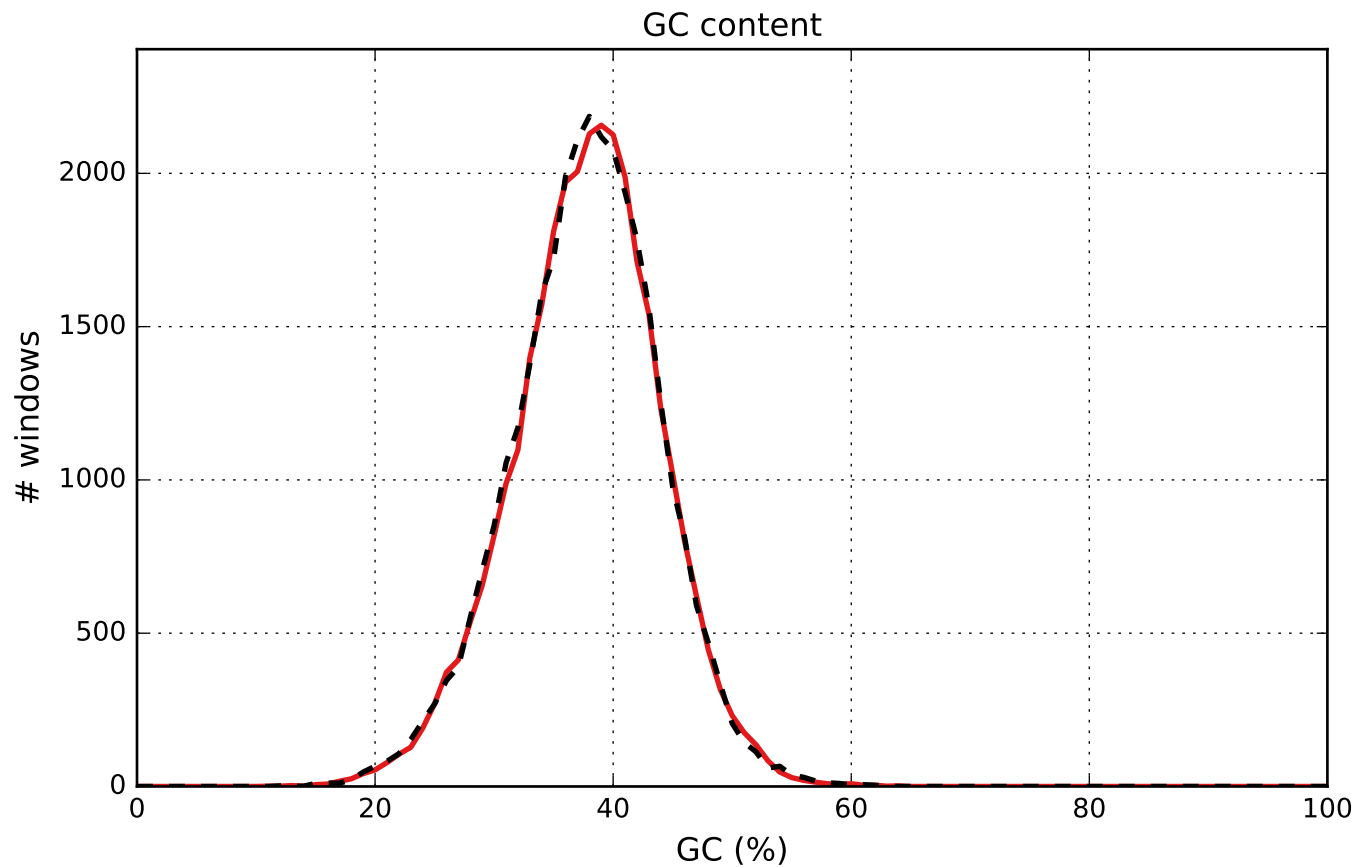


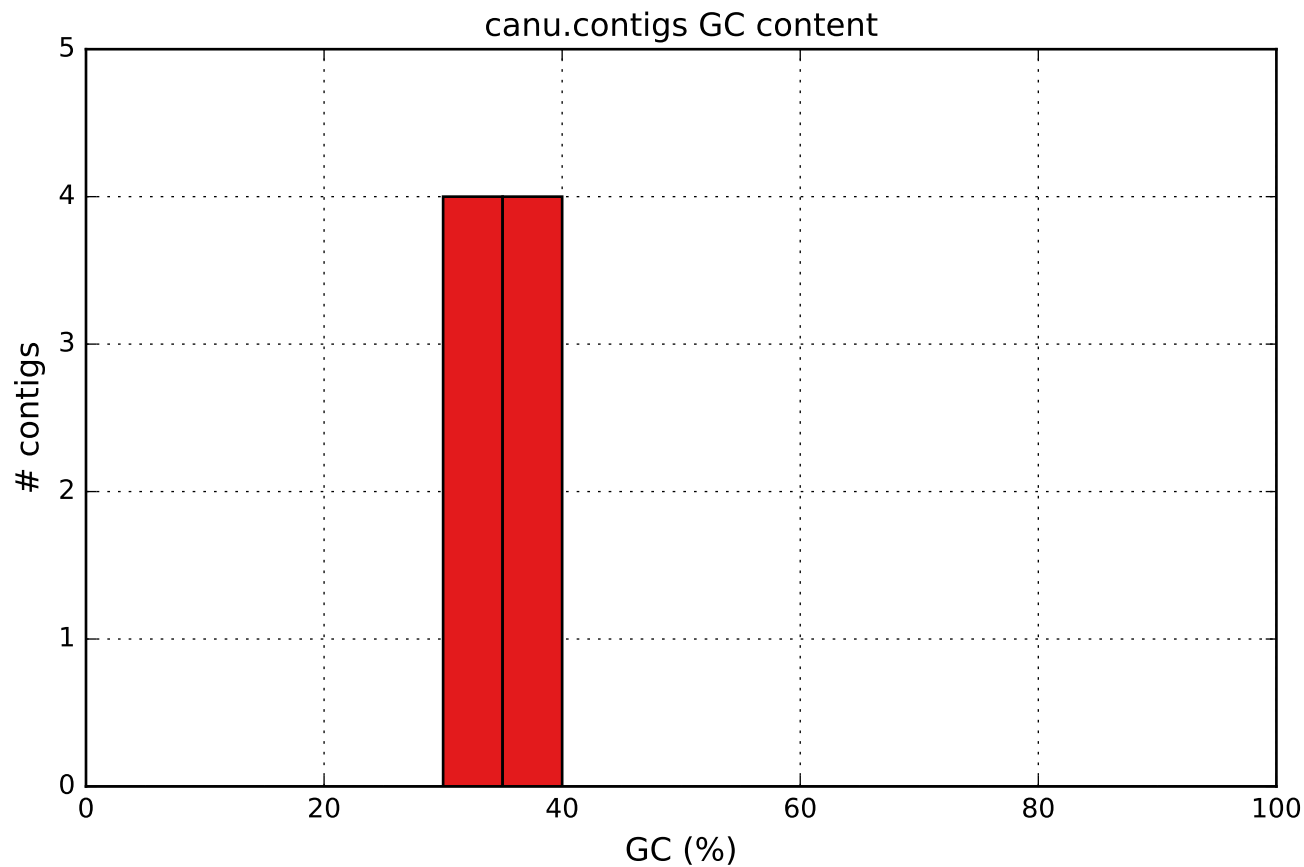
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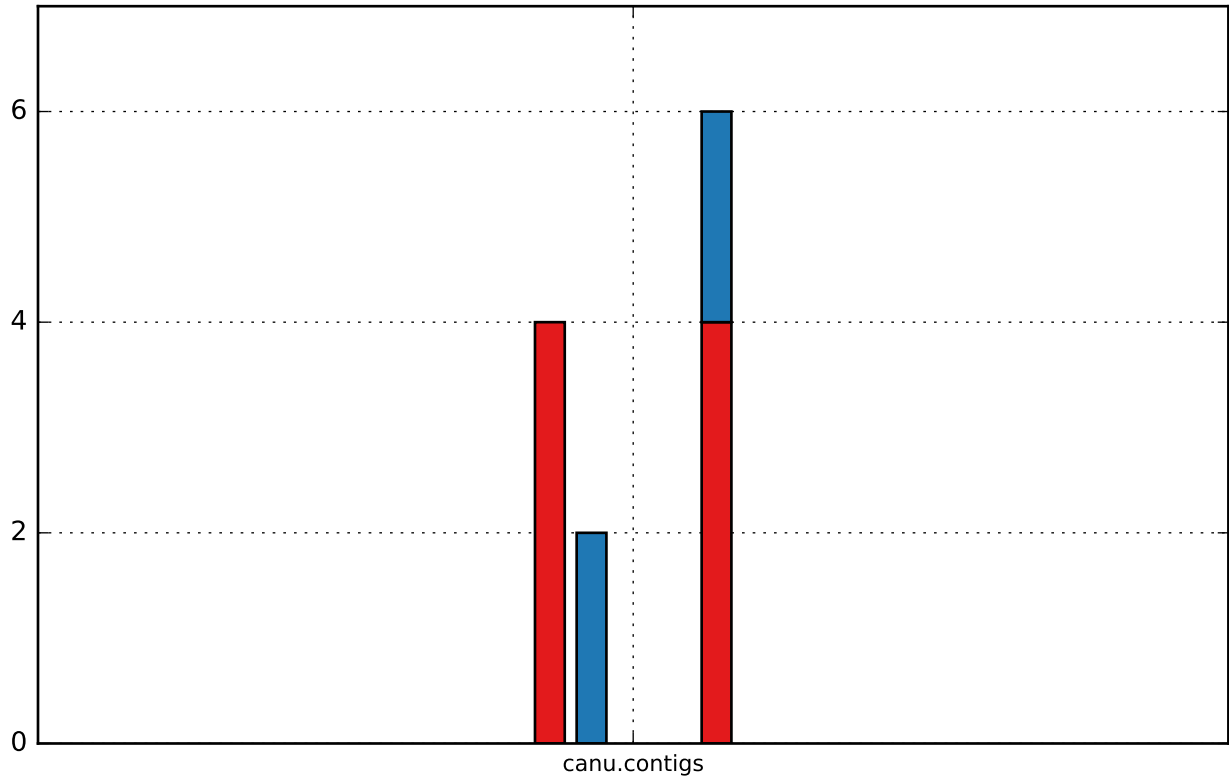






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Misassemblies

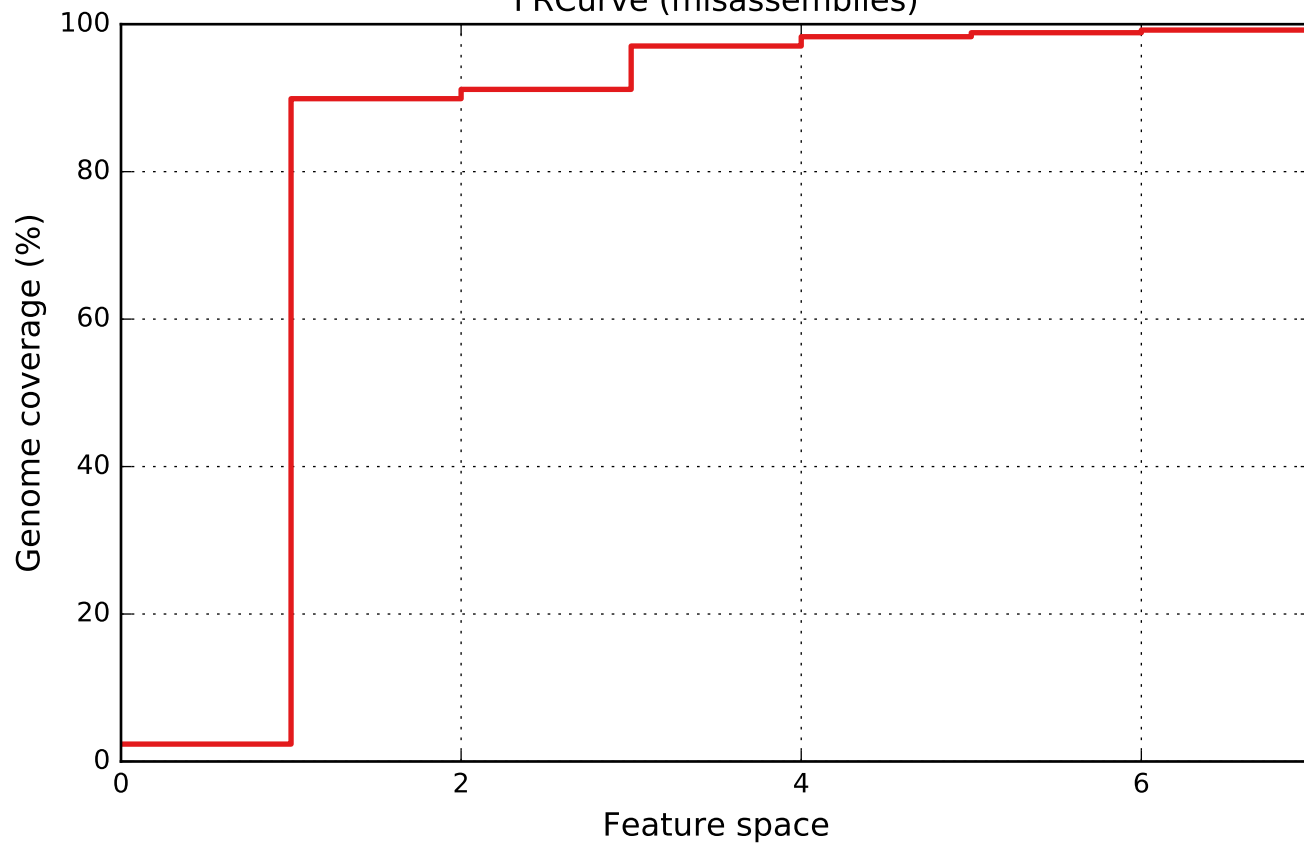


relocations



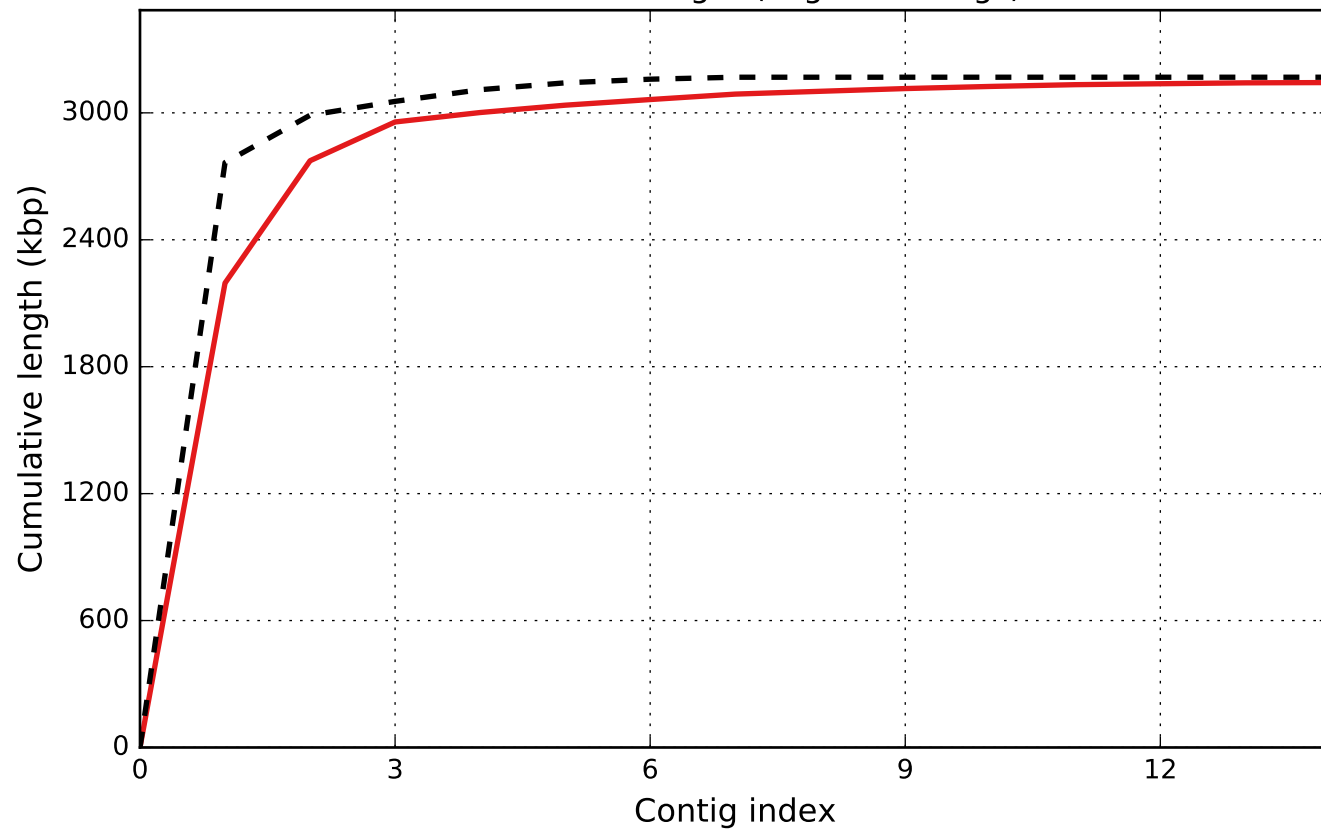
translocations

FRCurve (misassemblies)

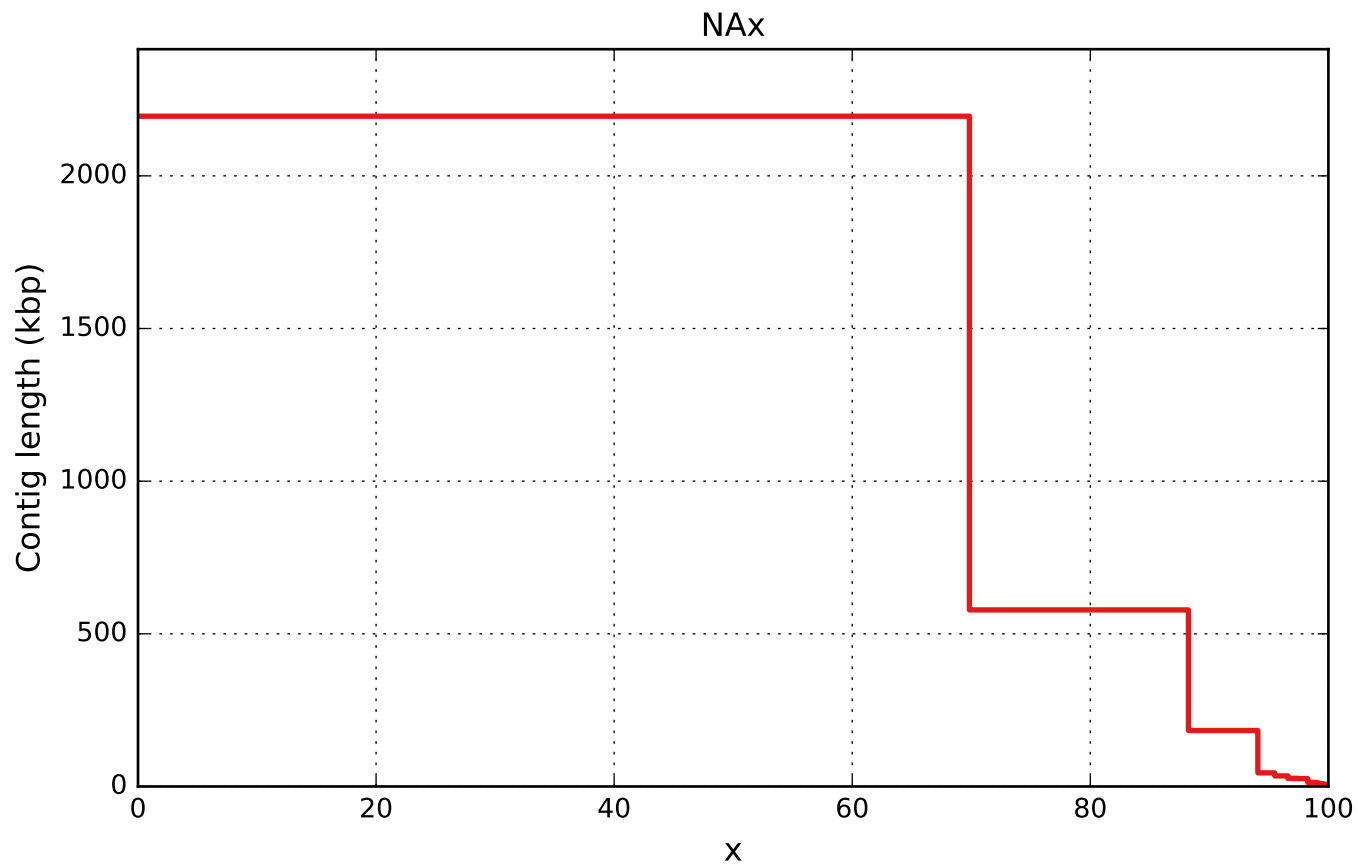


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Cumulative length (aligned contigs)

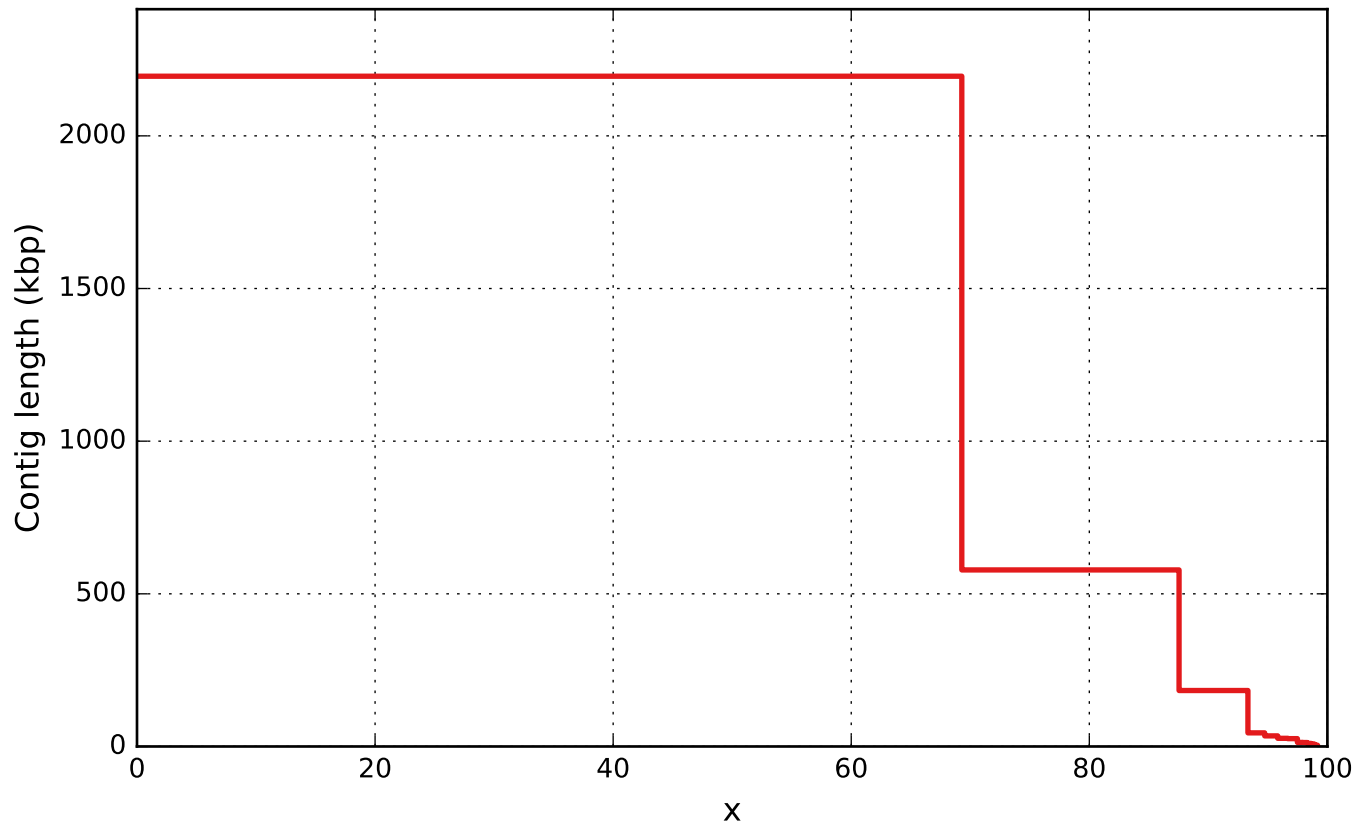


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NGAx



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