

Report

	SRR1190502_contigs_fw_30_complete
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	110044
Total length (>= 5000 bp)	95849
Total length (>= 10000 bp)	77502
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	33
Largest contig	16943
Total length	120827
Reference length	30114
GC (%)	40.95
Reference GC (%)	41.12
N50	14874
NG50	16943
N75	6102
NG75	16942
L50	4
LG50	1
L75	8
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.582
Duplication ratio	4.334
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2080.34
# indels per 100 kbp	7.17
Largest alignment	16884
Total aligned length	120379
NA50	14873
NGA50	16884
NA75	6101
NGA75	16882
LA50	4
LGA50	1
LA75	8
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

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# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	580
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

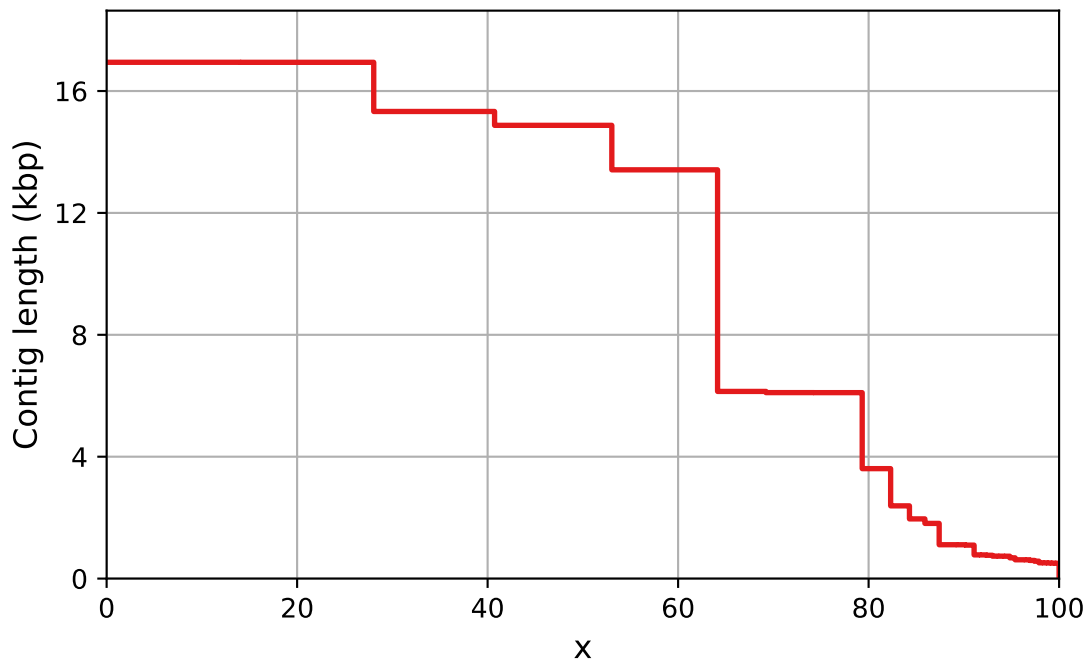
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR1190502_contigs_fw_30_complete
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

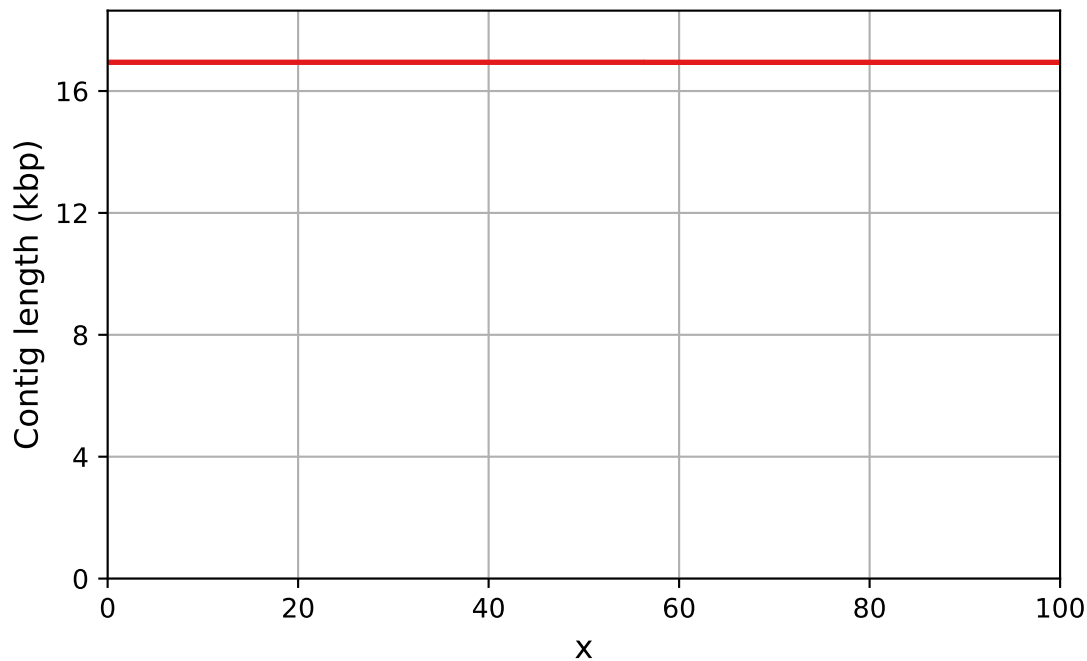
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

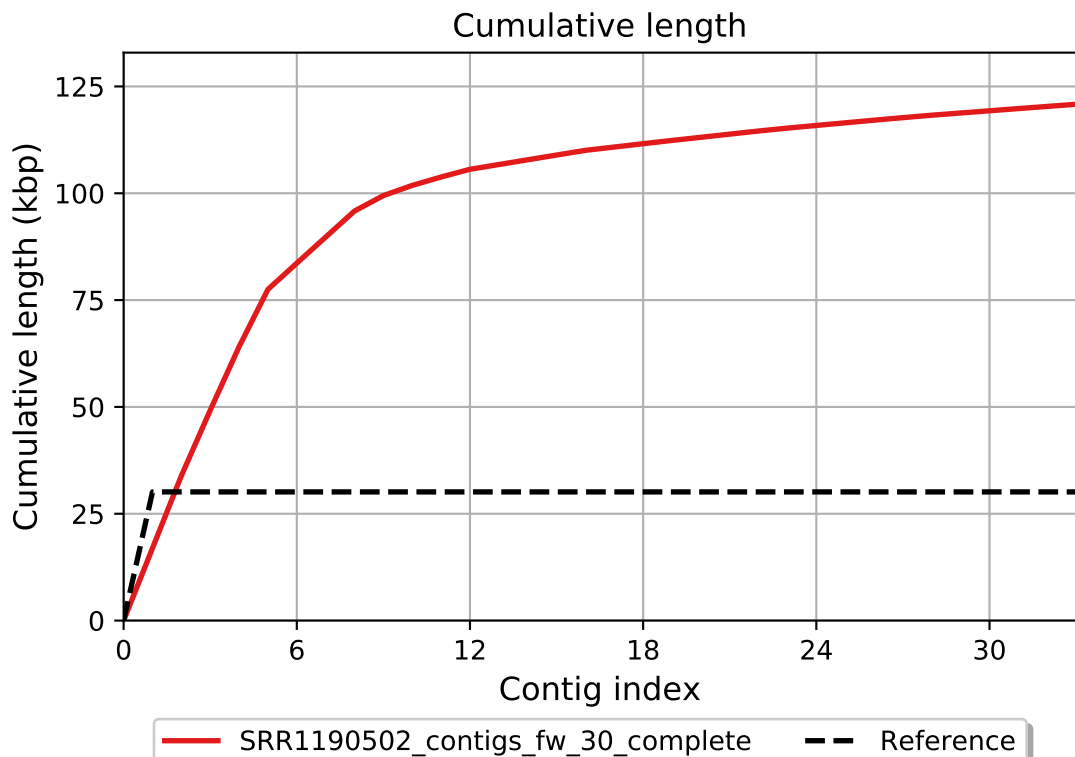


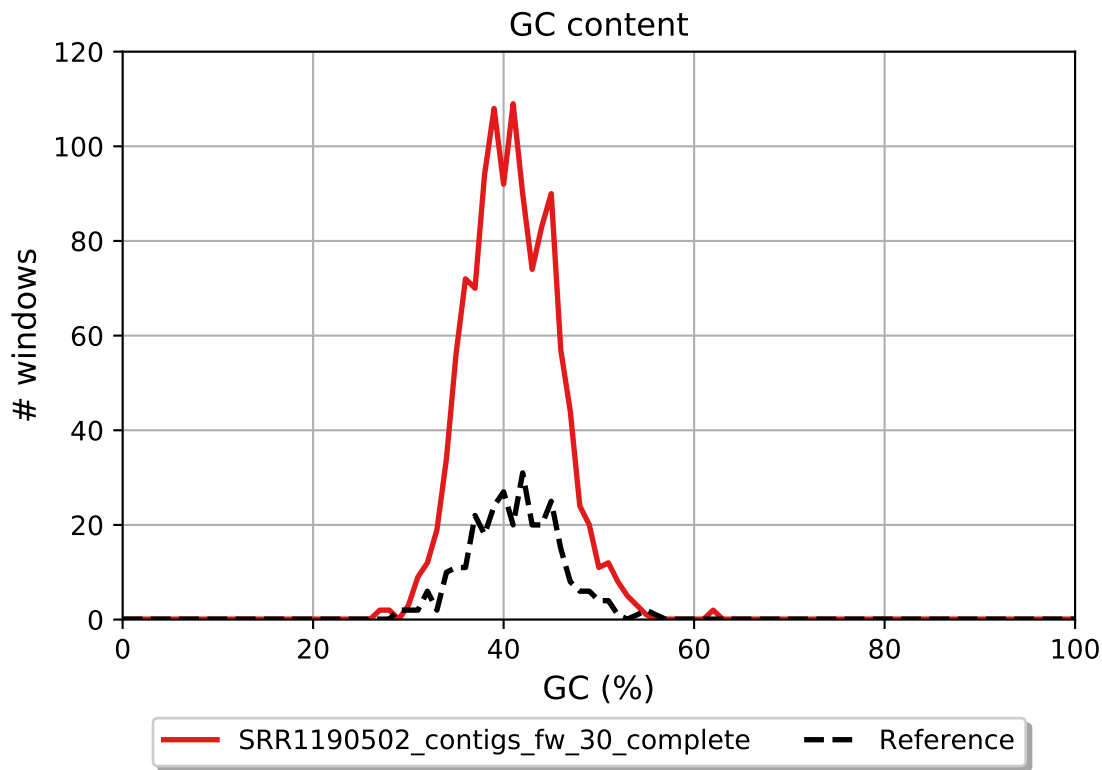
SRR1190502_contigs_fw_30_complete

NGx

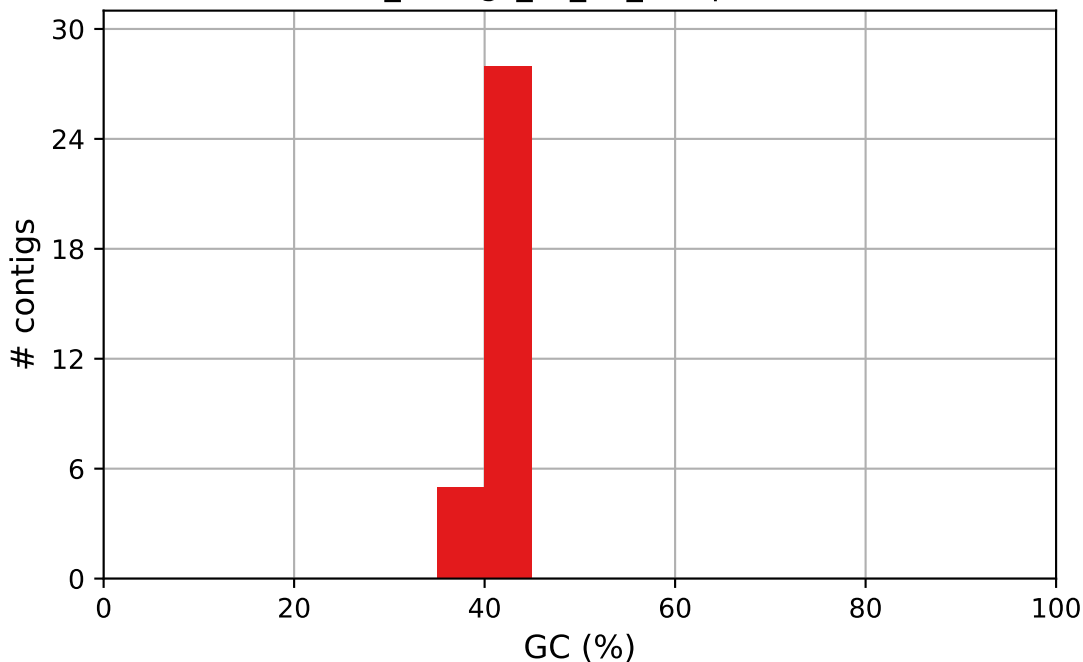


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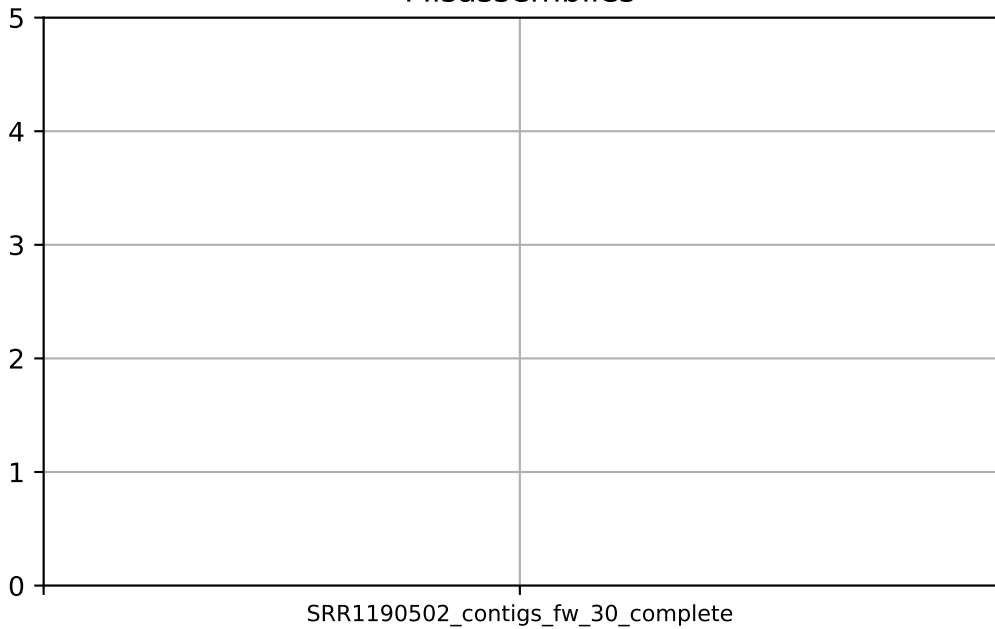


SRR1190502_contigs_fw_30_complete GC content

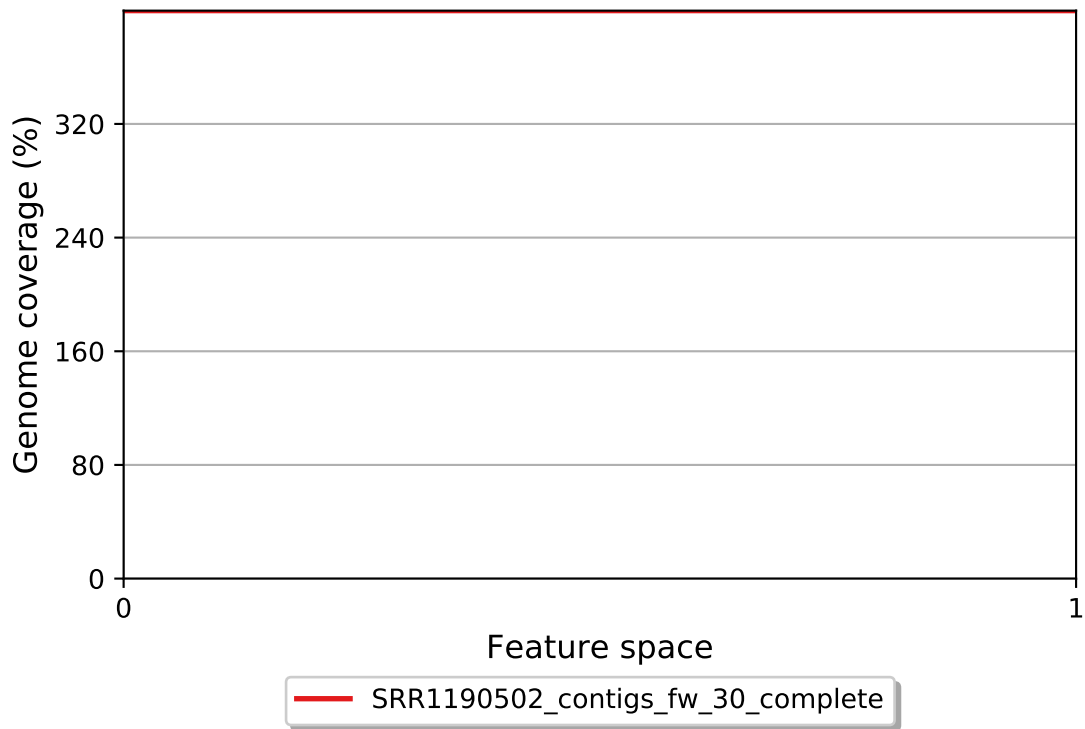


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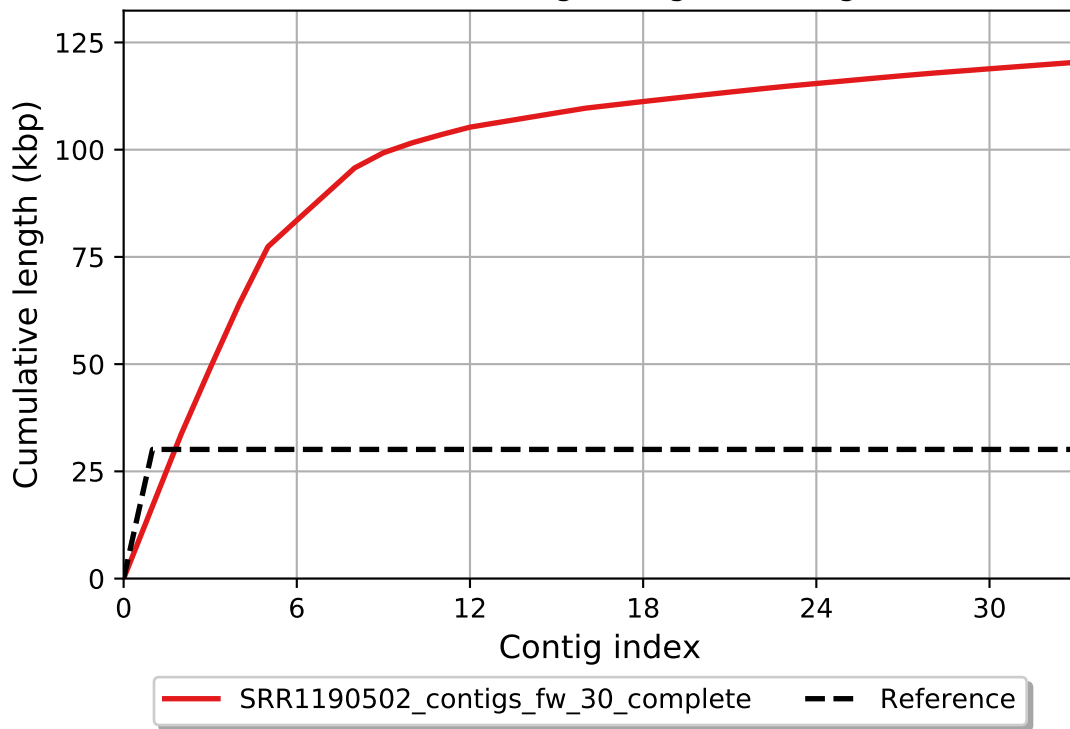
Misassemblies



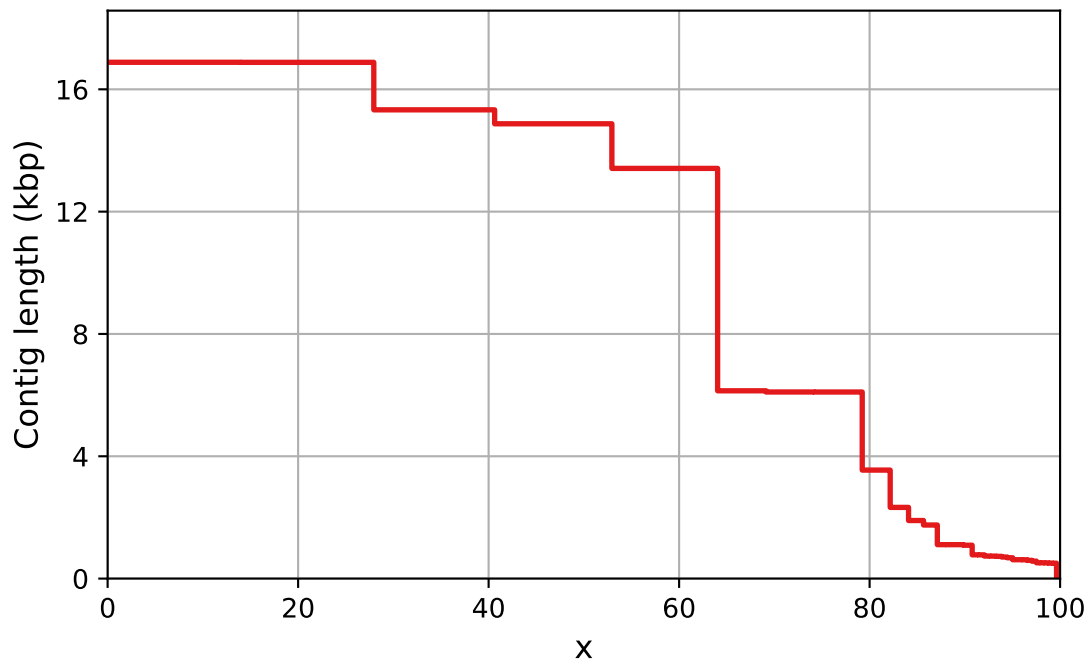
FRCurve (misassemblies)



Cumulative length (aligned contigs)

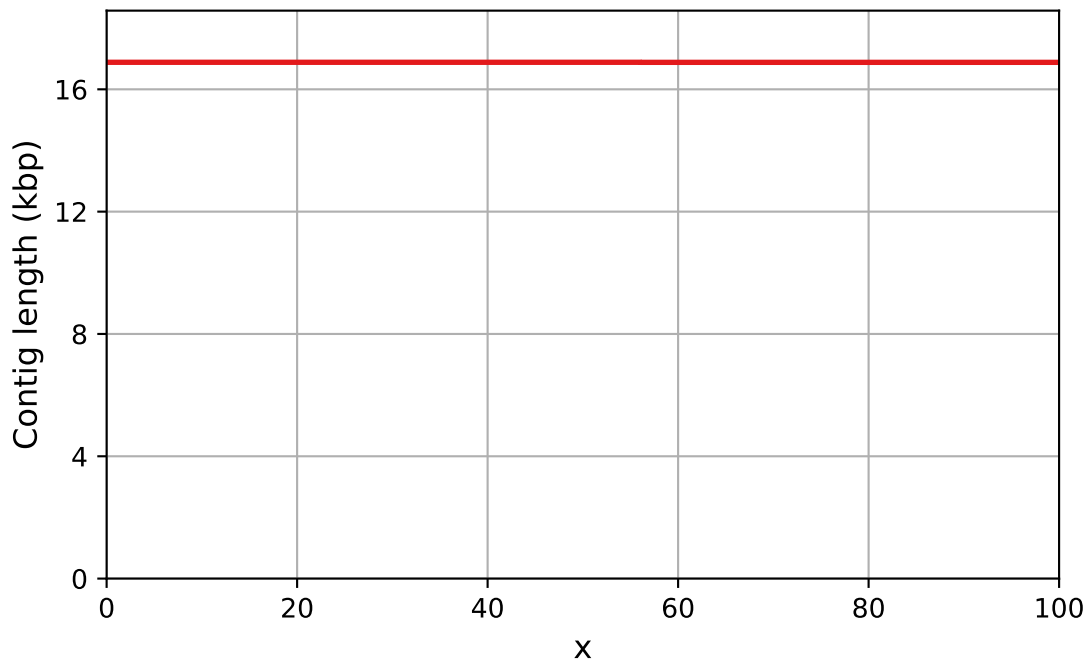


NAx



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NGAx



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