

Report

	no_error_reads_hiseq_5k_dbg_k_40
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29553
Total length (>= 1000 bp)	29553
Total length (>= 5000 bp)	29553
Total length (>= 10000 bp)	12290
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3
Largest contig	12290
Total length	29553
Reference length	30119
GC (%)	41.27
Reference GC (%)	41.24
N50	8725
NG50	8725
N90	8538
NG90	8538
auN	10153.5
auNG	9962.7
L50	2
LG50	2
L90	3
LG90	3
# 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 (%)	97.885
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	12290
Total aligned length	29553
NA50	8725
NGA50	8725
NA90	8538
NGA90	8538
auNA	10153.5
auNGA	9962.7
LA50	2
LGA50	2
LA90	3
LGA90	3

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

	no_error_reads_hiseq_5k_dbg_k_40
# 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
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

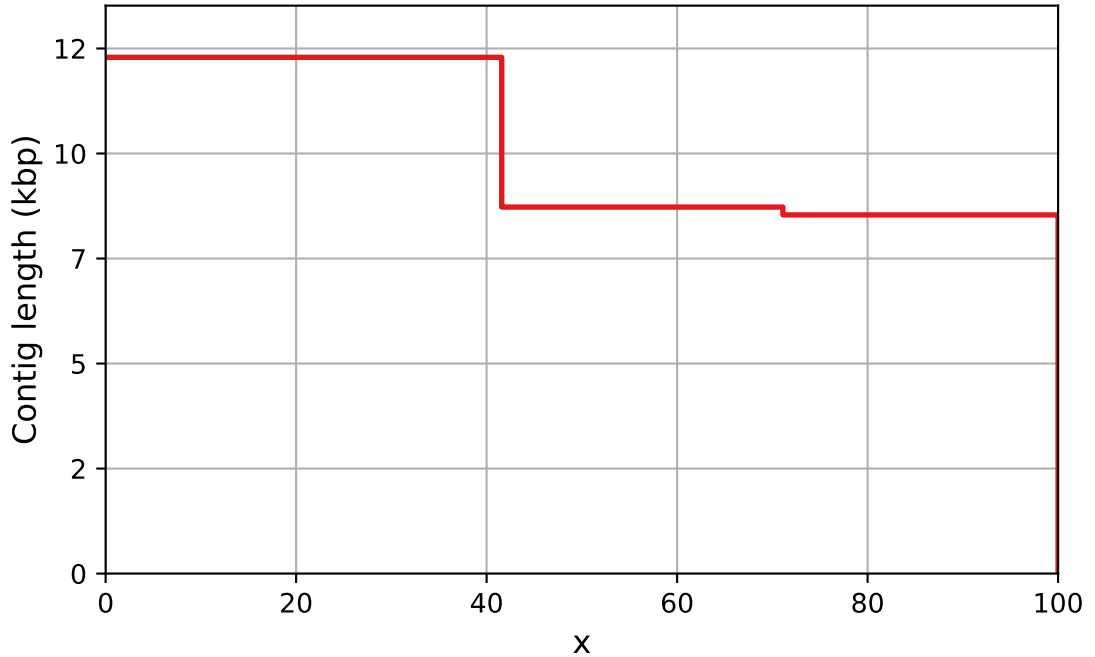
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	no_error_reads_hiseq_5k_dbg_k_40
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

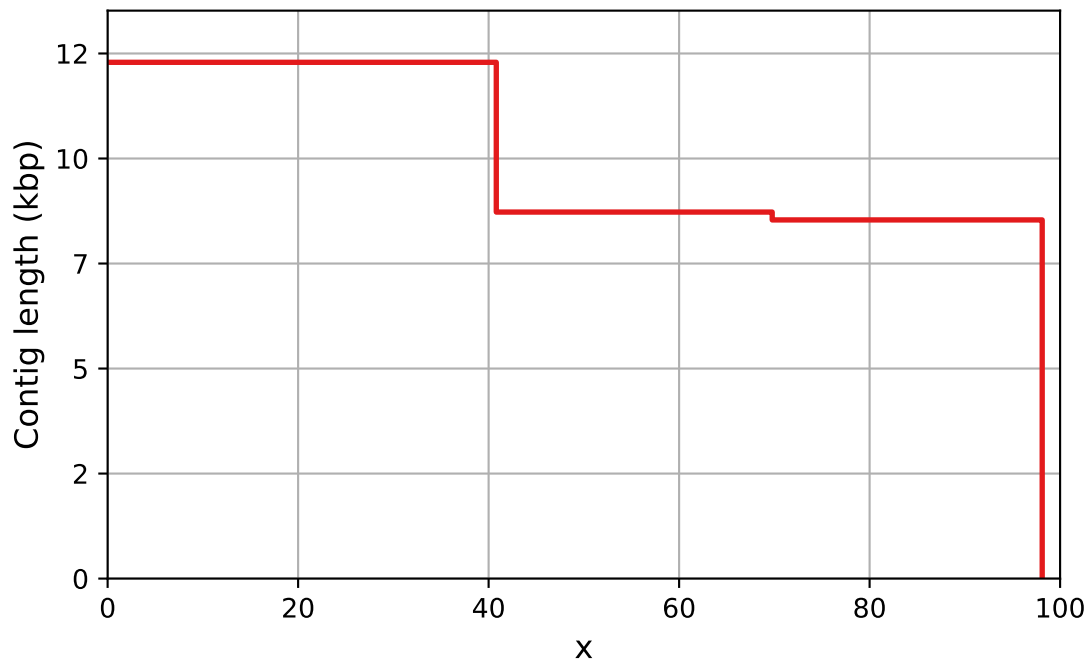
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



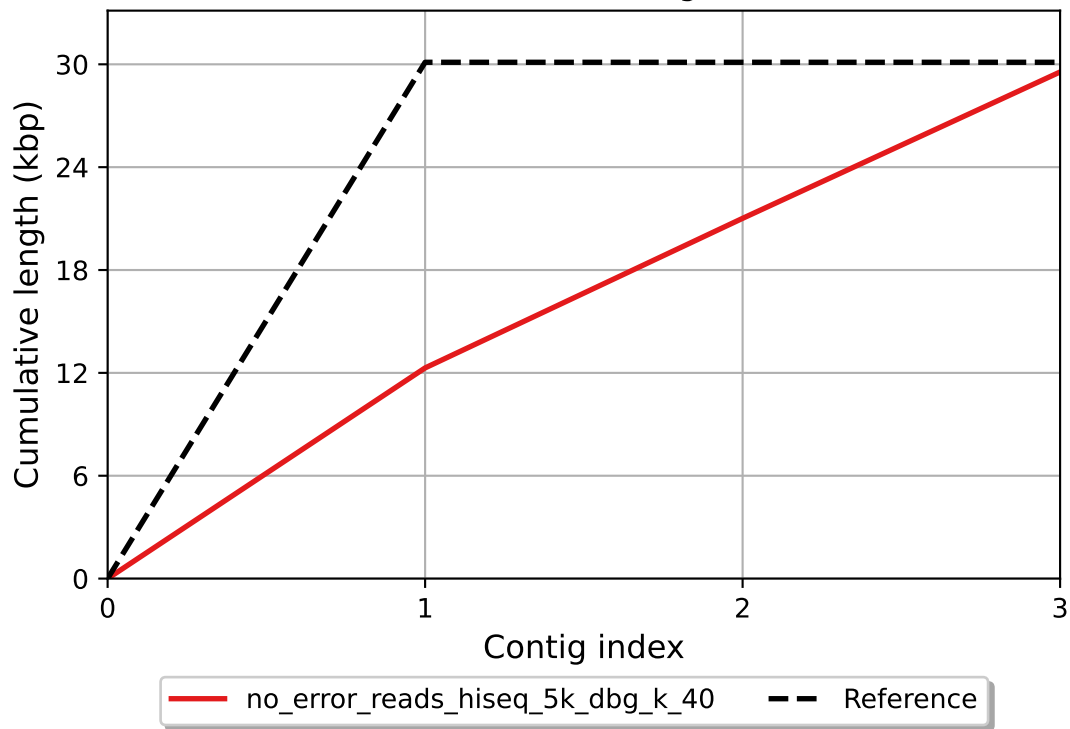
no_error_reads_hiseq_5k_dbg_k_40

NGx

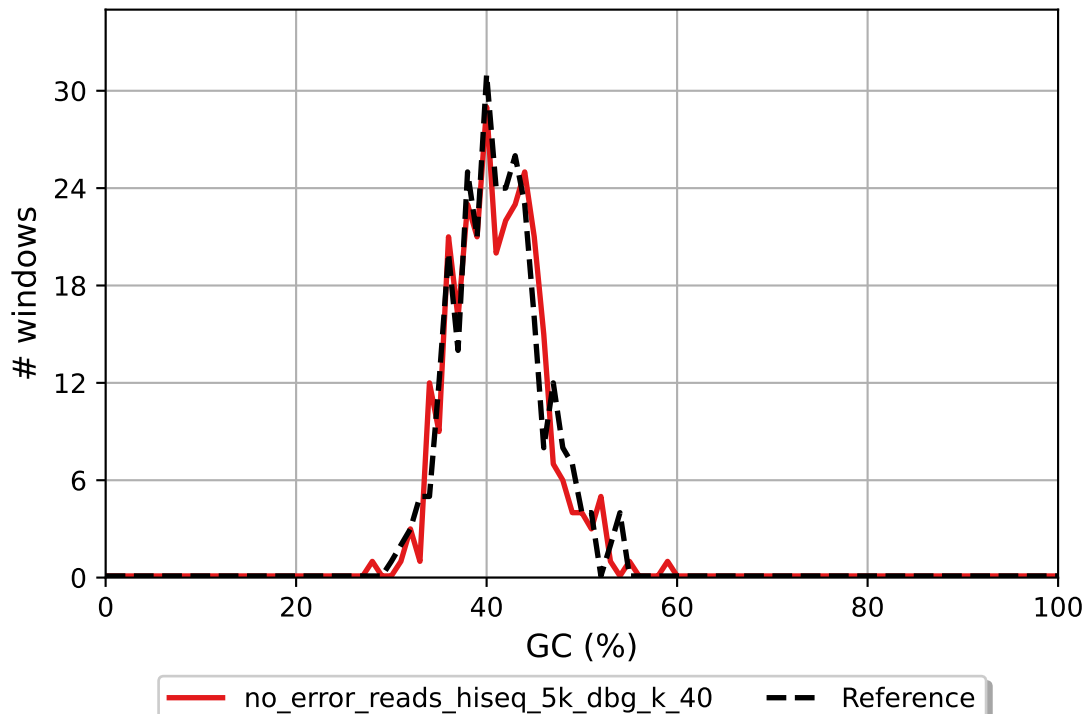


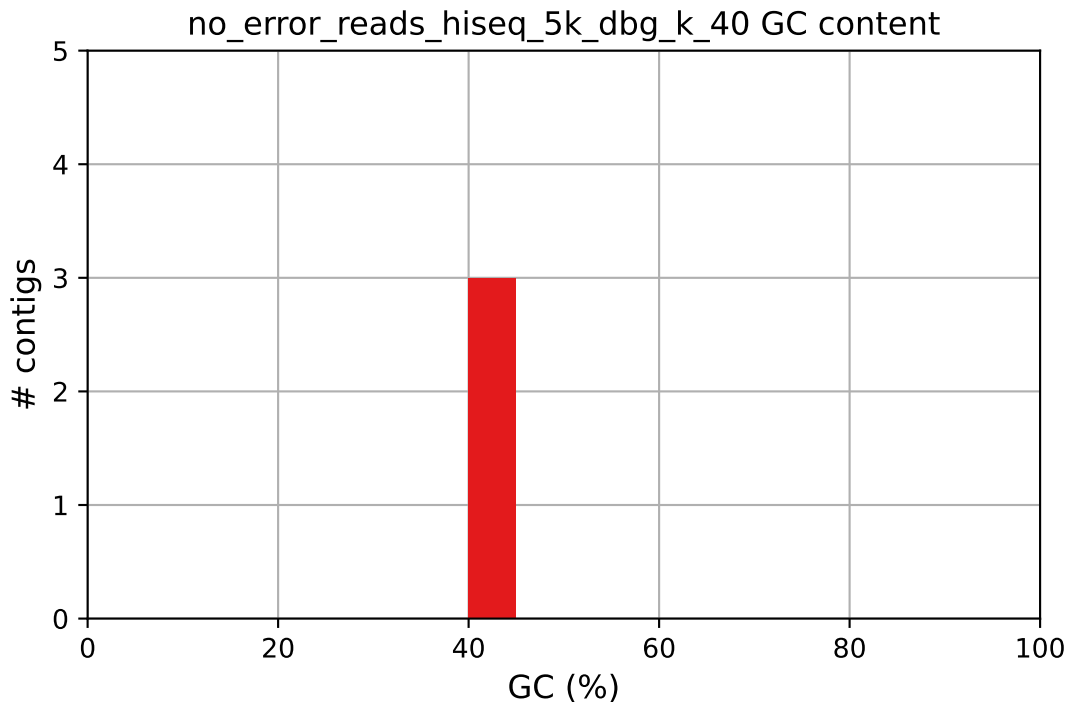
no_error_reads_hiseq_5k_dbg_k_40

Cumulative length



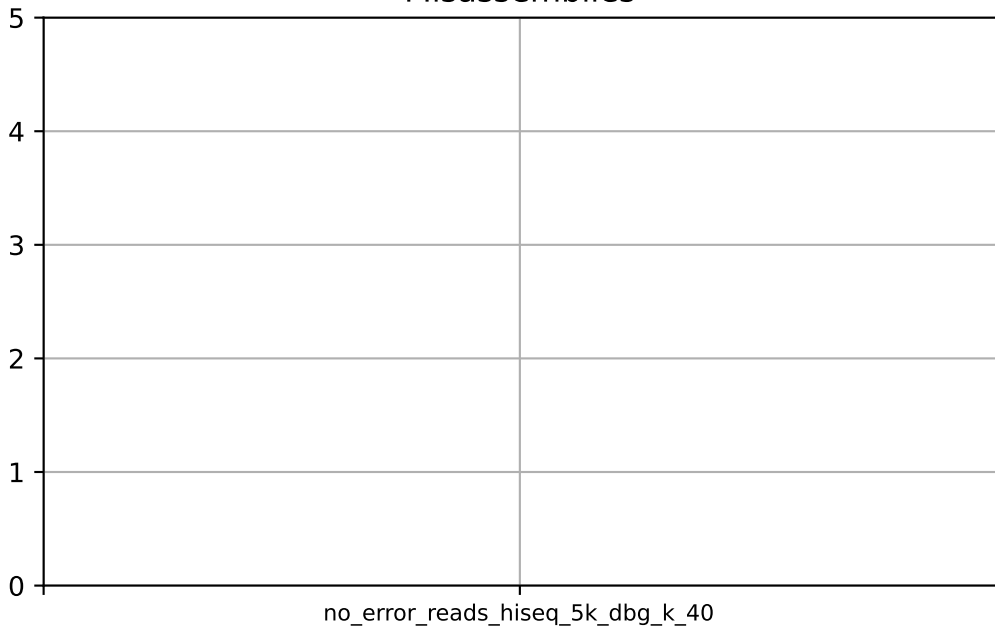
GC content



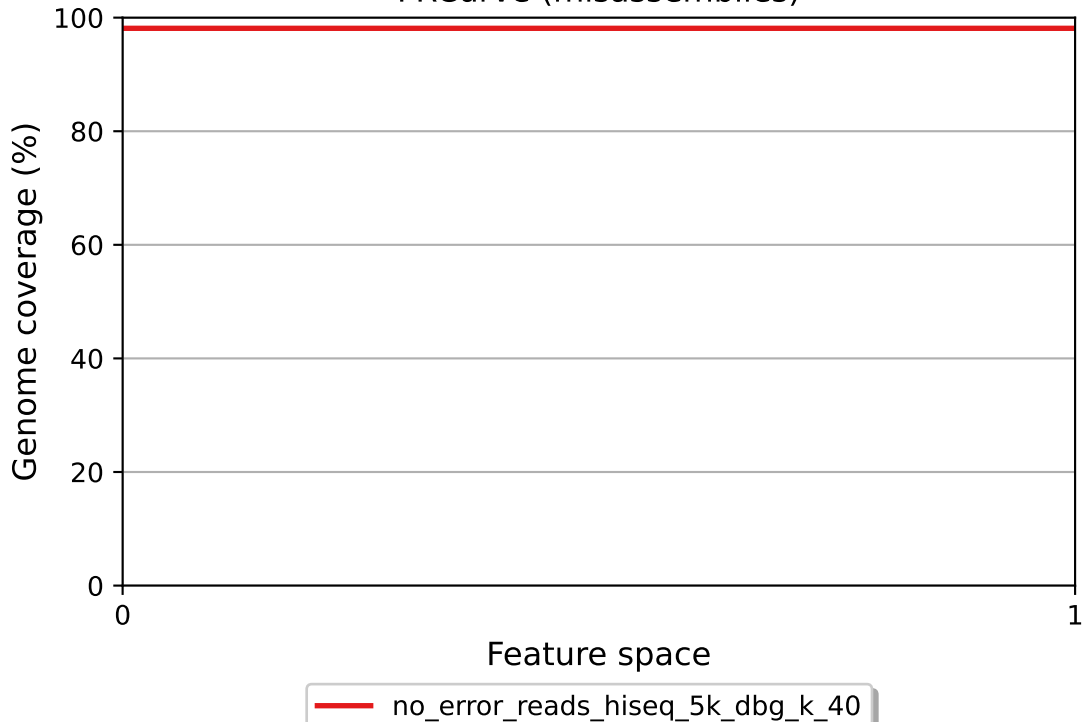


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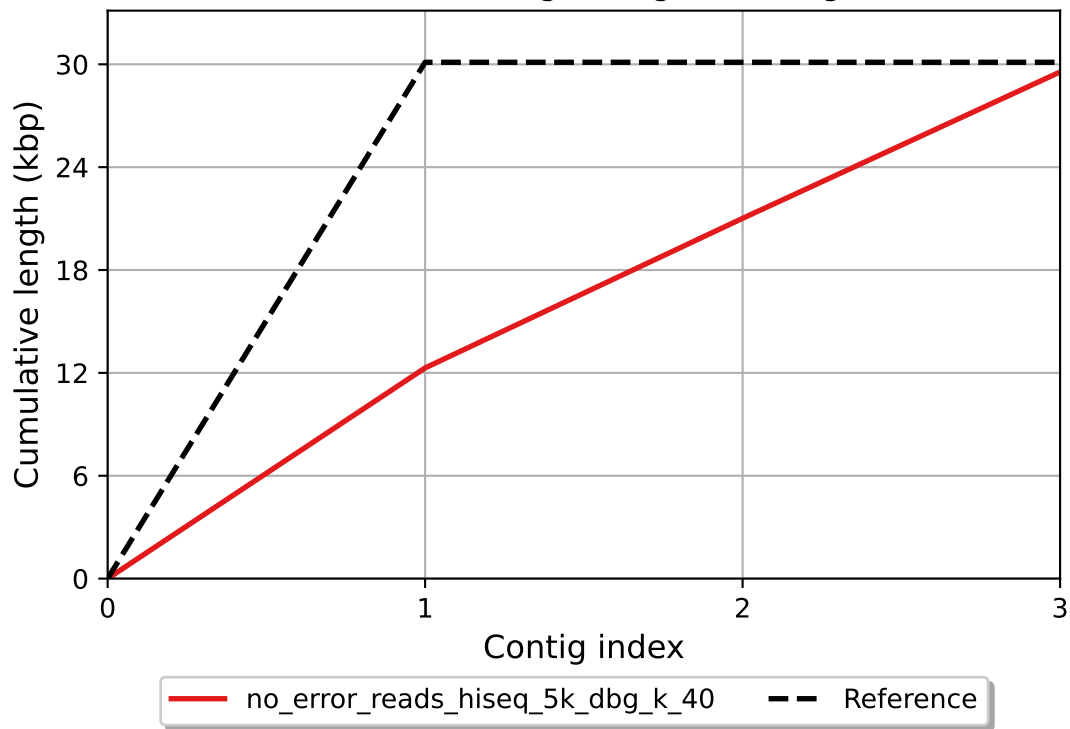
Misassemblies



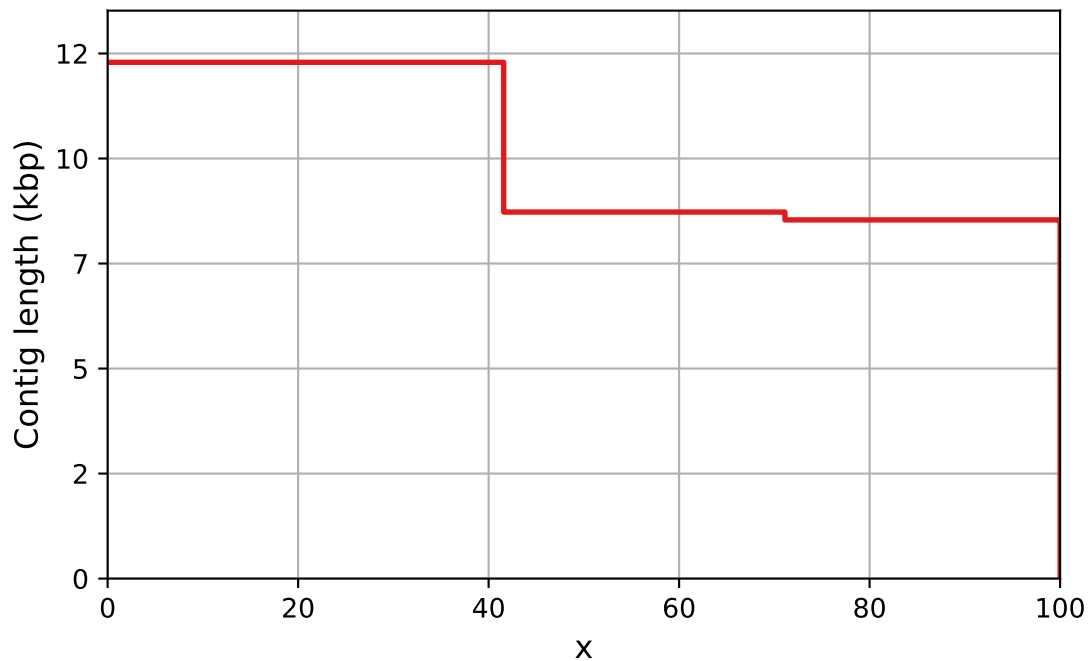
FRCurve (misassemblies)



Cumulative length (aligned contigs)

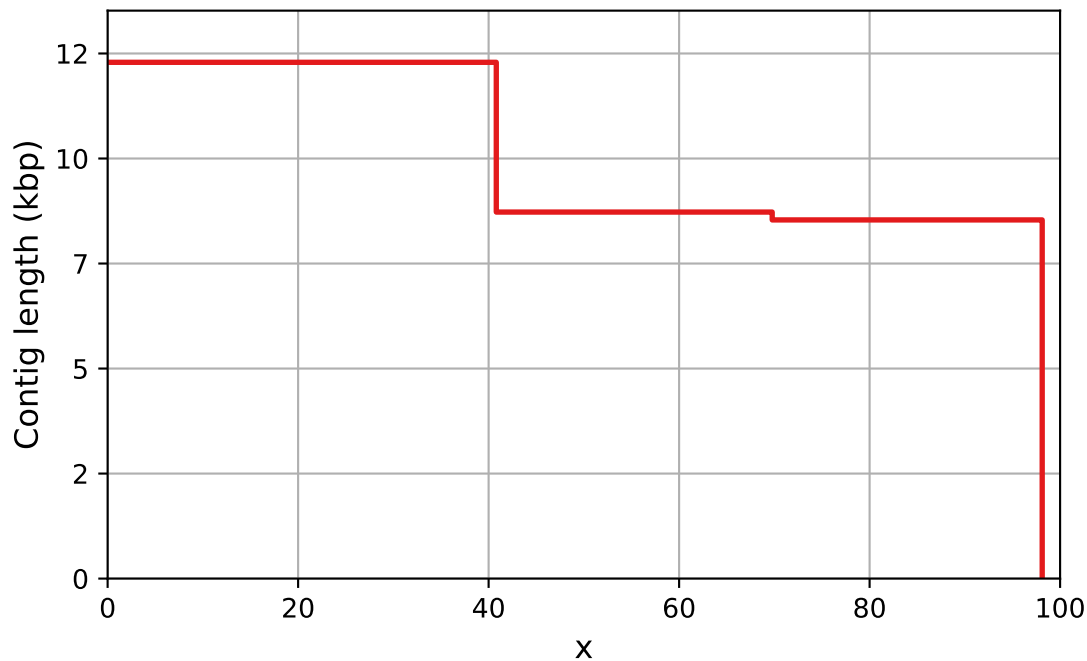


NAx



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NGAx



no_error_reads_hiseq_5k_dbg_k_40