

## Report

	no_error_reads_hiseq_5k_dbg_k40
# contigs (>= 0 bp)	42
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	30934
Total length (>= 1000 bp)	26330
Total length (>= 5000 bp)	8371
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	8371
Total length	28361
Reference length	30119
GC (%)	41.35
Reference GC (%)	41.24
N50	4173
NG50	4173
N90	1056
NG90	863
auN	4623.8
auNG	4354.0
L50	3
LG50	3
L90	8
LG90	9
# 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	3 + 0 part
Unaligned length	1168
Genome fraction (%)	89.907
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	8371
Total aligned length	27193
NA50	4173
NGA50	4173
NA90	1056
NGA90	863
auNA	4607.7
auNGA	4338.7
LA50	3
LGA50	3
LA90	8
LGA90	9

All statistics are based on contigs of size >= 300 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_k40
# 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

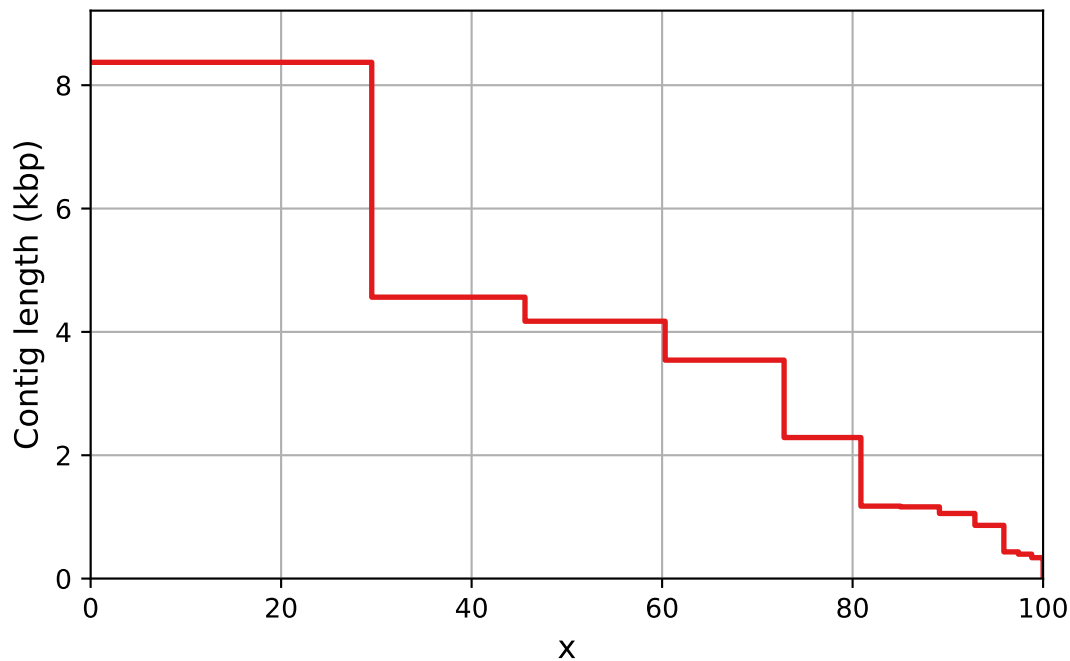
All statistics are based on contigs of size  $\geq 300$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	no_error_reads_hiseq_5k_dbg_k40
# fully unaligned contigs	3
Fully unaligned length	1168
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

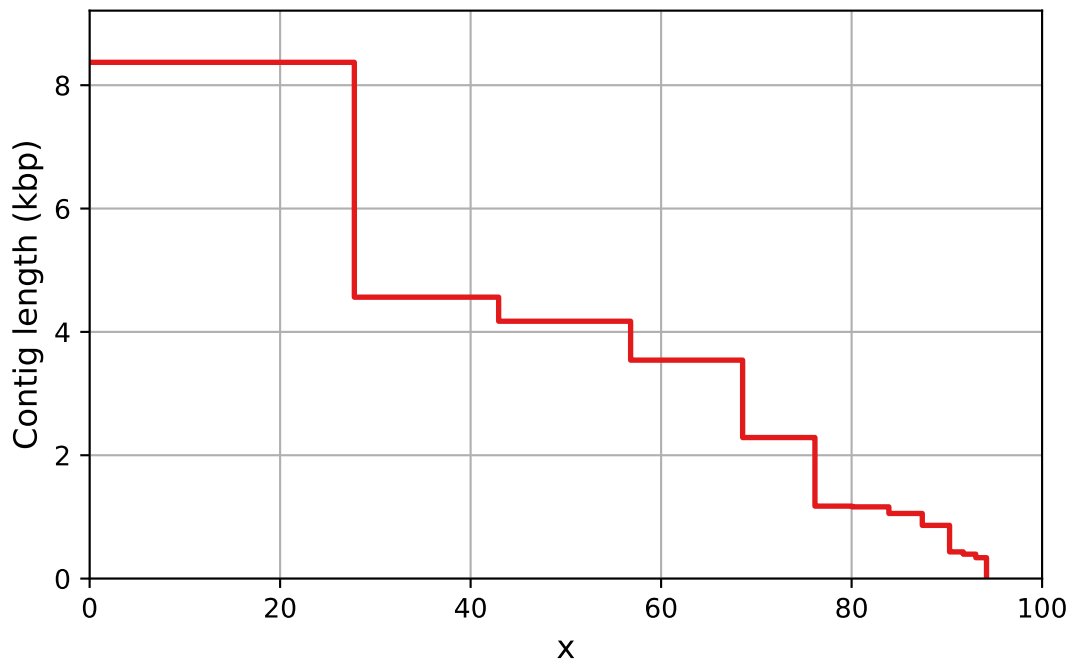
All statistics are based on contigs of size  $\geq 300$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



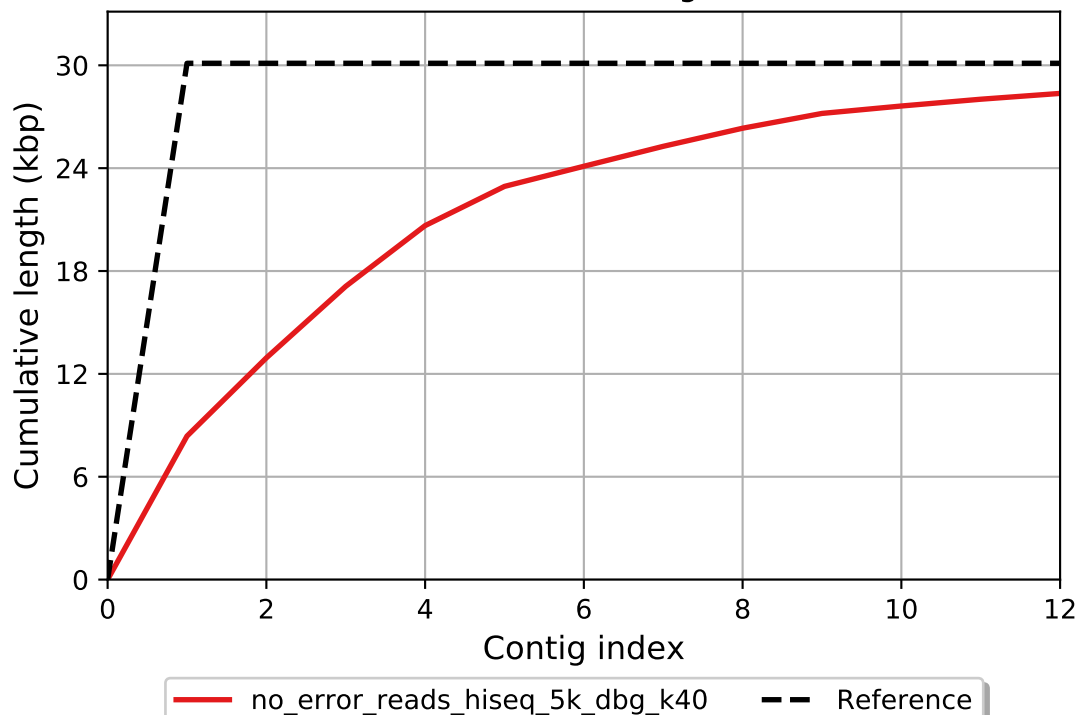
no\_error\_reads\_hiseq\_5k\_dbg\_k40

# NGx

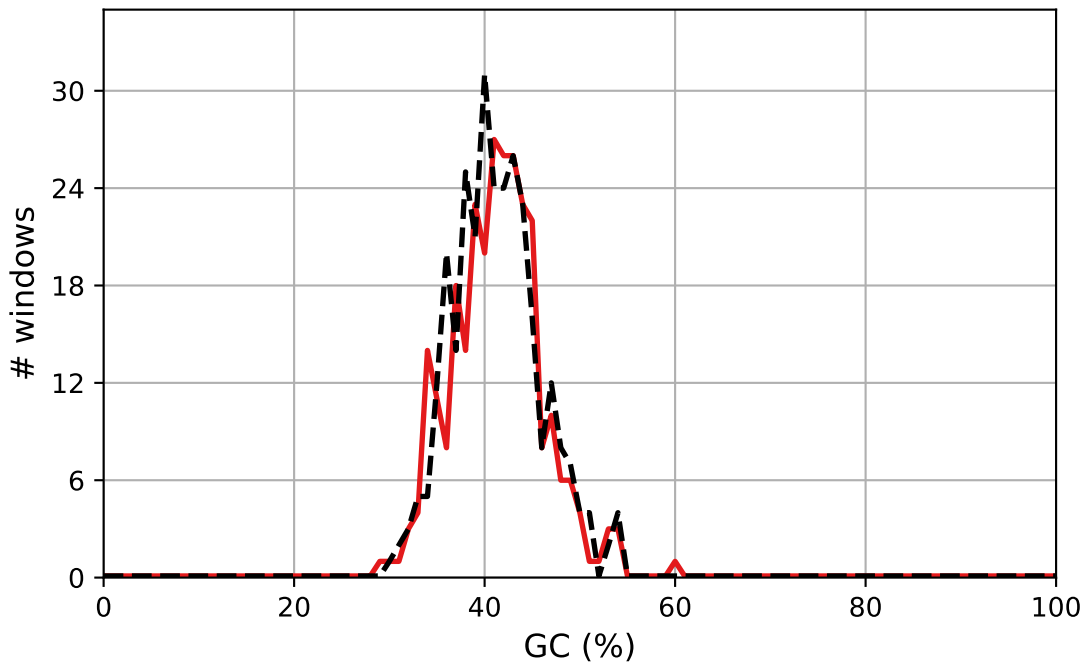


— no\_error\_reads\_hiseq\_5k\_dbg\_k40

Cumulative length

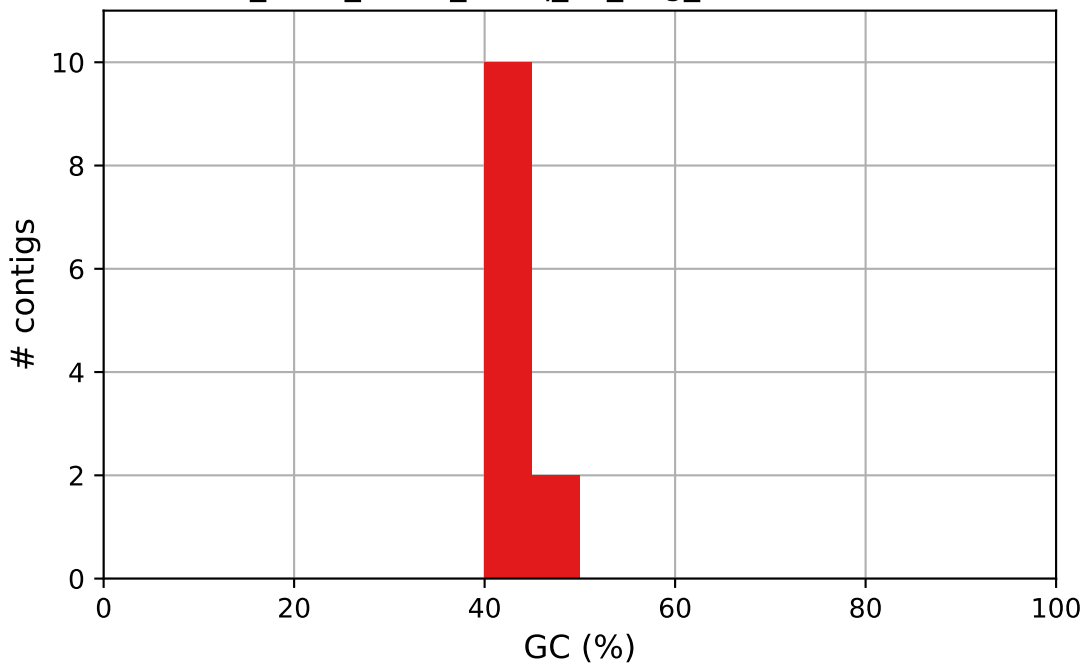


## GC content



no\_error\_reads\_hiseq\_5k\_dbg\_k40      Reference

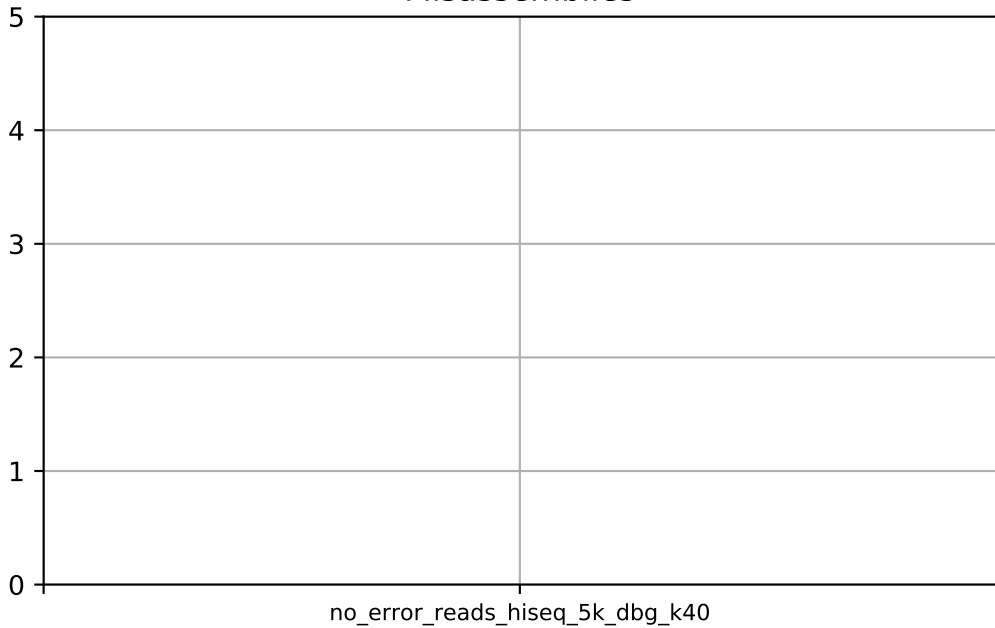
no\_error\_reads\_hiseq\_5k\_dbg\_k40 GC content



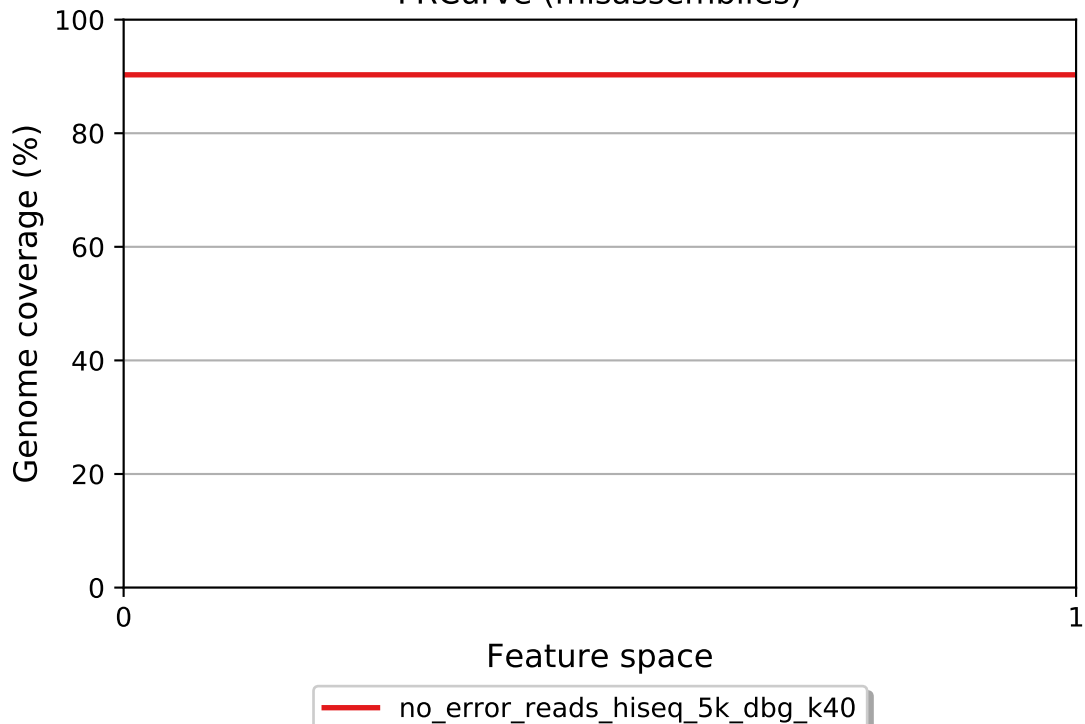
no\_error\_reads\_hiseq\_5k\_dbg\_k40



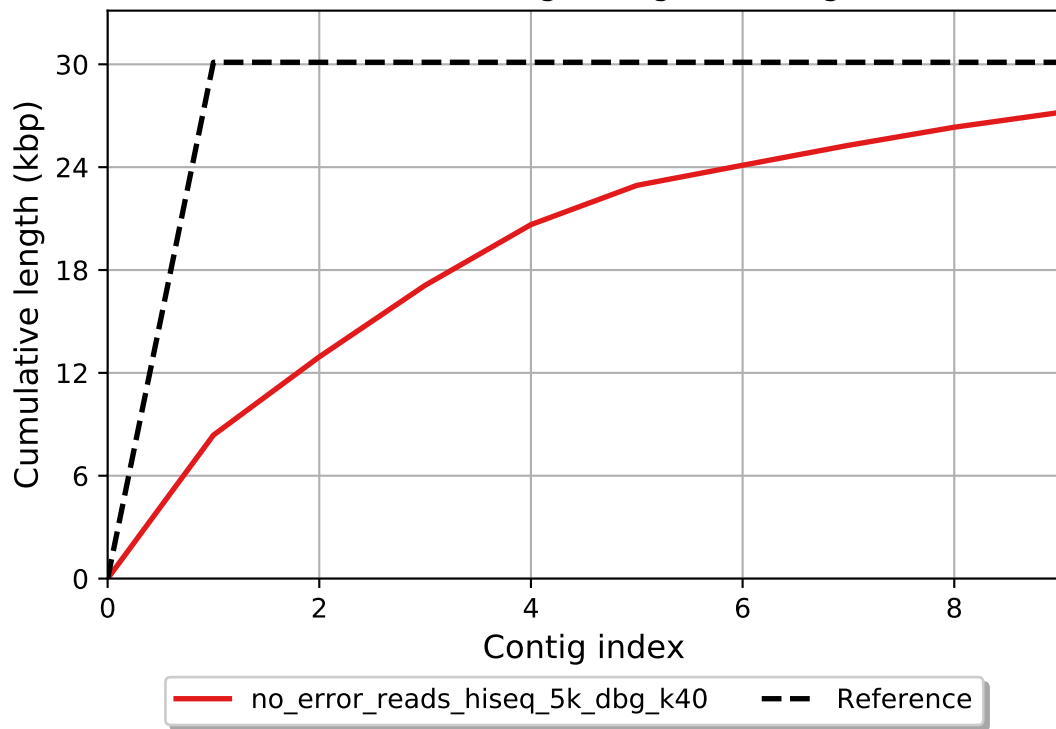
## Misassemblies



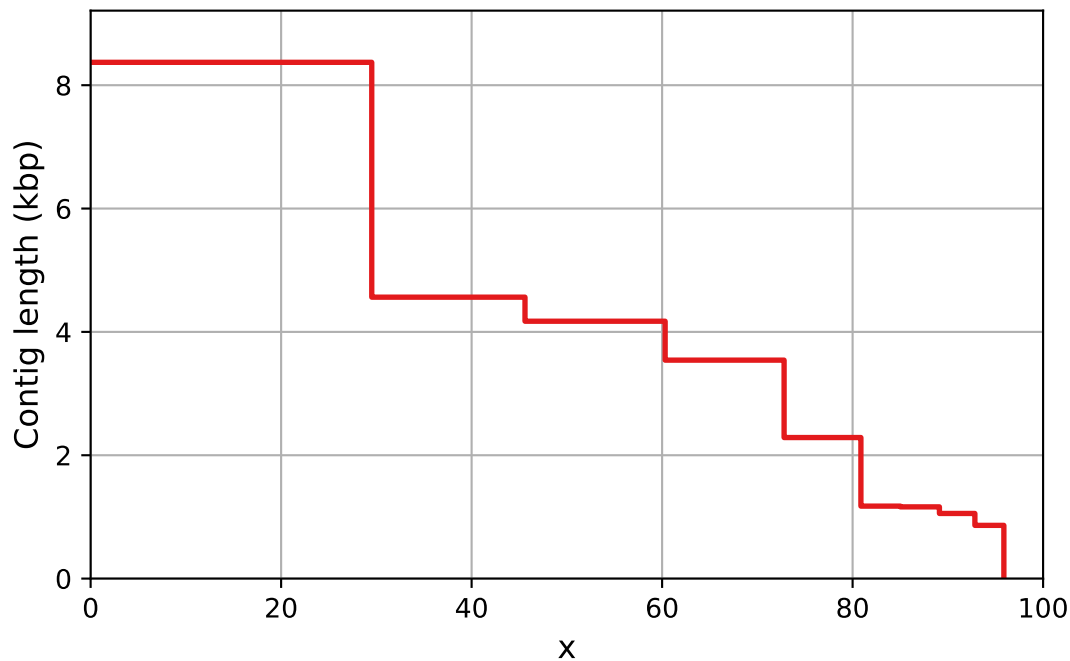
FRCurve (misassemblies)



Cumulative length (aligned contigs)

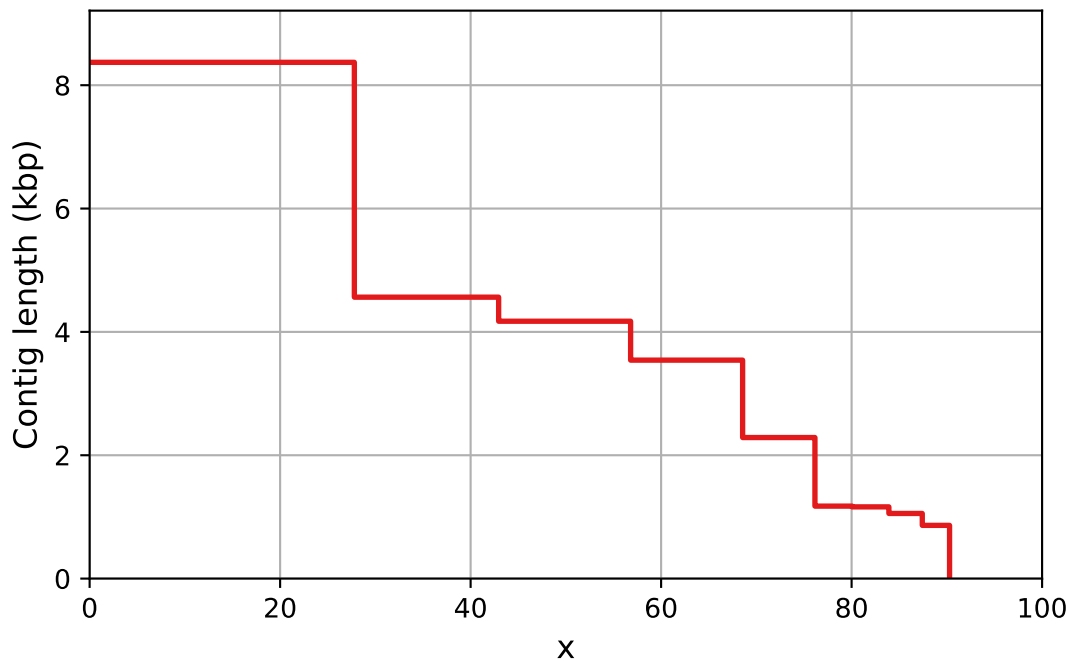


NAx



— no\_error\_reads\_hiseq\_5k\_dbg\_k40

# NGAx



— no\_error\_reads\_hiseq\_5k\_dbg\_k40