

Report

	DV3
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	8783868
Total length (>= 1000 bp)	8783868
Total length (>= 5000 bp)	8783868
Total length (>= 10000 bp)	8783868
Total length (>= 25000 bp)	8783868
Total length (>= 50000 bp)	8783868
# contigs	4
Largest contig	7007906
Total length	8783868
Reference length	10838897
GC (%)	72.00
Reference GC (%)	72.03
N50	7007906
NG50	7007906
N75	7007906
NG75	551129
L50	1
LG50	1
L75	1
LG75	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 (%)	80.838
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	0.82
Largest alignment	7007906
Total aligned length	8783795
NA50	7007906
NGA50	7007906
NA75	7007906
NGA75	551059
LA50	1
LGA50	1
LA75	1
LGA75	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

	DV3
# 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	16
# indels	72
# indels (<= 5 bp)	69
# indels (> 5 bp)	3
Indels length	116

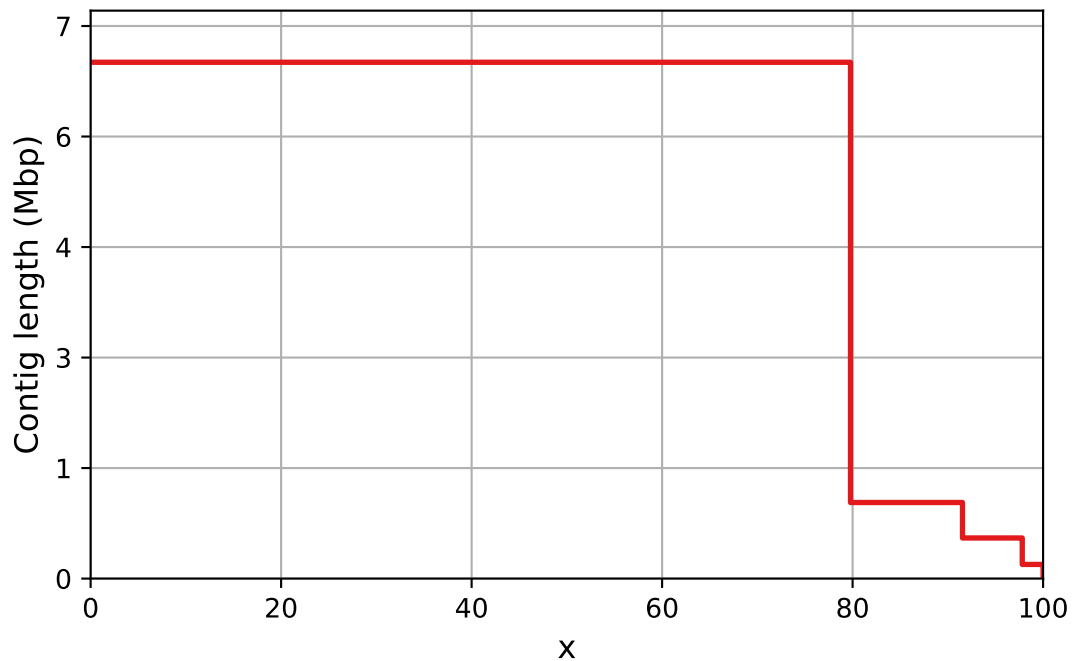
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	DV3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

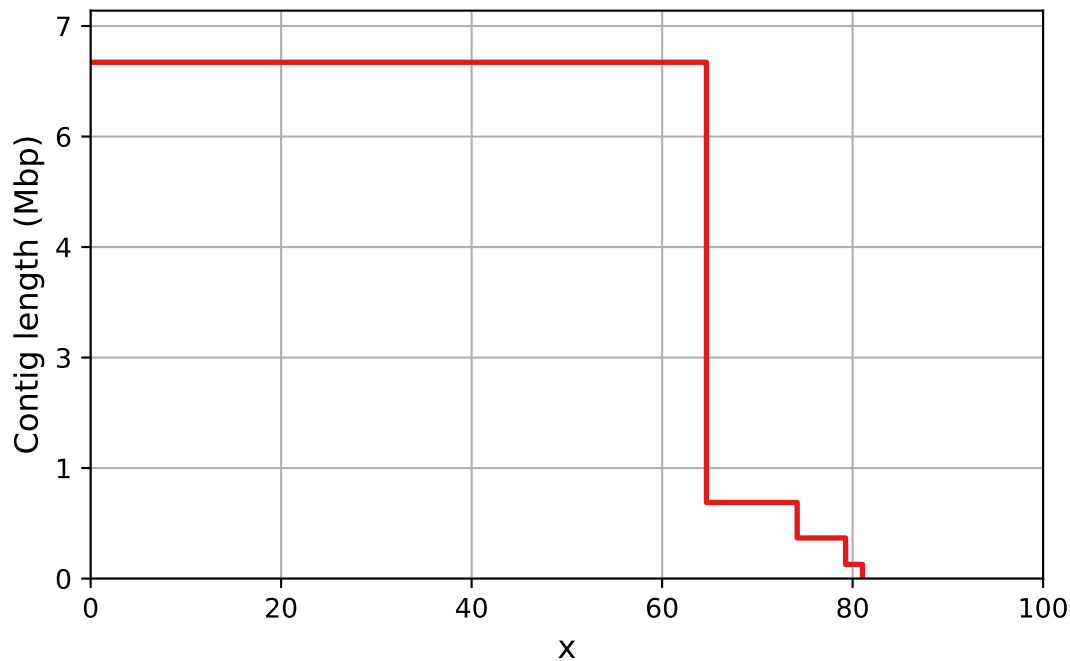
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



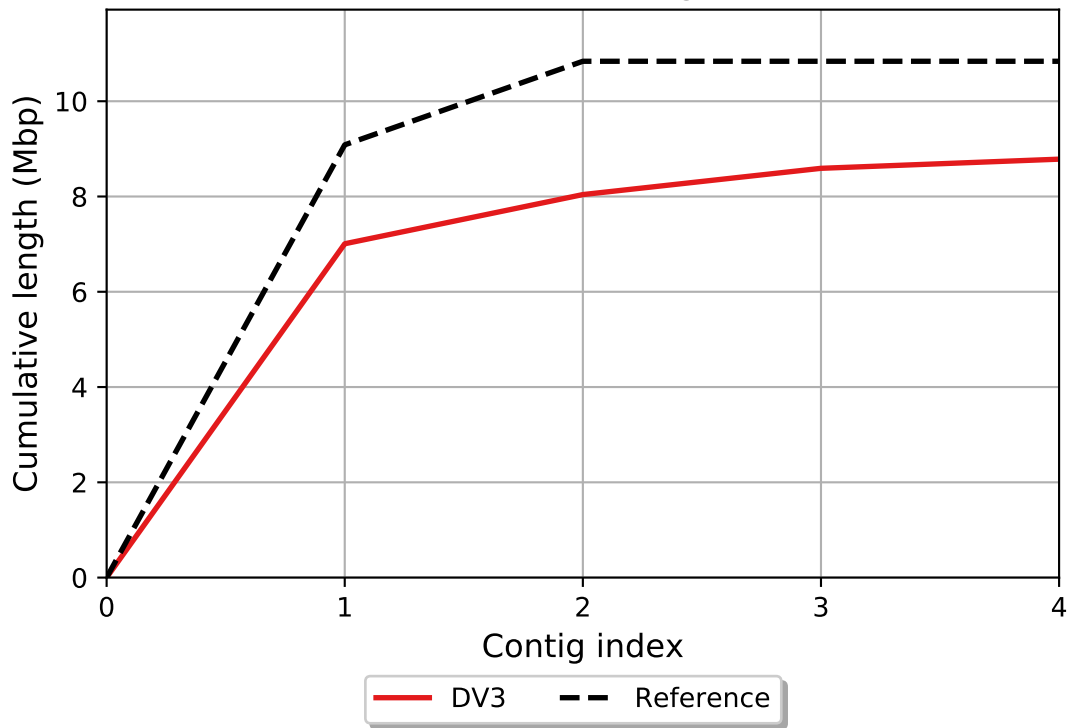
DV3

NGx

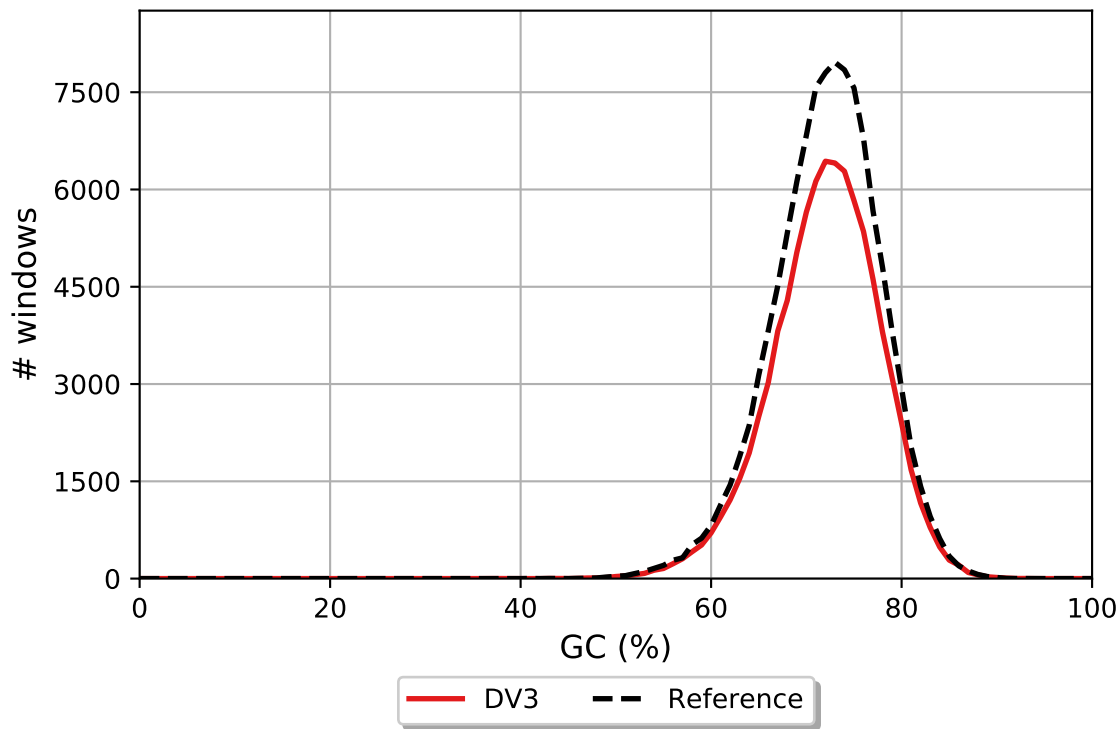


DV3

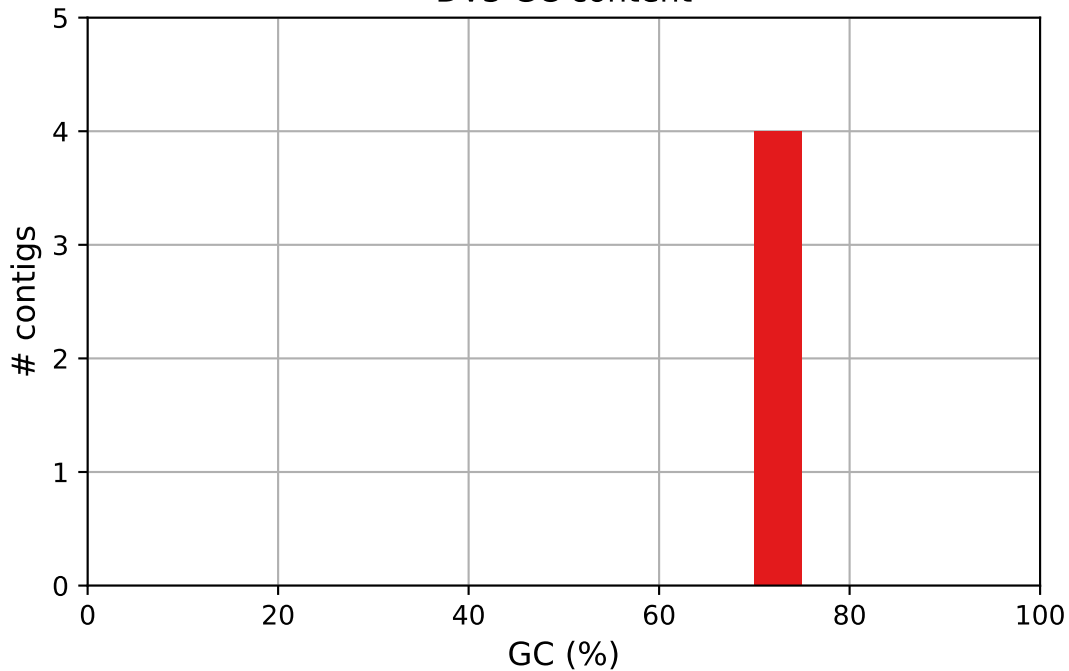
Cumulative length



GC content

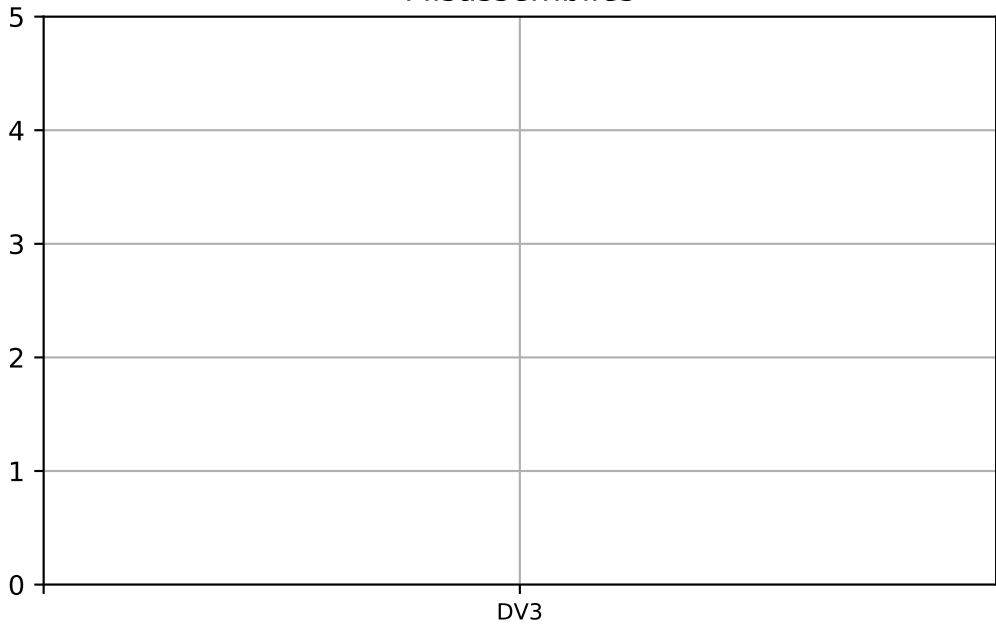


DV3 GC content

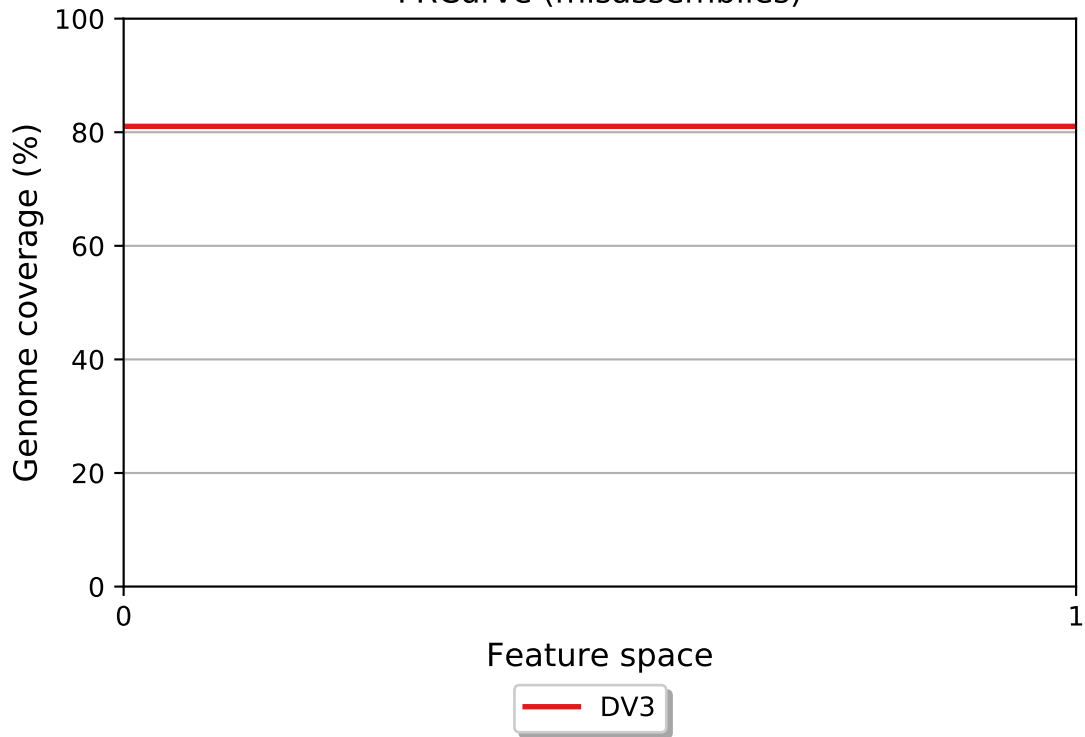


DV3

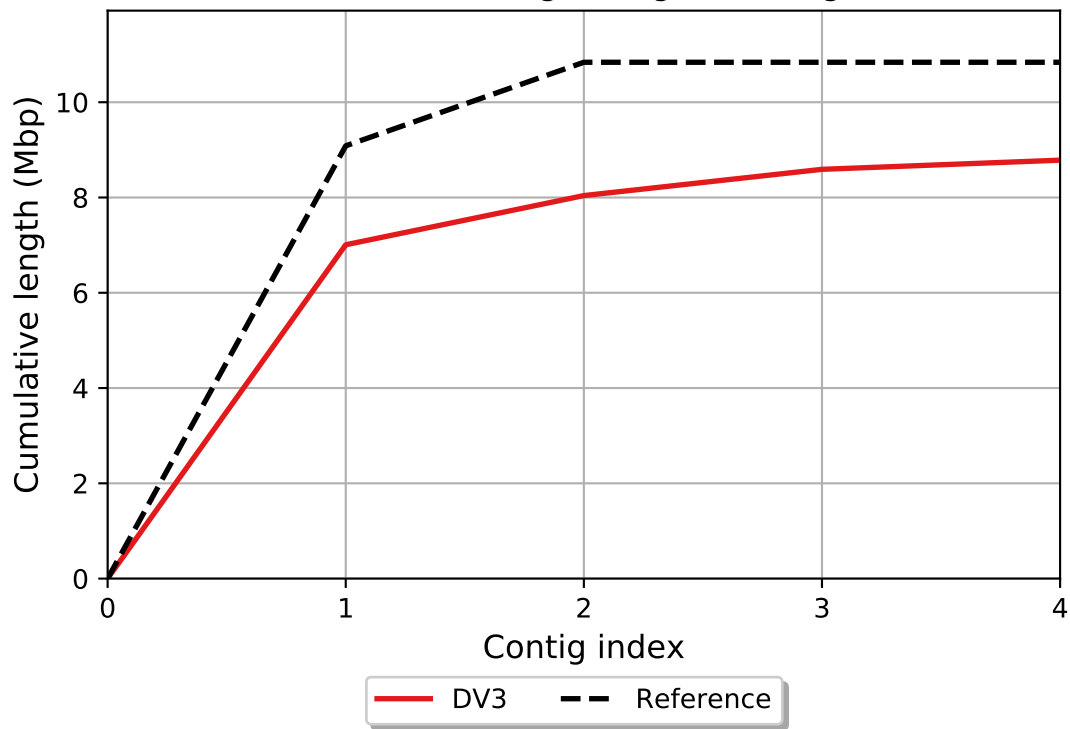
Misassemblies



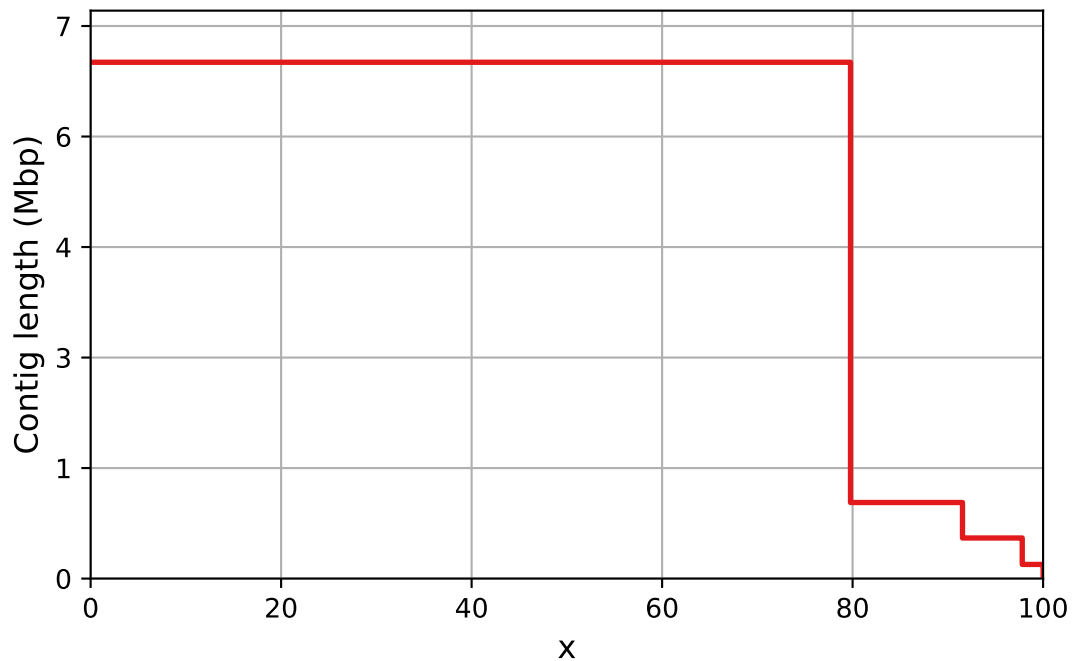
FRCurve (misassemblies)



Cumulative length (aligned contigs)

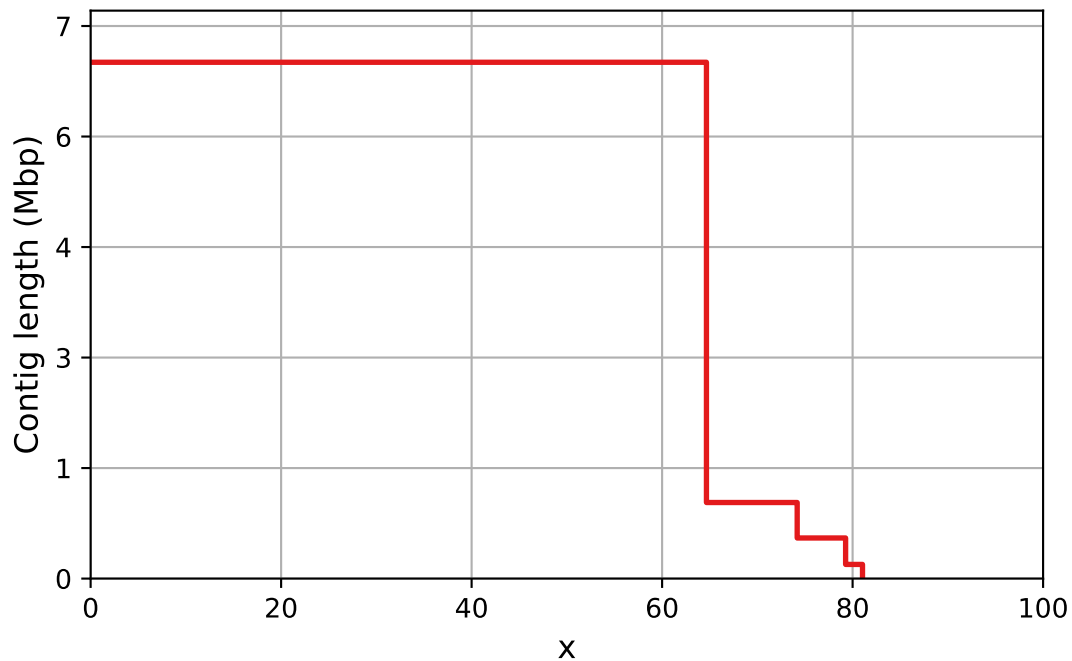


NAx



DV3

NGAx



DV3