

Report

	Shovill_on_data_6_and_data_5__Contigs
# contigs (>= 0 bp)	66
# contigs (>= 1000 bp)	30
Total length (>= 0 bp)	2748059
Total length (>= 1000 bp)	2735948
# contigs	35
Largest contig	723862
Total length	2739341
Reference length	2913900
GC (%)	32.84
Reference GC (%)	32.80
N50	346280
NG50	346280
N75	114772
NG75	61803
L50	3
LG50	3
L75	7
LG75	9
# misassemblies	60
# misassembled contigs	16
Misassembled contigs length	2462218
# local misassemblies	117
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 21 part
Unaligned length	287966
Genome fraction (%)	83.877
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1782.13
# indels per 100 kbp	62.23
Largest alignment	282948
Total aligned length	2449039
NA50	52616
NGA50	46345
NA75	21512
NGA75	15204
LA50	13
LGA50	15
LA75	33
LGA75	41

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

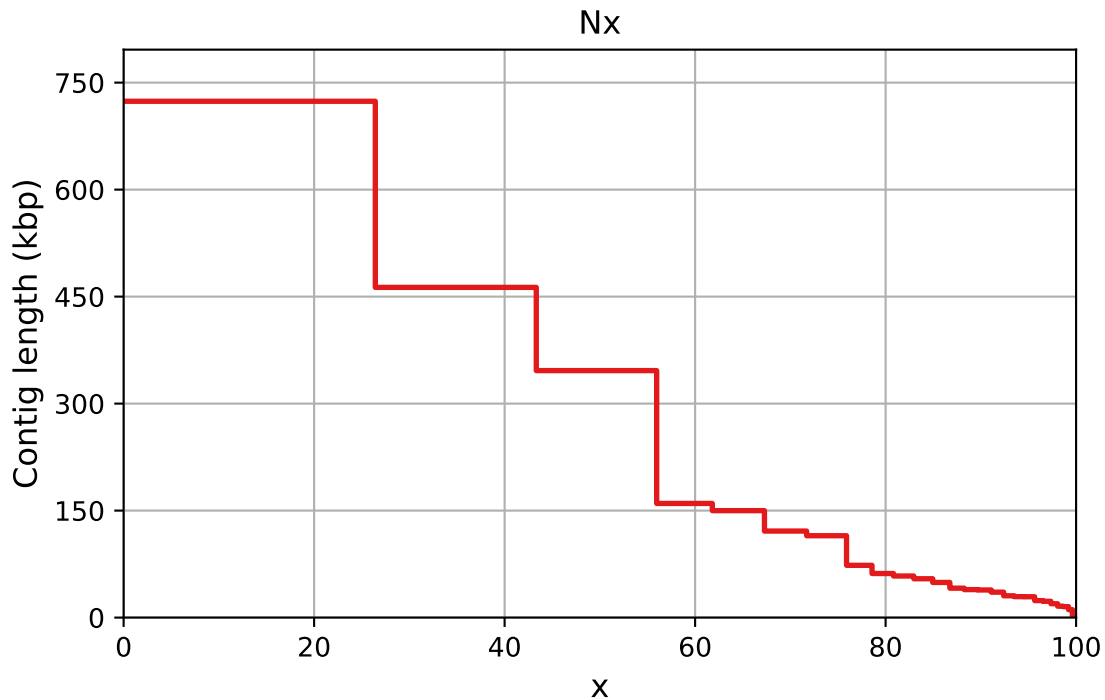
	Shovill_on_data_6_and_data_5_Contigs
# misassemblies	60
# contig misassemblies	60
# c. relocations	60
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	16
Misassembled contigs length	2462218
# local misassemblies	117
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	43557
# indels	1521
# indels (<= 5 bp)	1380
# indels (> 5 bp)	141
Indels length	5603

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

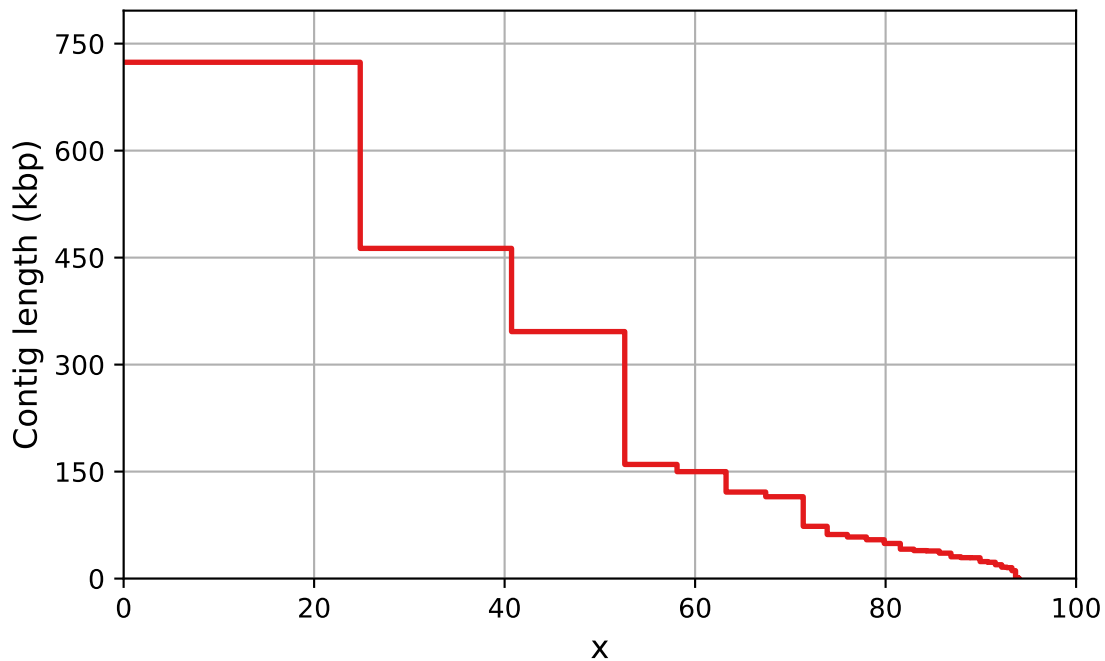
	Shovill_on_data_6_and_data_5__Contigs
# fully unaligned contigs	3
Fully unaligned length	2149
# partially unaligned contigs	21
Partially unaligned length	285817
# N's	0

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).

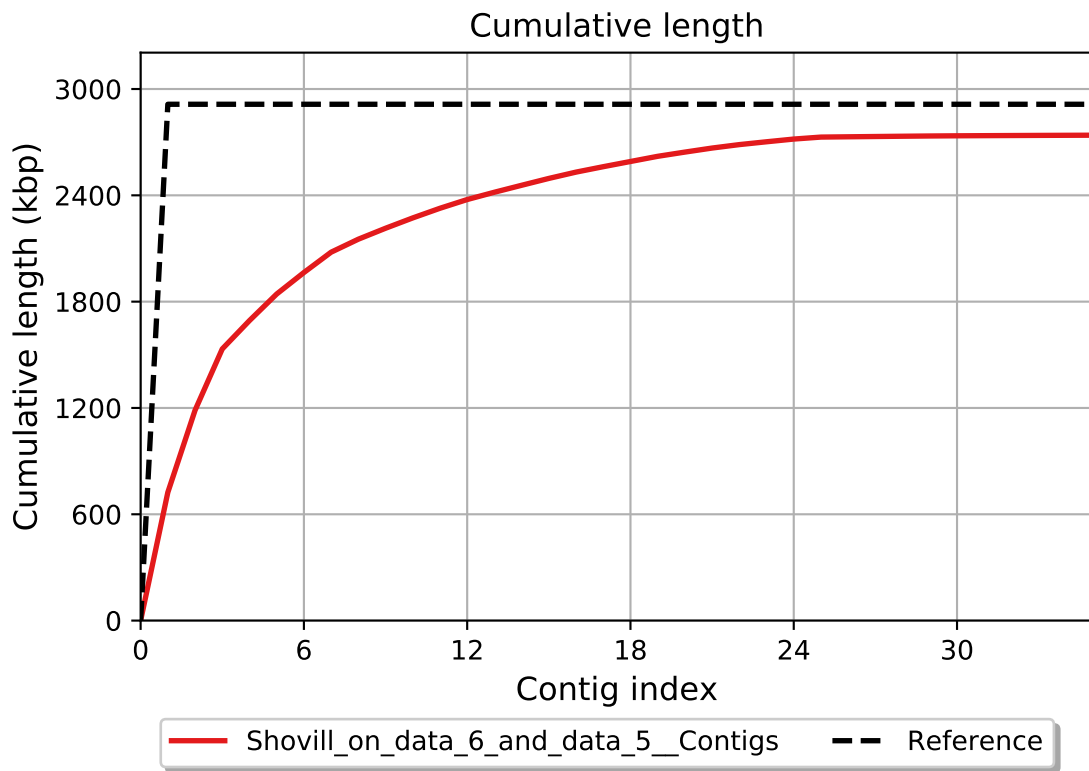


Shovill_on_data_6_and_data_5__Contigs

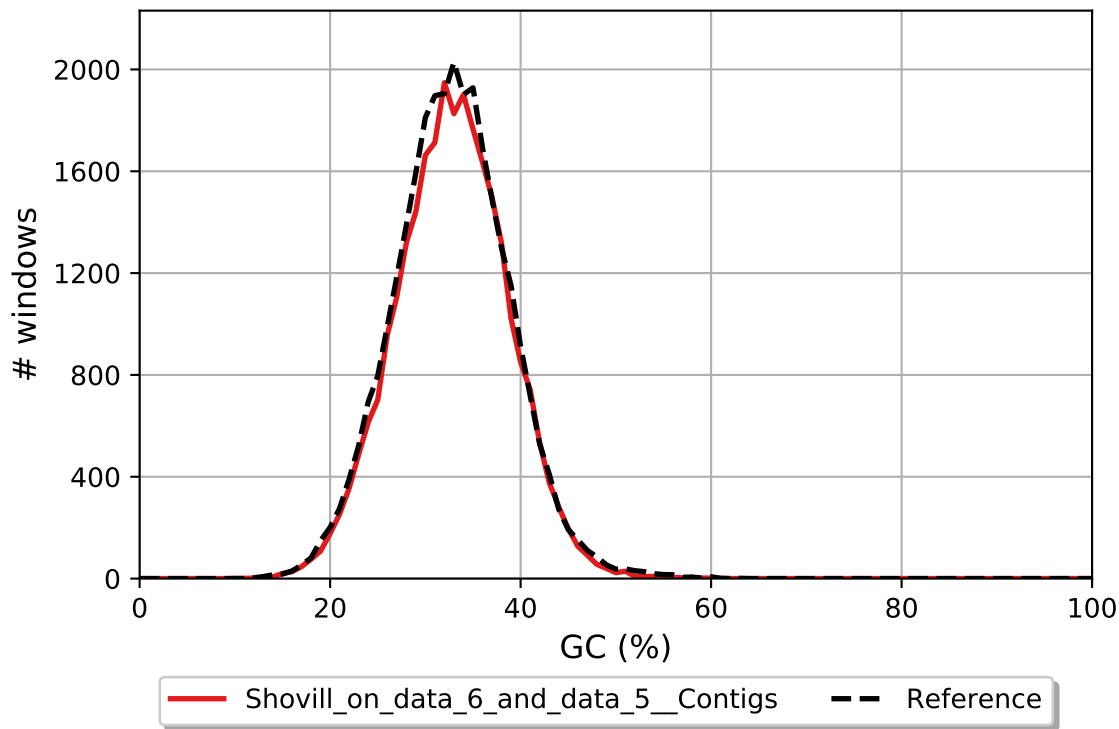
NGx



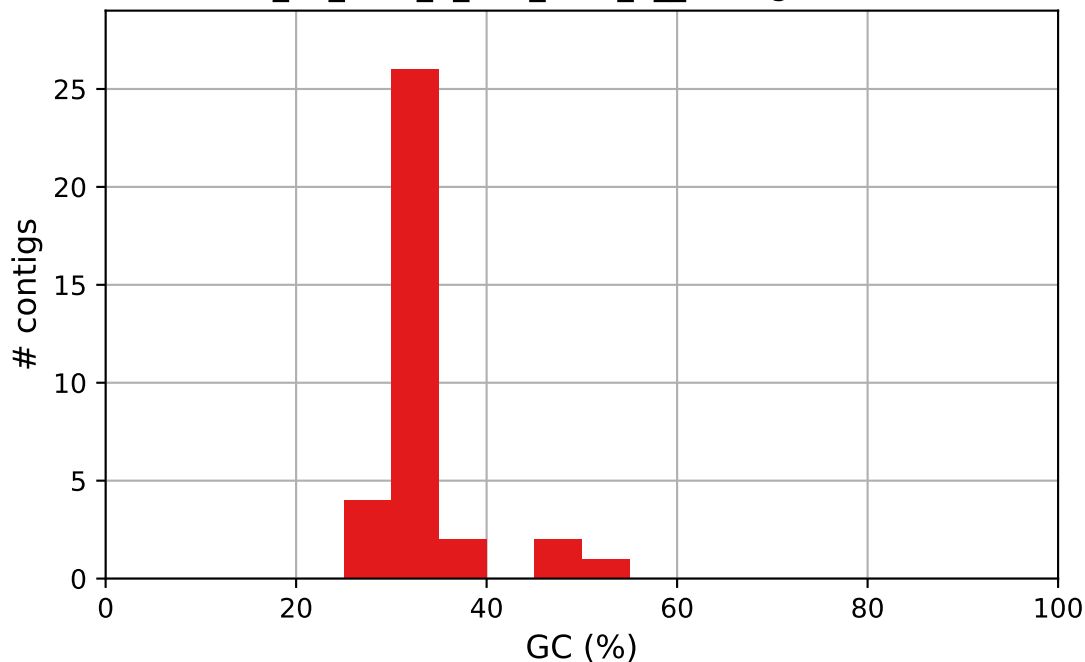
Shovill_on_data_6_and_data_5_Contigs



GC content

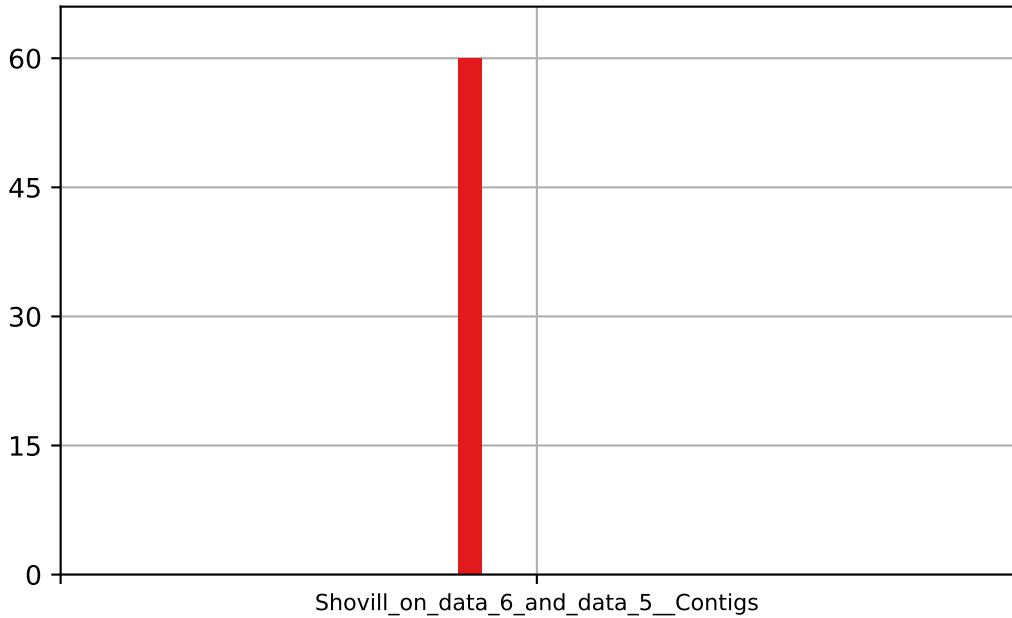


Shovill_on_data_6_and_data_5__Contigs GC content

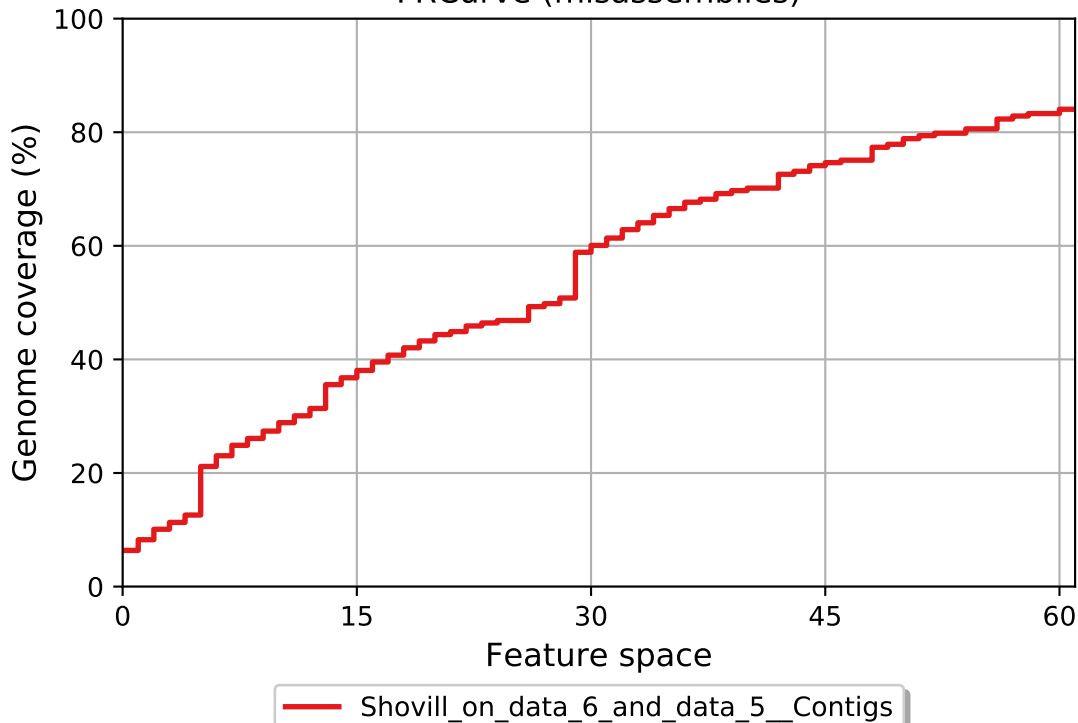


Shovill_on_data_6_and_data_5__Contigs

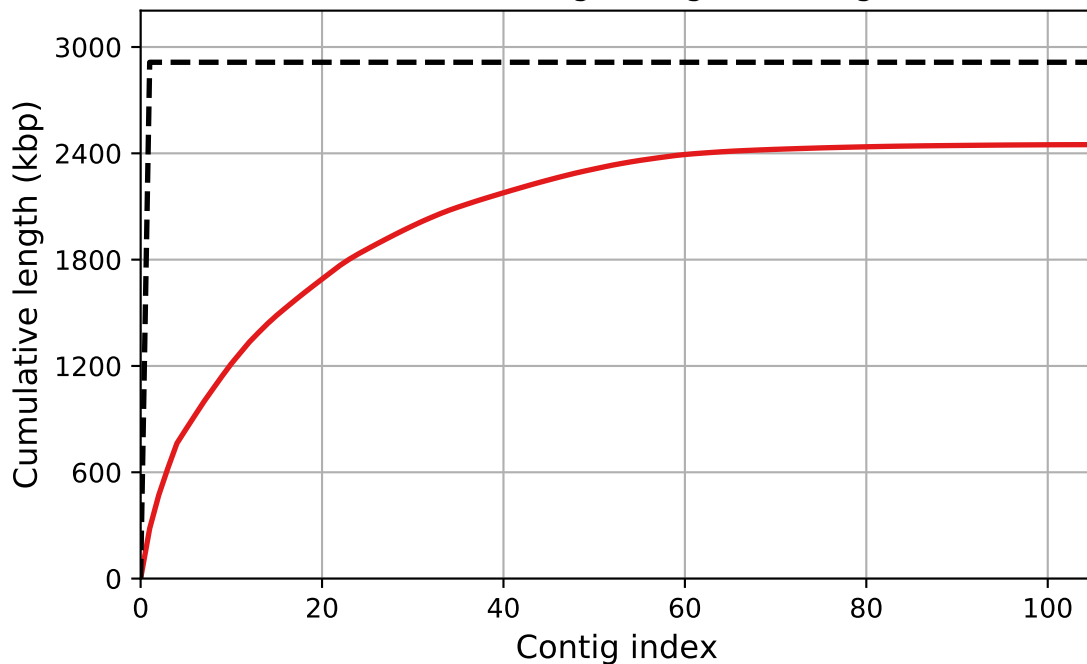
Misassemblies



FRCurve (misassemblies)

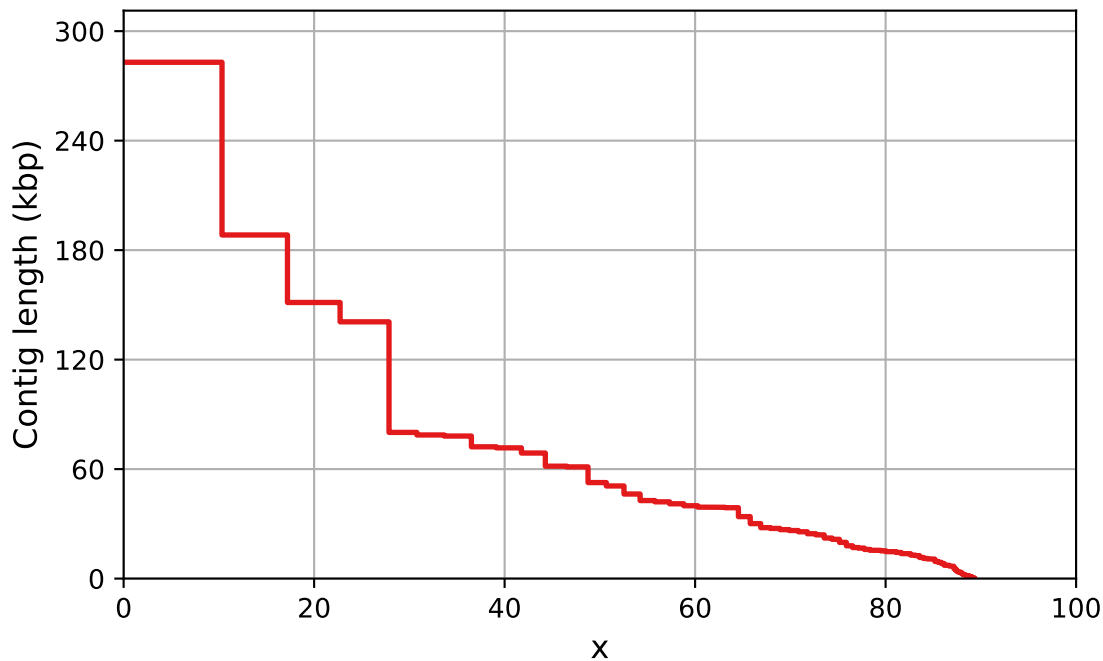


Cumulative length (aligned contigs)



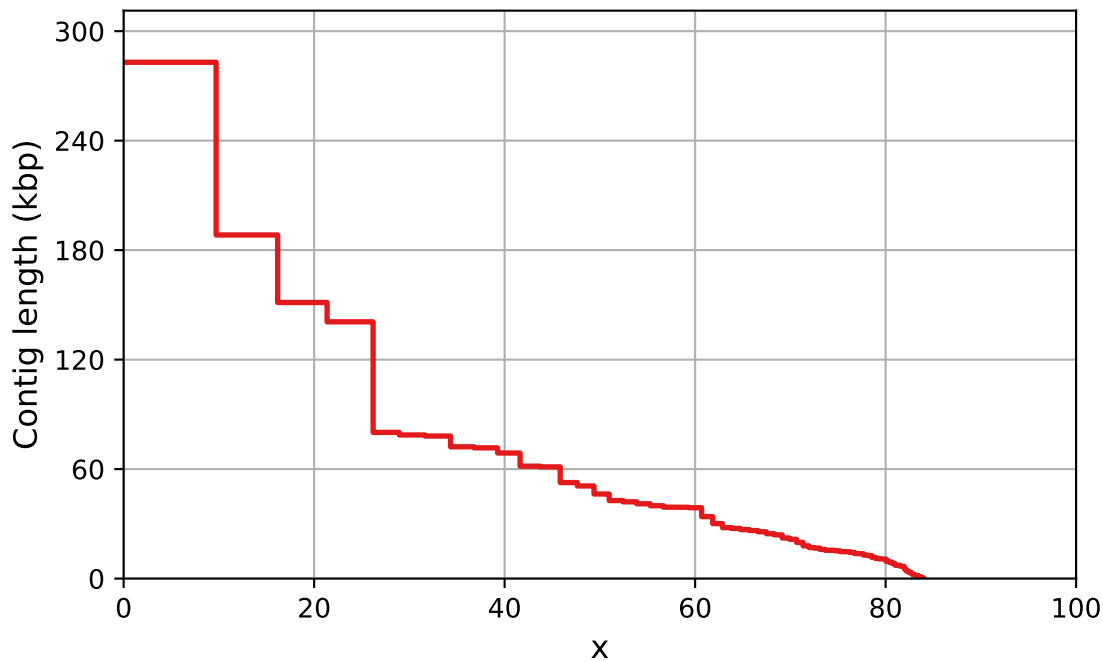
— Shovill_on_data_6_and_data_5_Contigs - - Reference

NAx



— Shovill_on_data_6_and_data_5_Contigs

NGAx



Shovill_on_data_6_and_data_5_Contigs