

Report

	Aba1_unmappedregions
# contigs (>= 0 bp)	64
# contigs (>= 1000 bp)	25
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	143467
Total length (>= 1000 bp)	114259
Total length (>= 5000 bp)	93320
Total length (>= 10000 bp)	59873
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	55
Largest contig	12482
Total length	141367
Reference length	4297393
GC (%)	41.06
Reference GC (%)	39.42
N50	5668
N75	1172
L50	7
L75	18
# 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 (%)	2.243
Duplication ratio	1.467
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	12482
Total aligned length	141367
NA50	5668
NGA50	-
NA75	1172
LA50	7
LA75	18

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

	Aba1_unmappedregions
# 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

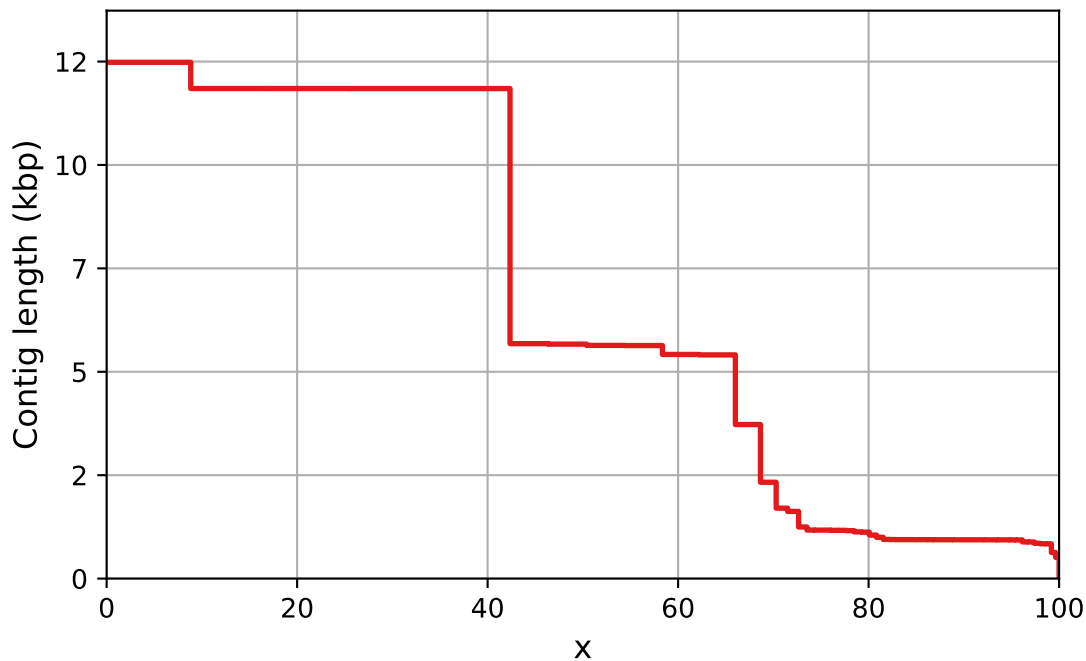
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	Aba1_unmappedregions
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

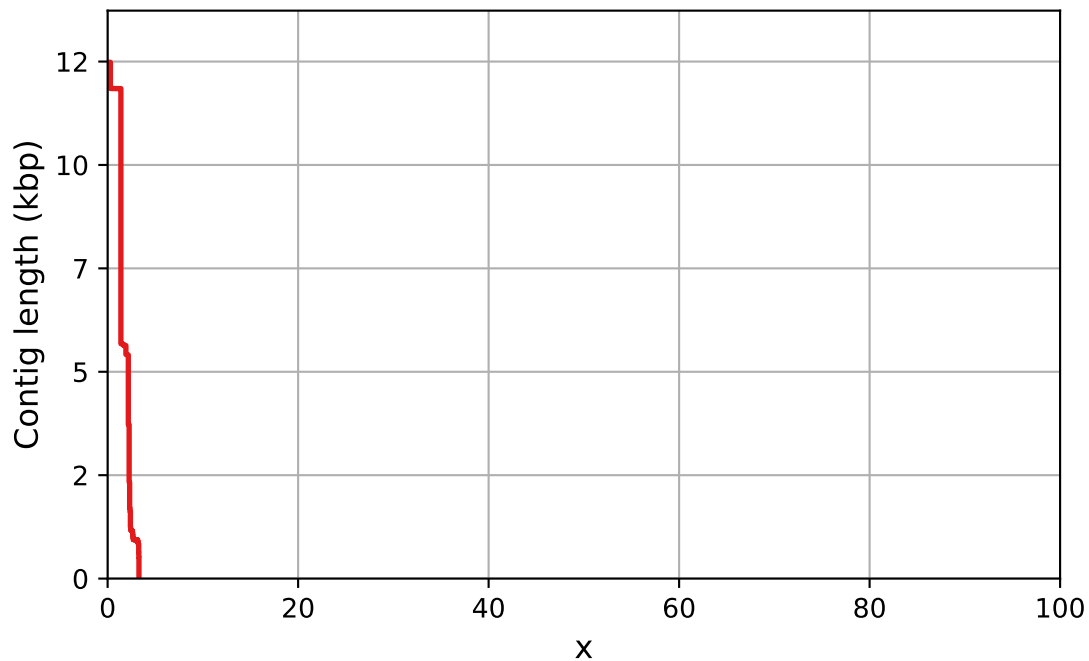
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

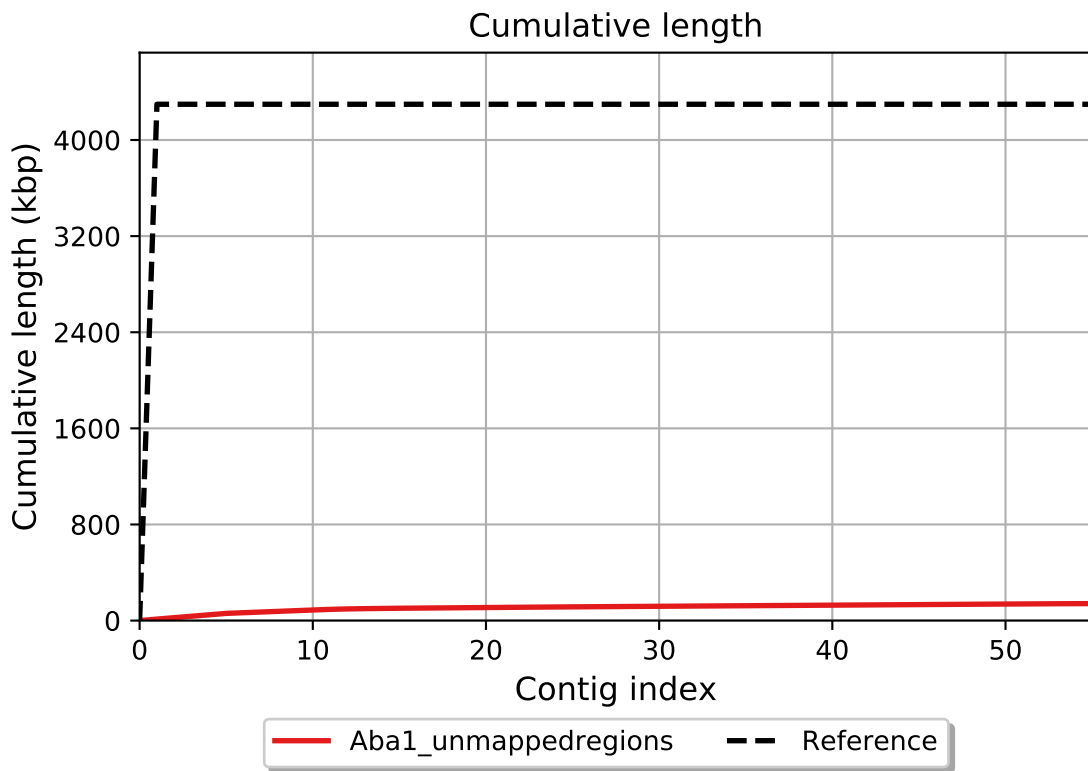


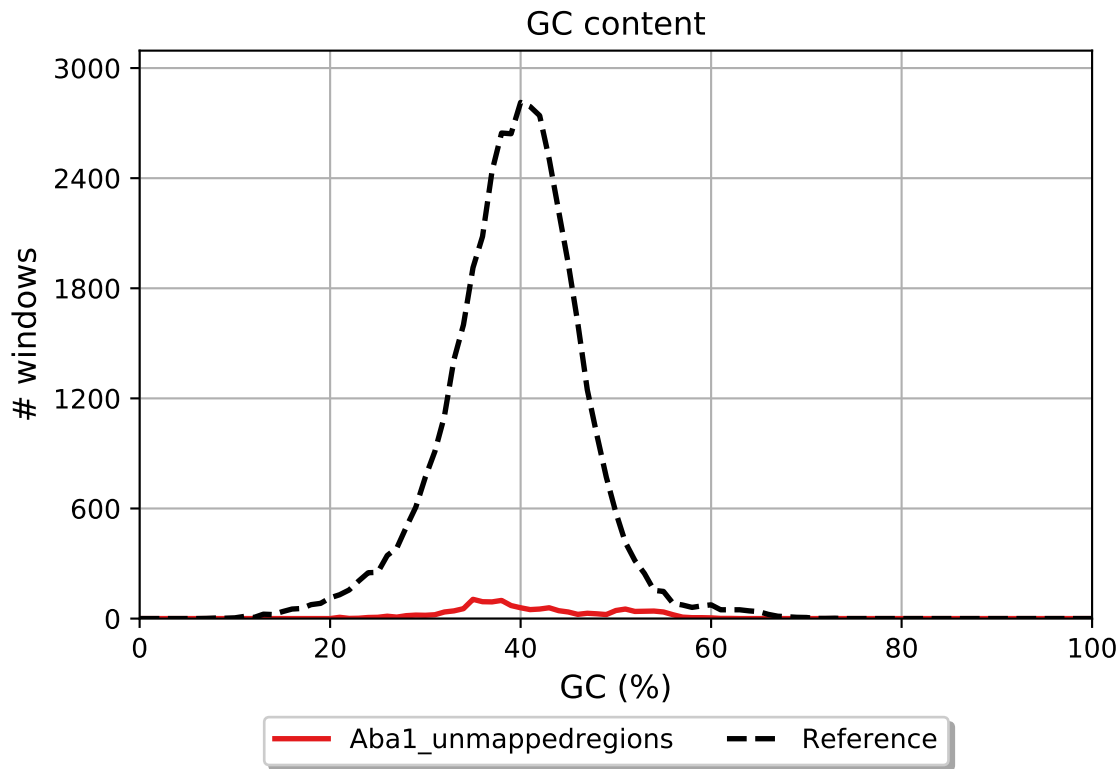
— Aba1_unmappedregions

NGx

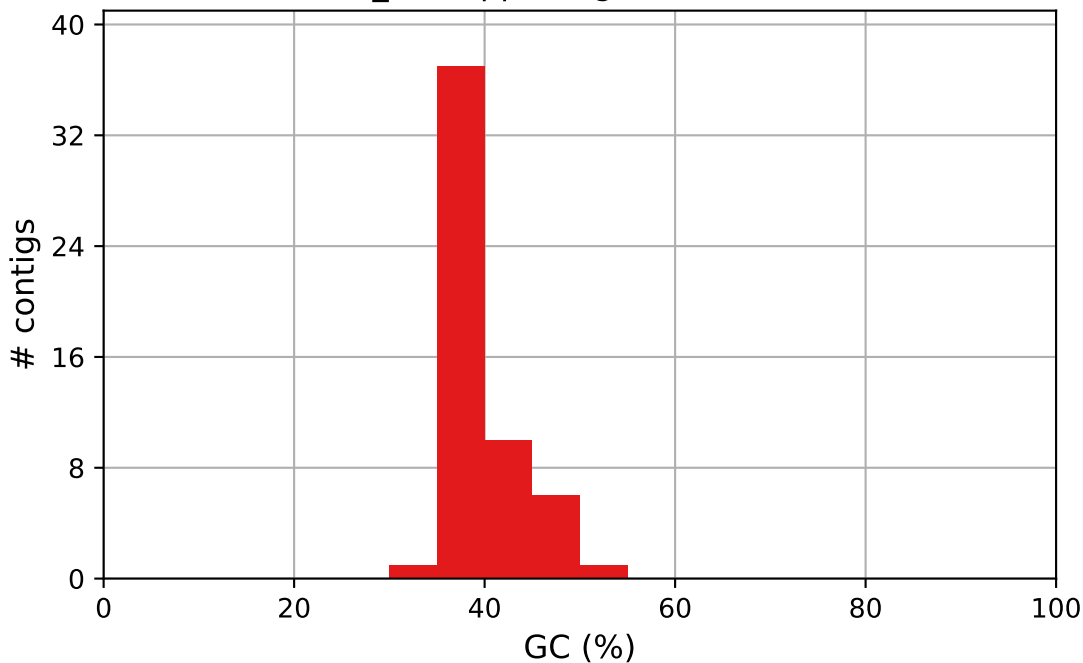


— Aba1_unmappedregions



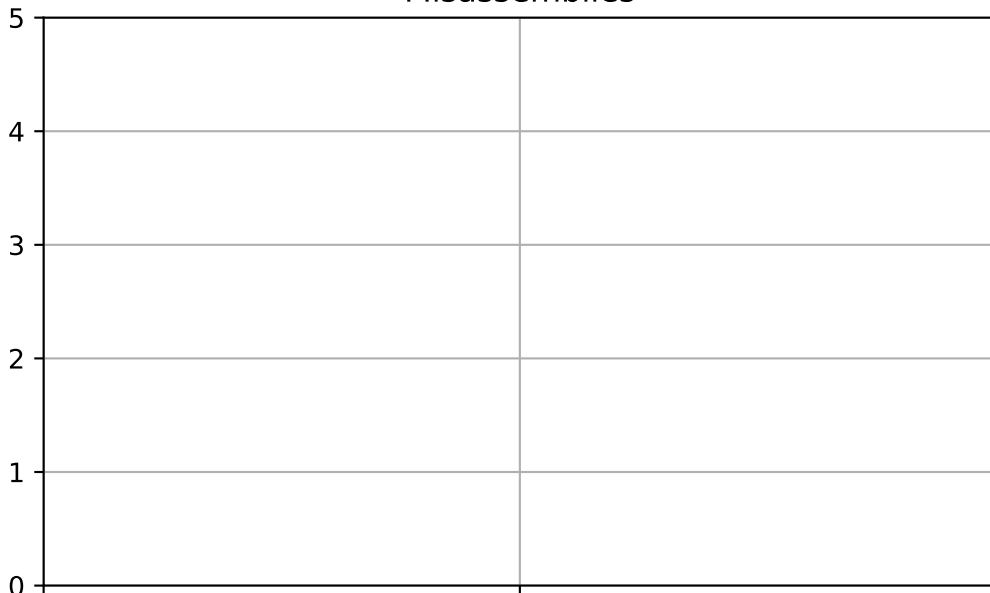


Aba1_unmappedregions GC content



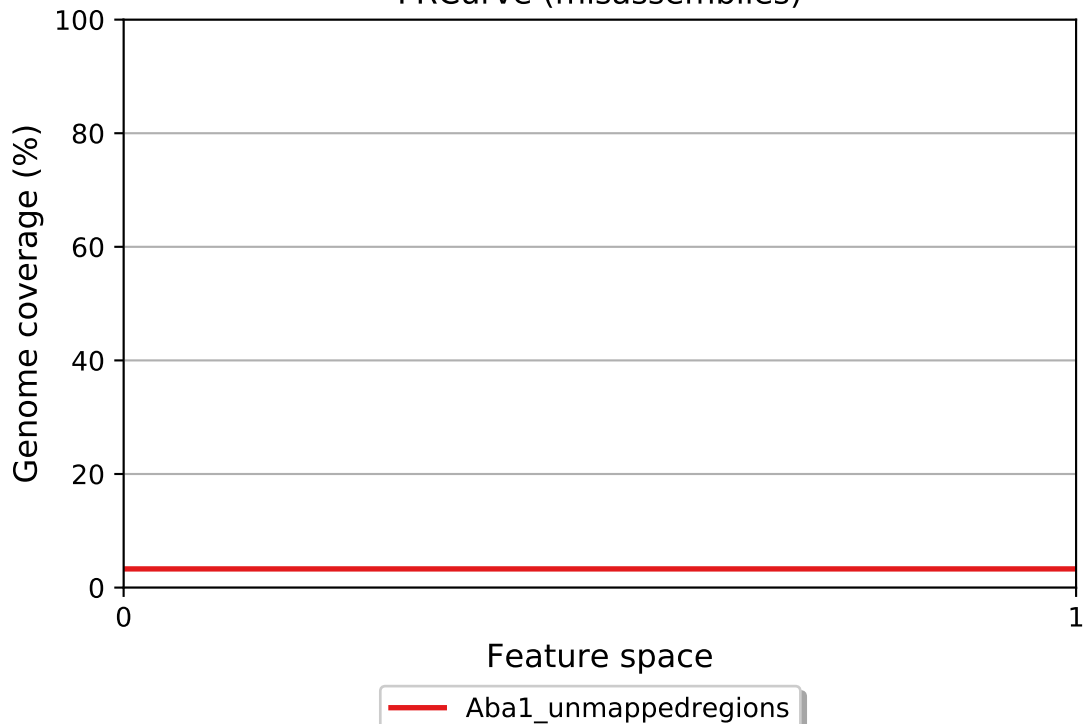
Aba1_unmappedregions

Misassemblies

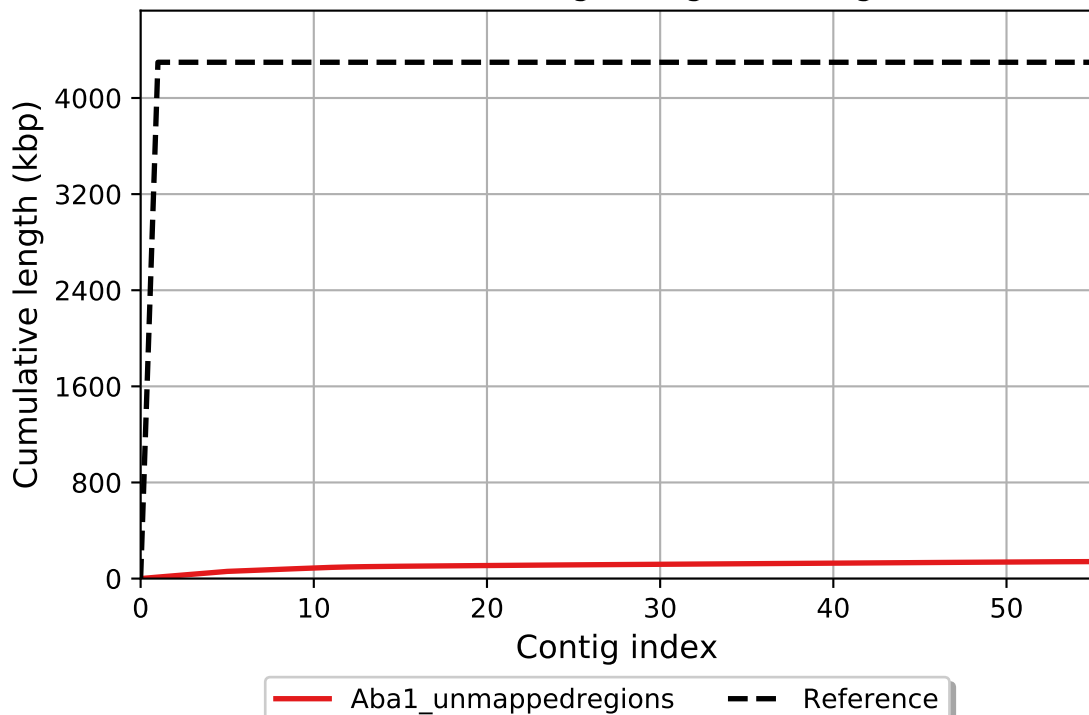


Aa1_unmappedregions

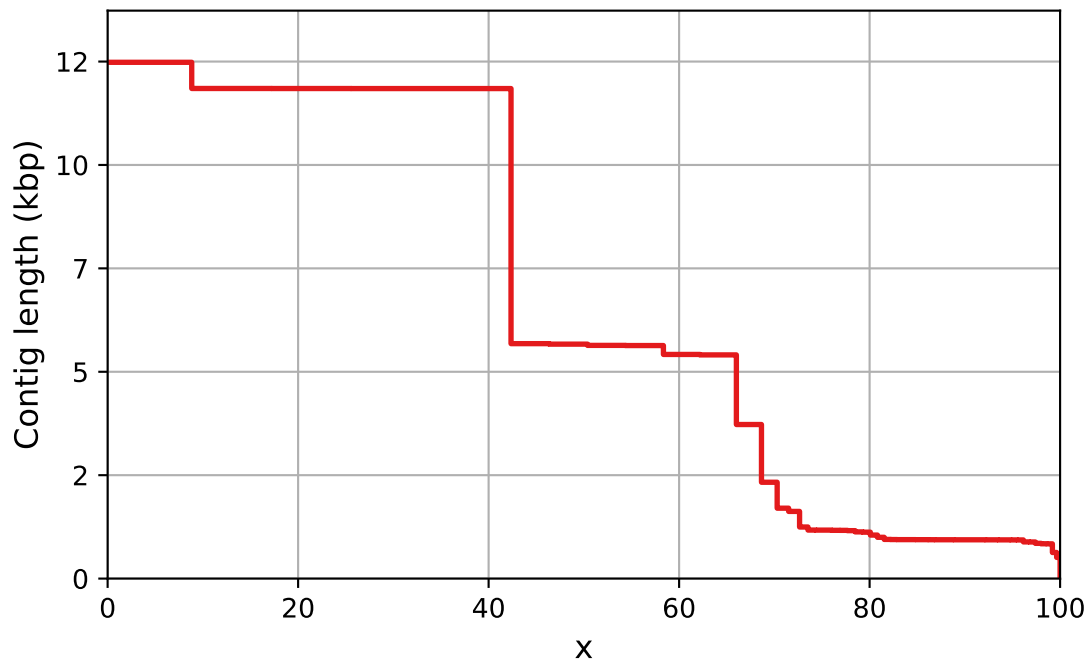
FRCurve (misassemblies)



Cumulative length (aligned contigs)

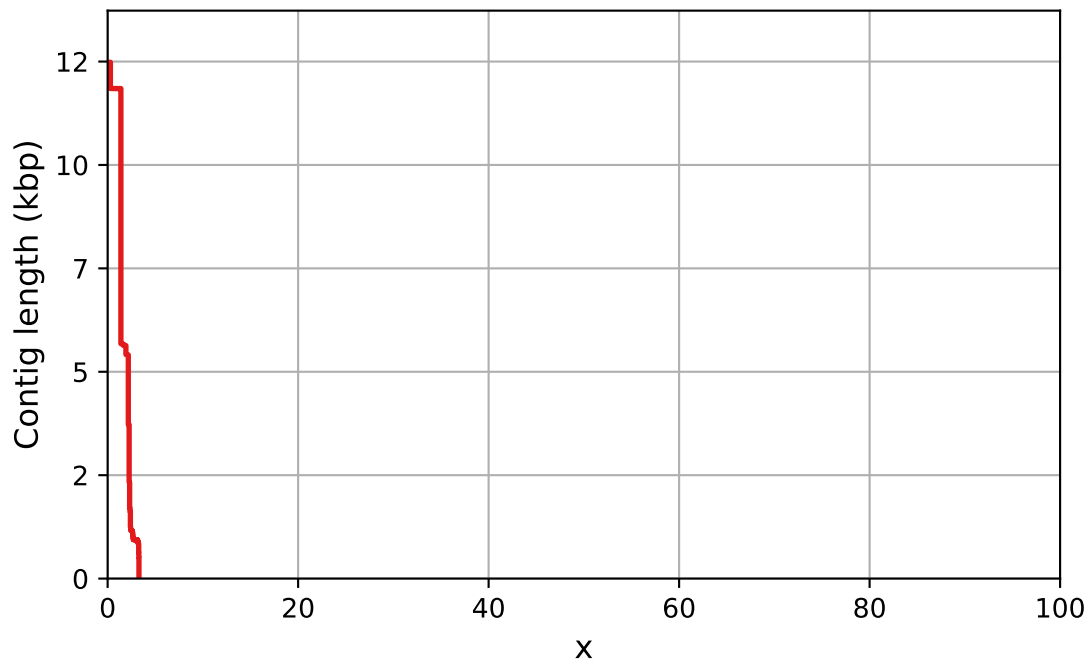


NAx



— Aba1_unmappedregions

NGAx



— Aba1_unmappedregions