

Report

SRR13577846.asm.bp.hap2.p_ctg	
# contigs (>= 0 bp)	26
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	26
# contigs (>= 10000 bp)	26
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	18
Total length (>= 0 bp)	11724748
Total length (>= 1000 bp)	11724748
Total length (>= 5000 bp)	11724748
Total length (>= 10000 bp)	11724748
Total length (>= 25000 bp)	11589613
Total length (>= 50000 bp)	11562764
# contigs	26
Largest contig	1410597
Total length	11724748
Reference length	12157105
GC (%)	38.30
Reference GC (%)	38.15
N50	809047
NG50	809047
N90	441569
NG90	255977
auN	834149.4
auNG	804483.6
L50	6
LG50	6
L90	13
LG90	15
# misassemblies	96
# misassembled contigs	24
Misassembled contigs length	11495549
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 17 part
Unaligned length	95996
Genome fraction (%)	92.674
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	215.26
# indels per 100 kbp	23.75
Largest alignment	843303
Total aligned length	11612235
NA50	273893
NGA50	247983
NA90	89236
NGA90	65917
auNA	363715.3
auNGA	350780.1
LA50	12
LGA50	13
LA90	41
LGA90	46

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

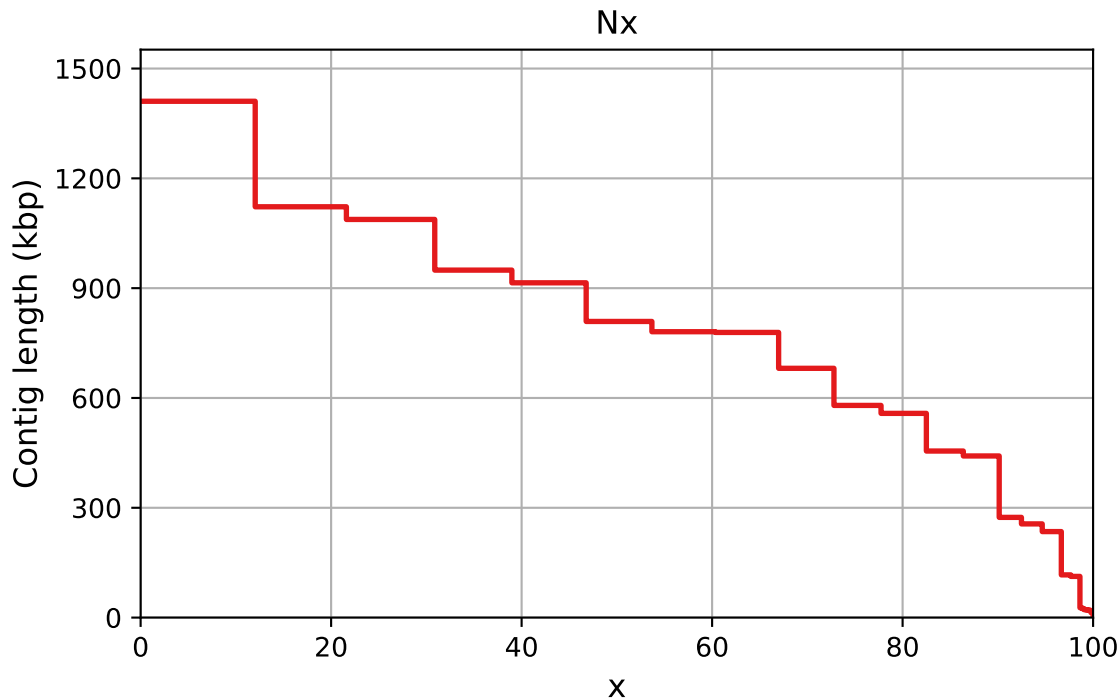
	SRR13577846.asm.bp.hap2.p_ctg
# misassemblies	96
# contig misassemblies	96
# c. relocations	39
# c. translocations	57
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	24
Misassembled contigs length	11495549
# local misassemblies	34
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	24996
# indels	2758
# indels (<= 5 bp)	2324
# indels (> 5 bp)	434
Indels length	15744

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

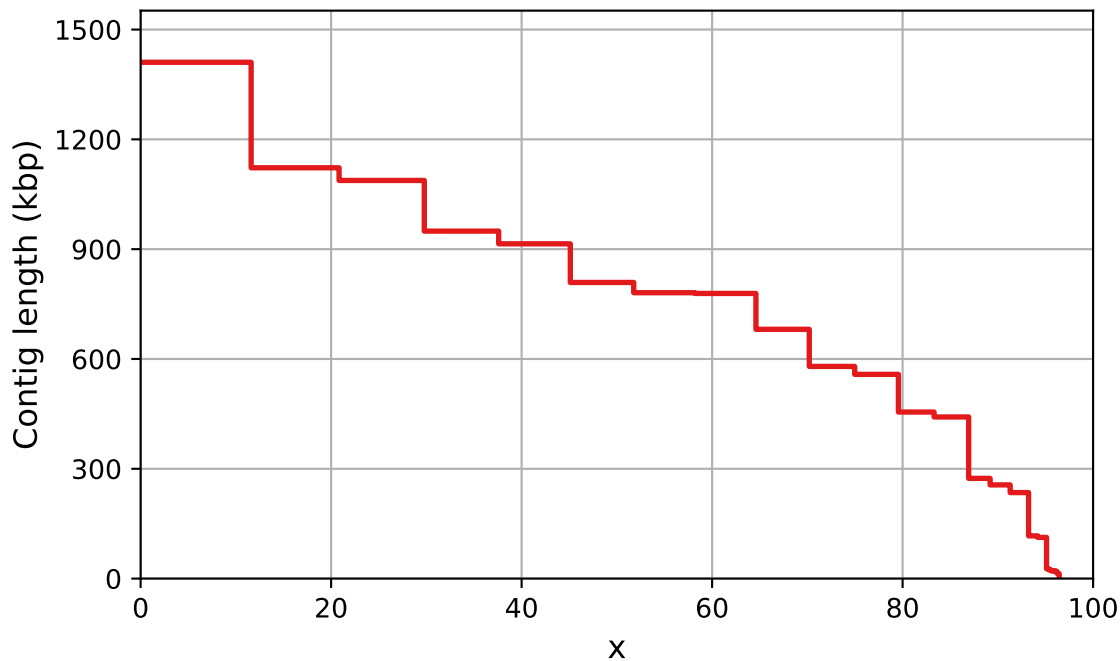
	SRR13577846.asm.bp.hap2.p_ctg
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	17
Partially unaligned length	95996
# N's	0

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).



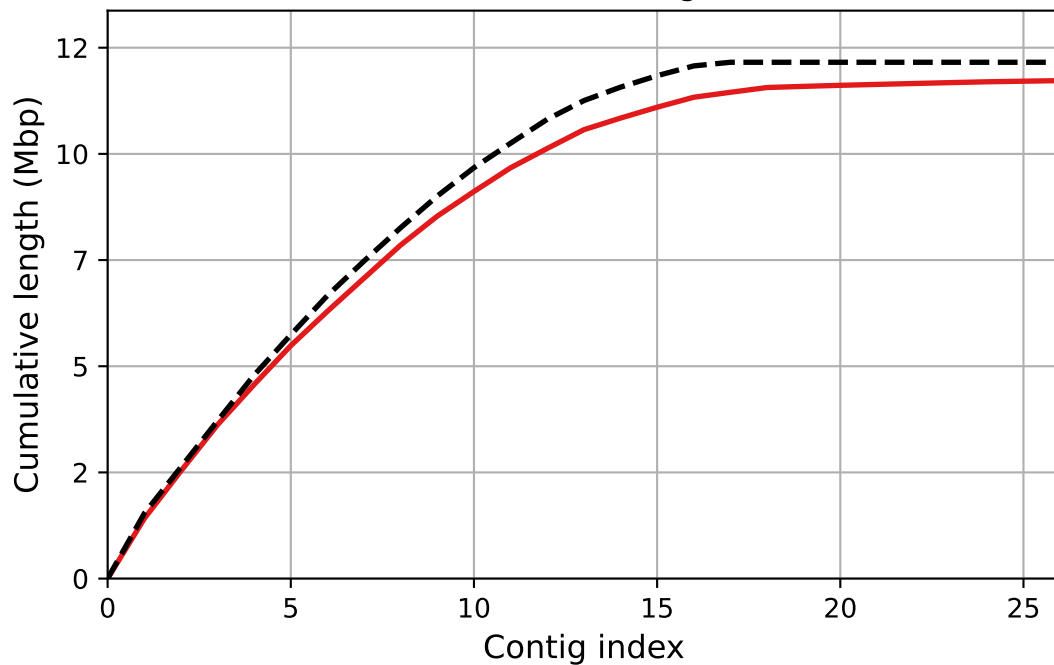
— SRR13577846.asm.bp.hap2.p_ctg

NGx



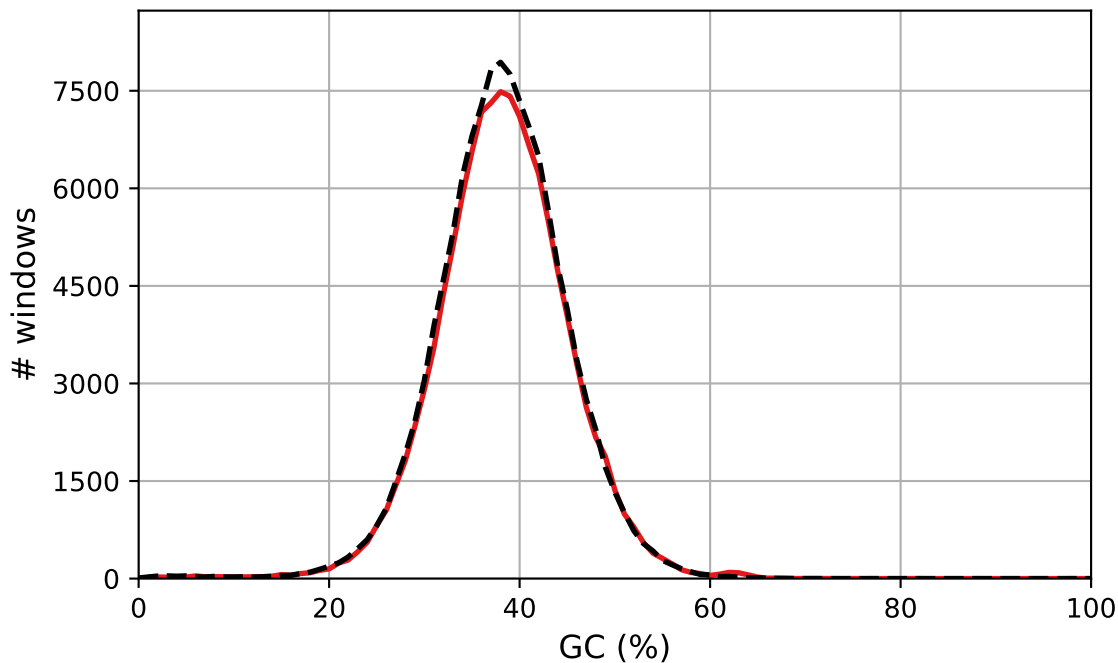
SRR13577846.asm.bp.hap2.p_ctg

Cumulative length



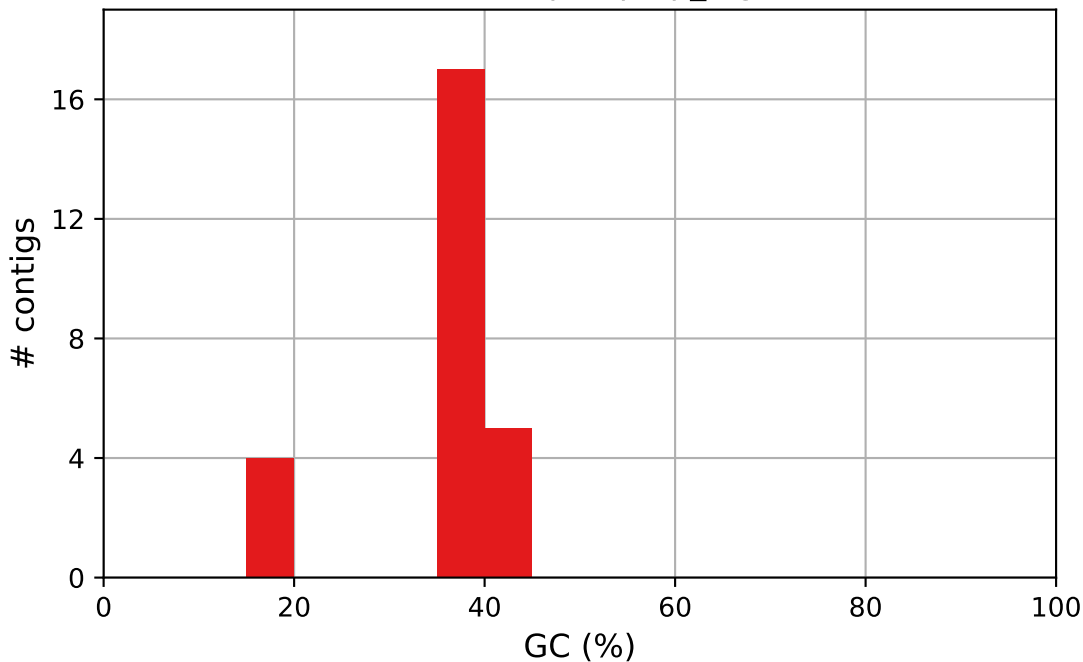
SRR13577846.asm.bp.hap2.p_ctg Reference

GC content



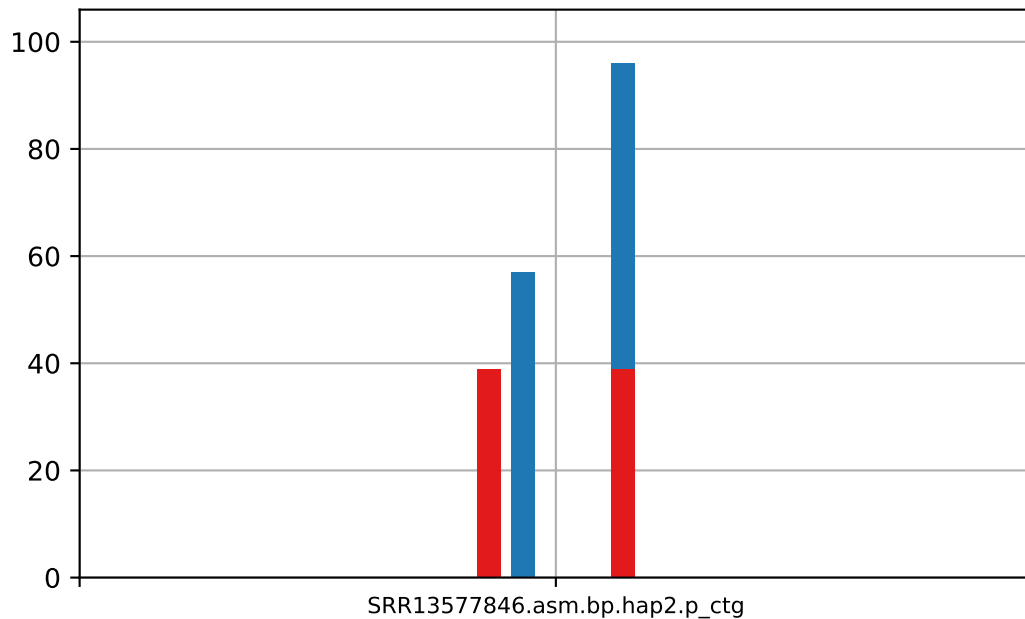
SRR13577846.asm.bp.hap2.p_ctg Reference

SRR13577846.asm.bp.hap2.p_ctg GC content



SRR13577846.asm.bp.hap2.p_ctg

Misassemblies

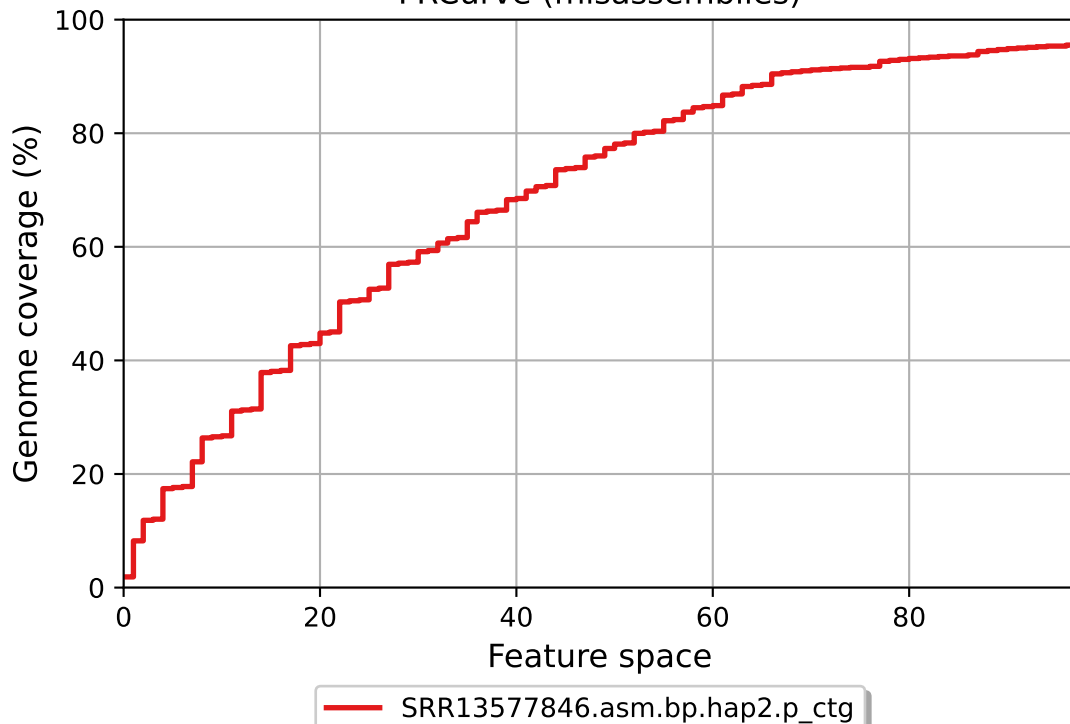


relocations

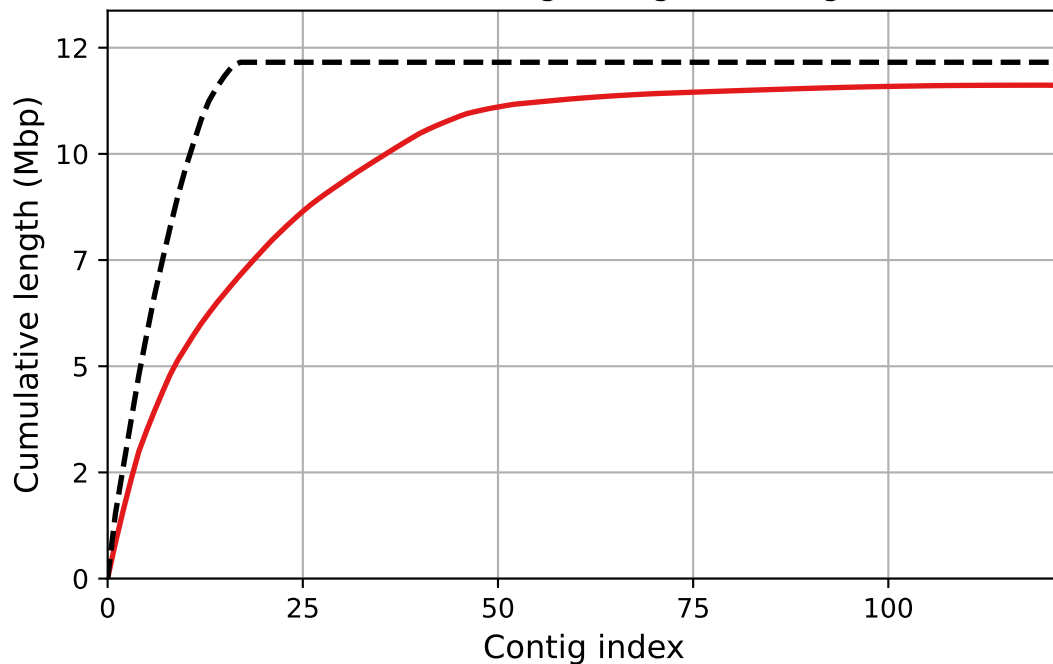


translocations

FRCurve (misassemblies)

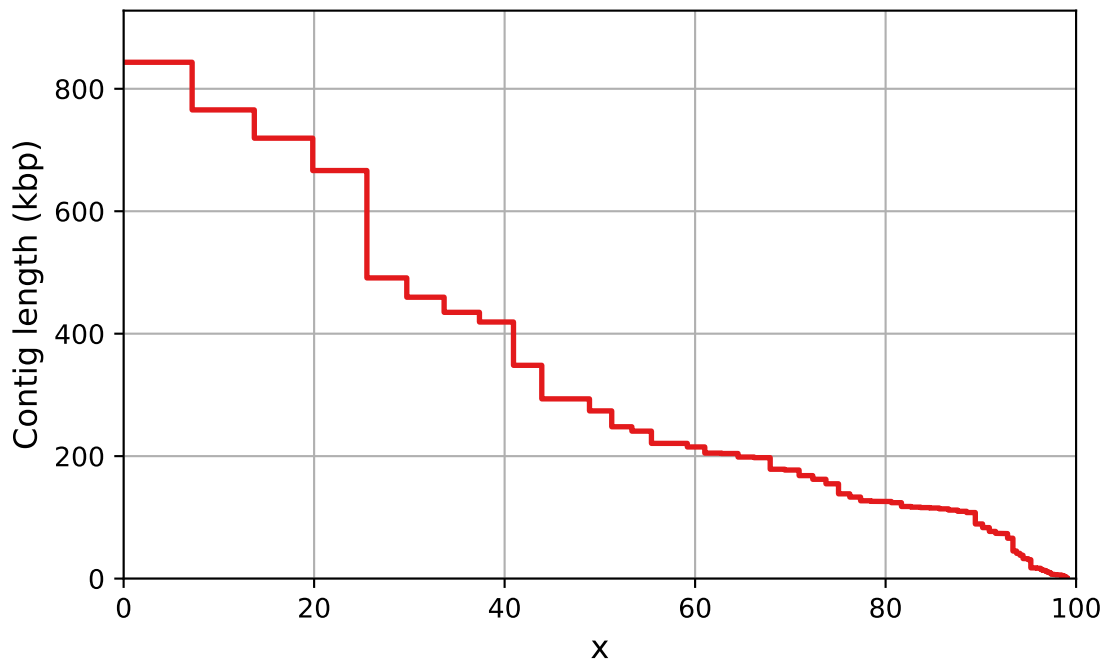


Cumulative length (aligned contigs)



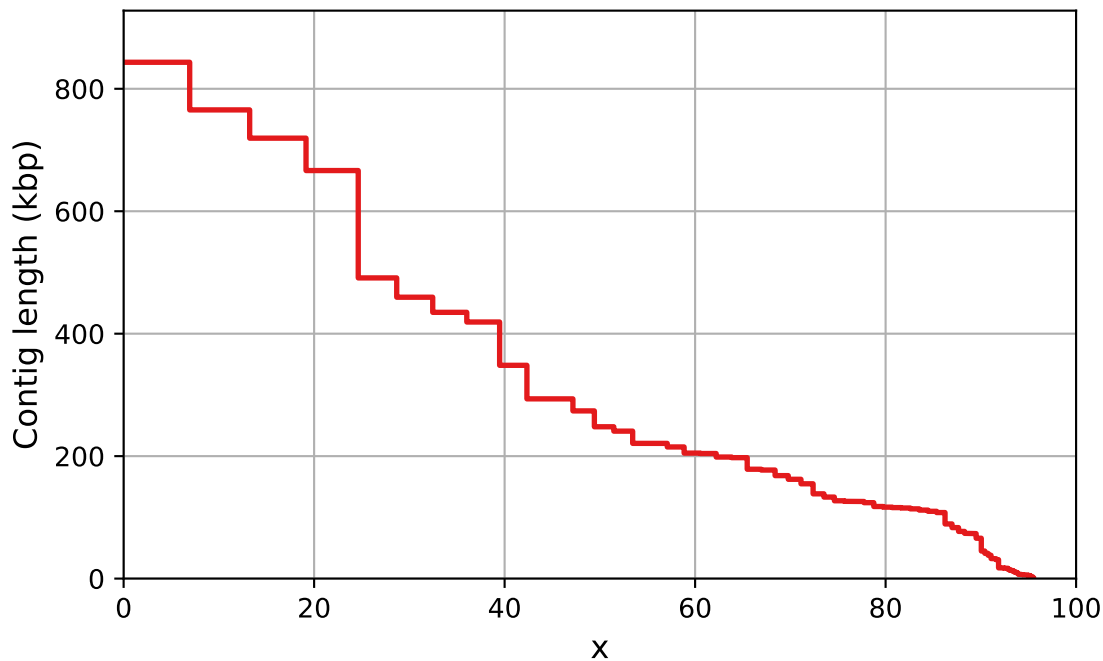
SRR13577846.asm.bp.hap2.p_ctg Reference

NAx



— SRR13577846.asm.bp.hap2.p_ctg

NGAx



— SRR13577846.asm.bp.hap2.p_ctg