

Report

	AJ055.CanuH
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	5727073
Total length (>= 1000 bp)	5727073
Total length (>= 5000 bp)	5727073
Total length (>= 10000 bp)	5727073
Total length (>= 25000 bp)	5702958
Total length (>= 50000 bp)	5675085
# contigs	4
Largest contig	5496970
Total length	5727073
Reference length	5504133
GC (%)	57.18
Reference GC (%)	57.38
N50	5496970
NG50	5496970
N75	5496970
NG75	5496970
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 1 part
Unaligned length	229009
Genome fraction (%)	99.877
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.27
# indels per 100 kbp	34.76
Largest alignment	5496967
Total aligned length	5498061
NA50	5496967
NGA50	5496967
NA75	5496967
NGA75	5496967
LA50	1
LGA50	1
LA75	1
LGA75	1

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

	AJ055.CanuH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	15
# indels	1911
# indels (≤ 5 bp)	1910
# indels (> 5 bp)	1
Indels length	1951

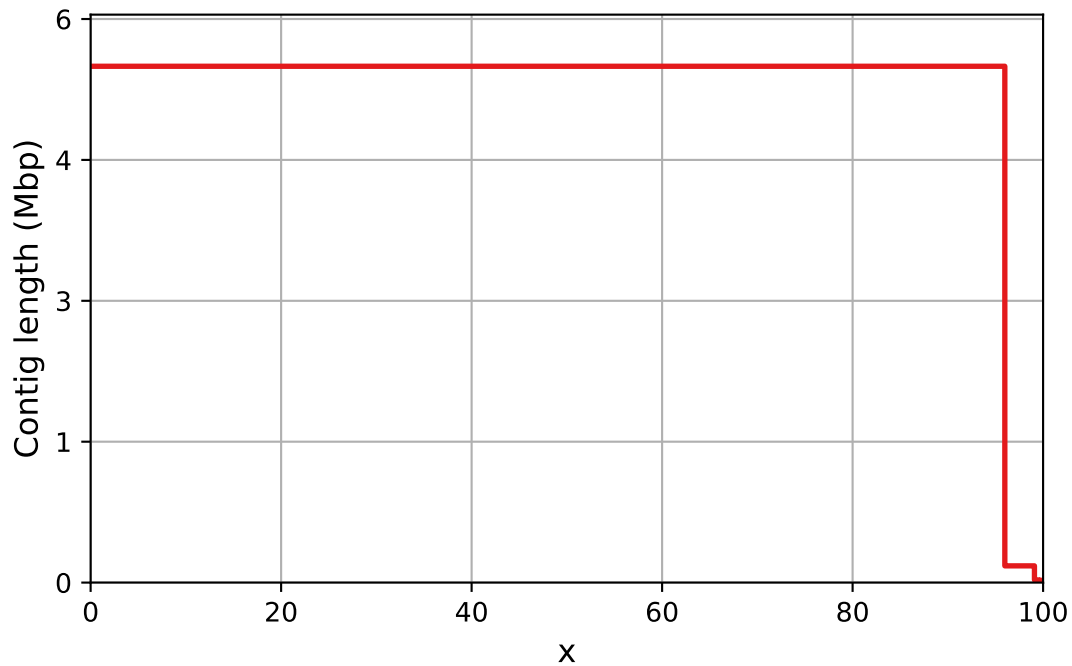
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.CanuH
# fully unaligned contigs	2
Fully unaligned length	51988
# partially unaligned contigs	1
Partially unaligned length	177021
# N's	0

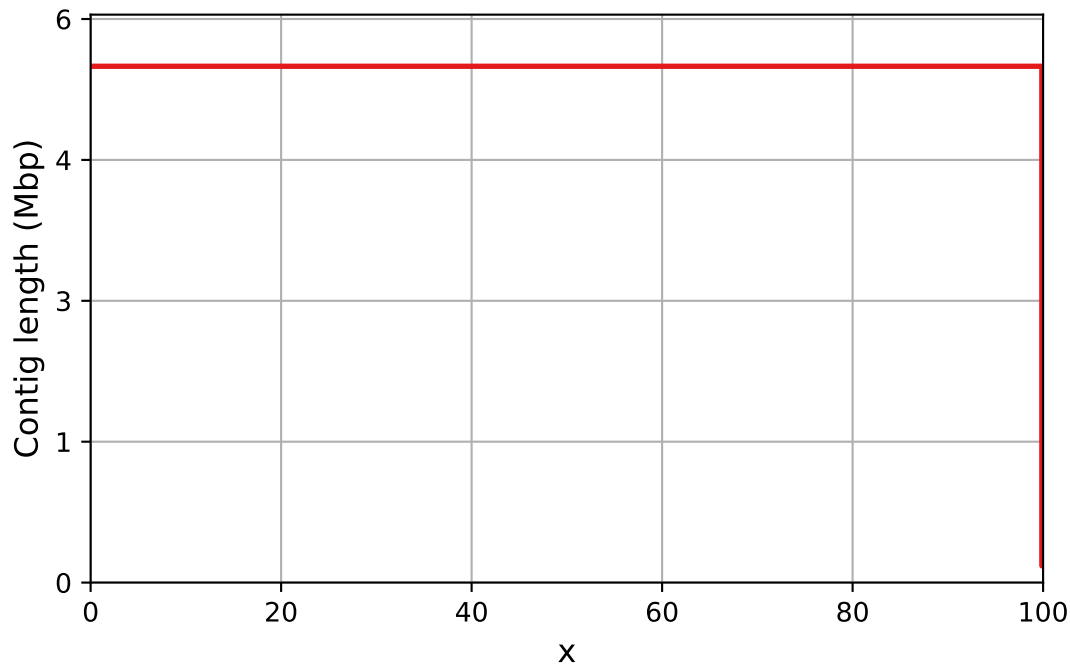
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



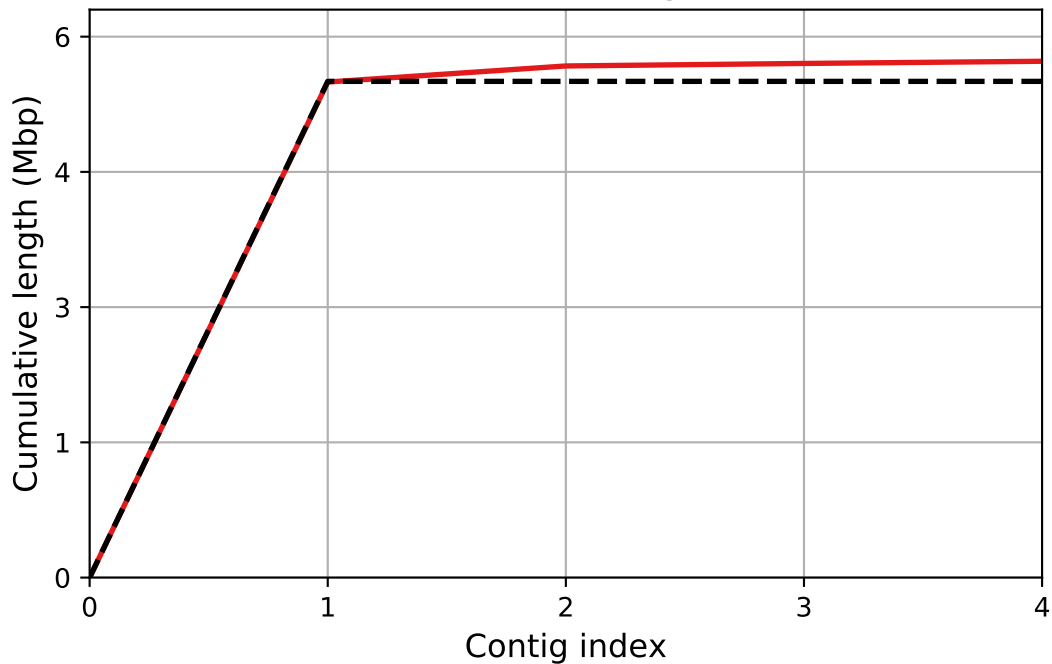
AJ055.CanuH

NGx



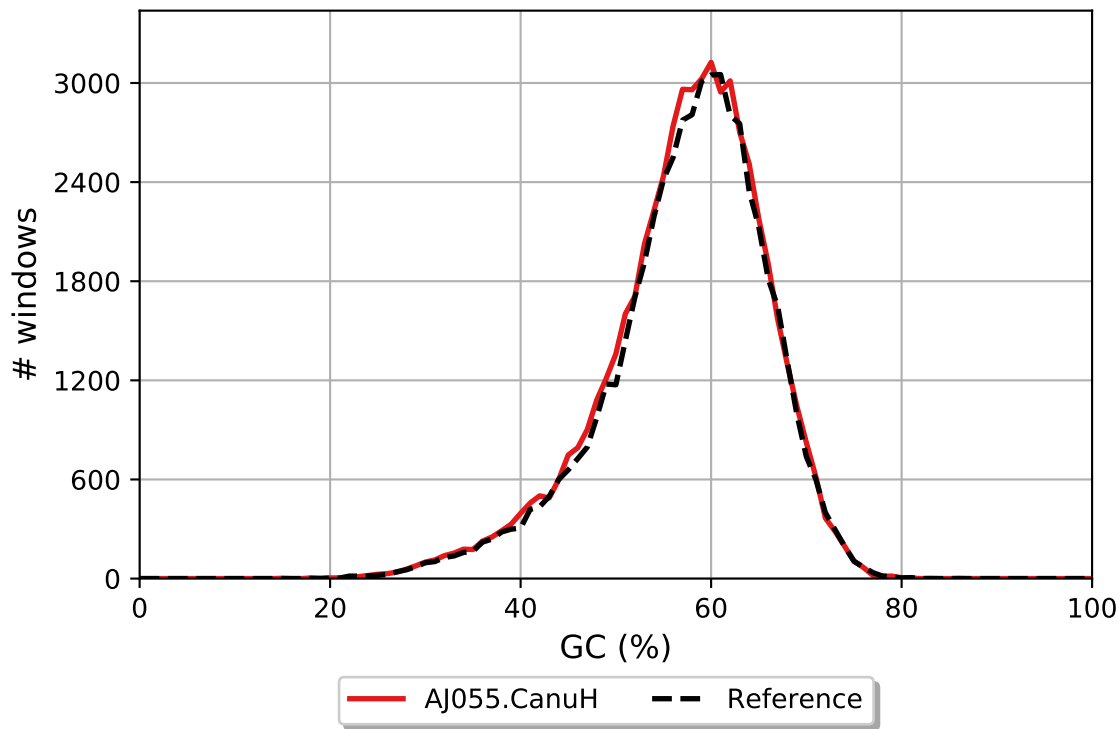
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Cumulative length

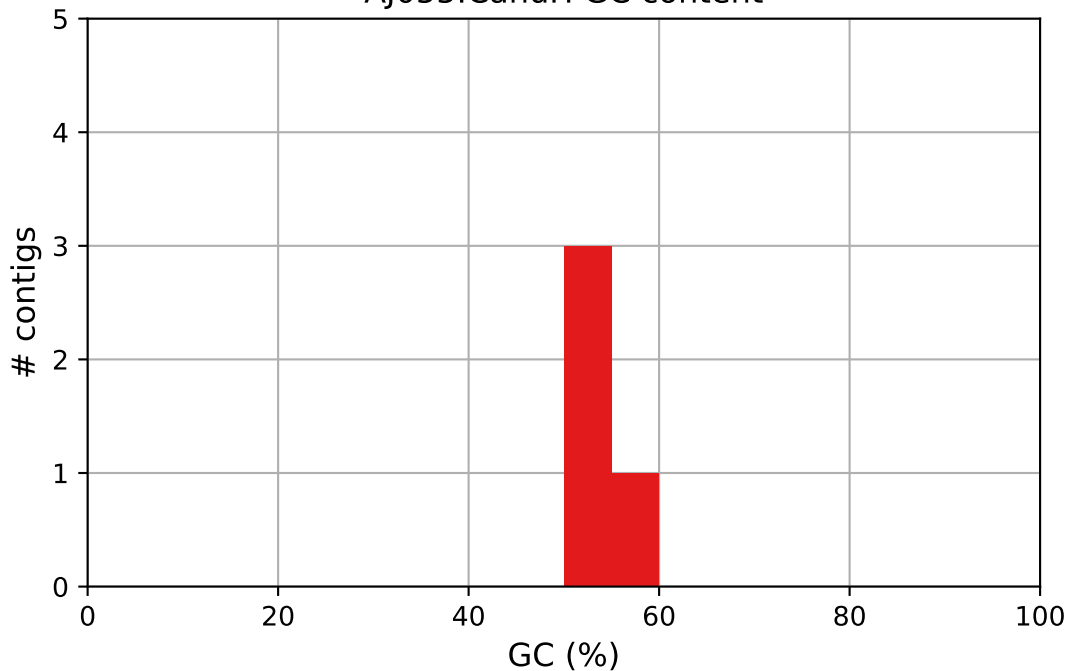


AJ055.CanuH Reference

GC content



AJ055.CanuH GC content

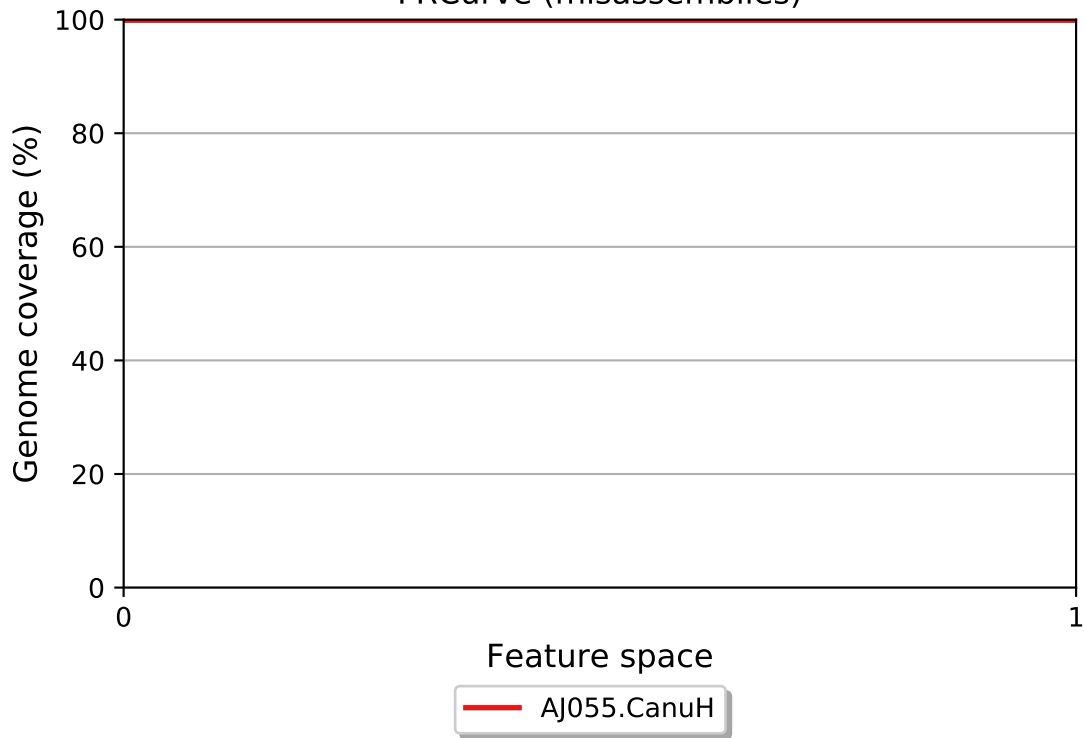


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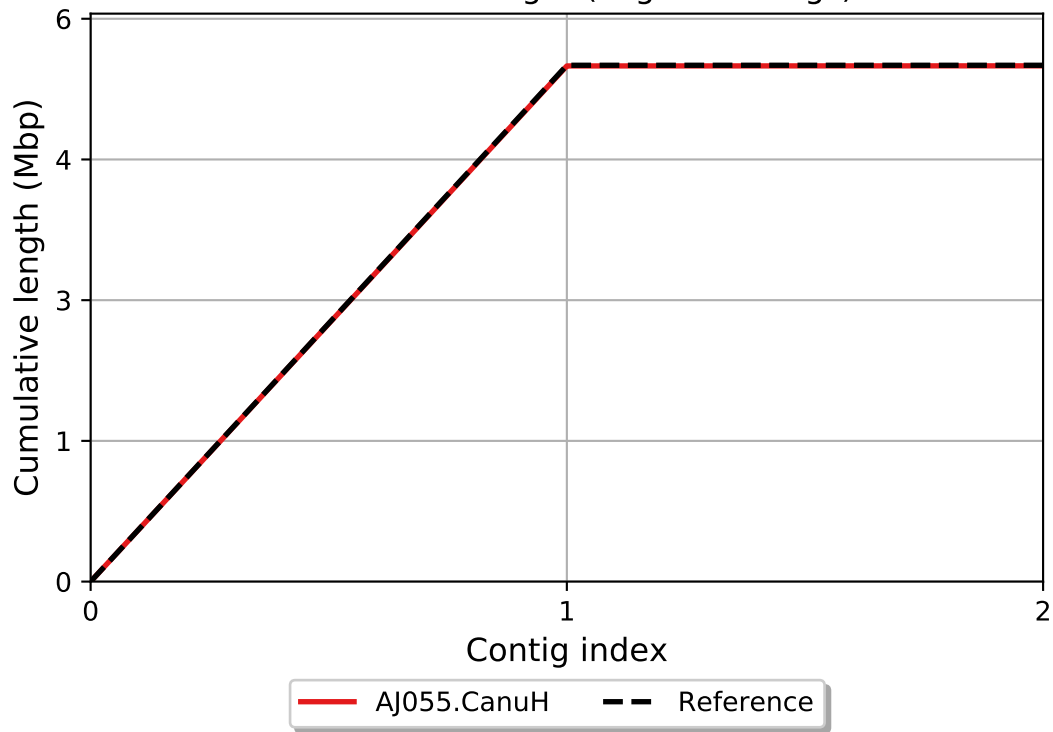
Misassemblies



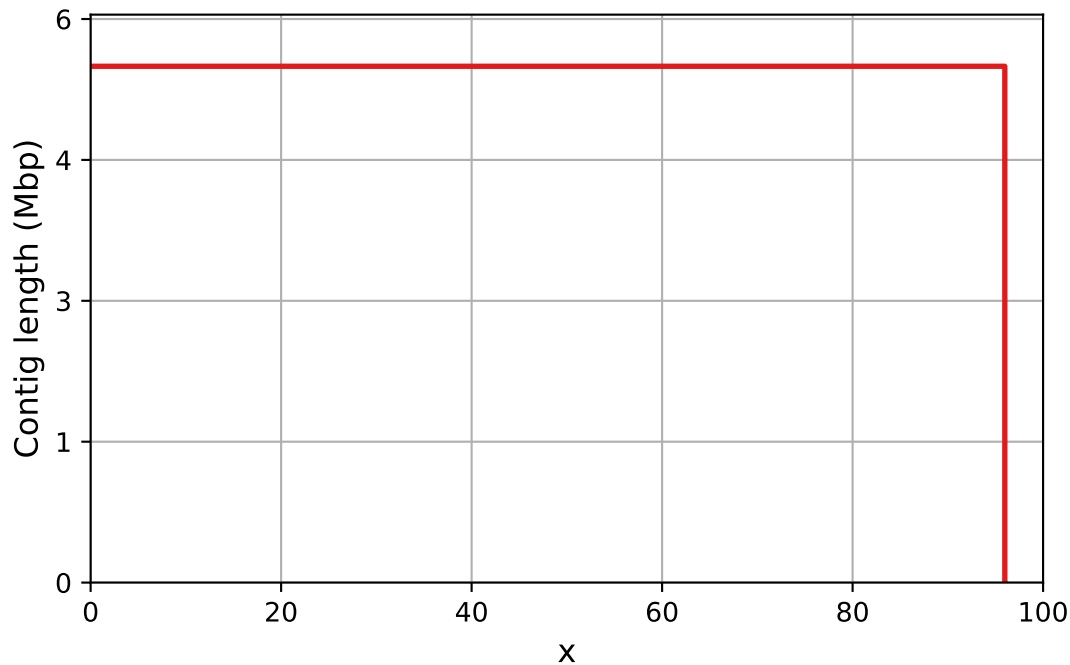
FRCurve (misassemblies)



Cumulative length (aligned contigs)

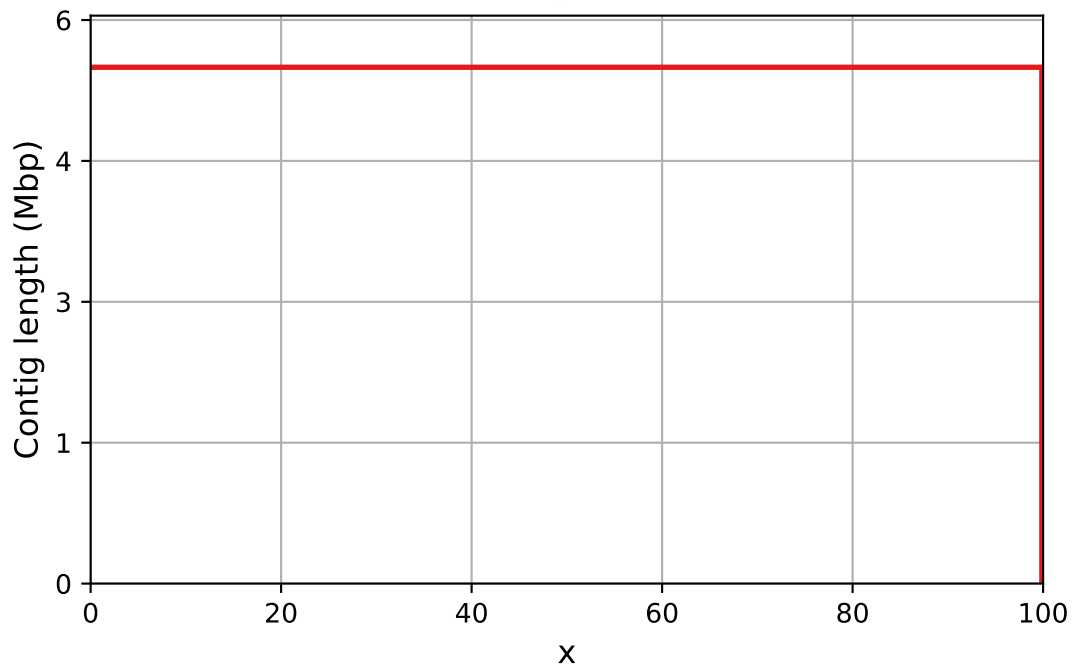


NAx



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NGAx



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