

Report

	AJ055.MiniH
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	5700578
Total length (>= 1000 bp)	5700578
Total length (>= 5000 bp)	5700578
Total length (>= 10000 bp)	5700578
Total length (>= 25000 bp)	5700578
Total length (>= 50000 bp)	5700578
# contigs	2
Largest contig	5534010
Total length	5700578
Reference length	5504133
GC (%)	57.19
Reference GC (%)	57.38
N50	5534010
NG50	5534010
N75	5534010
NG75	5534010
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	170176
Genome fraction (%)	99.934
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.62
# indels per 100 kbp	466.43
Largest alignment	5529303
Total aligned length	5530402
NA50	5529303
NGA50	5529303
NA75	5529303
NGA75	5529303
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.MiniH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned mis. contigs	0
# mismatches	1629
# indels	25656
# indels (≤ 5 bp)	25432
# indels (> 5 bp)	224
Indels length	38590

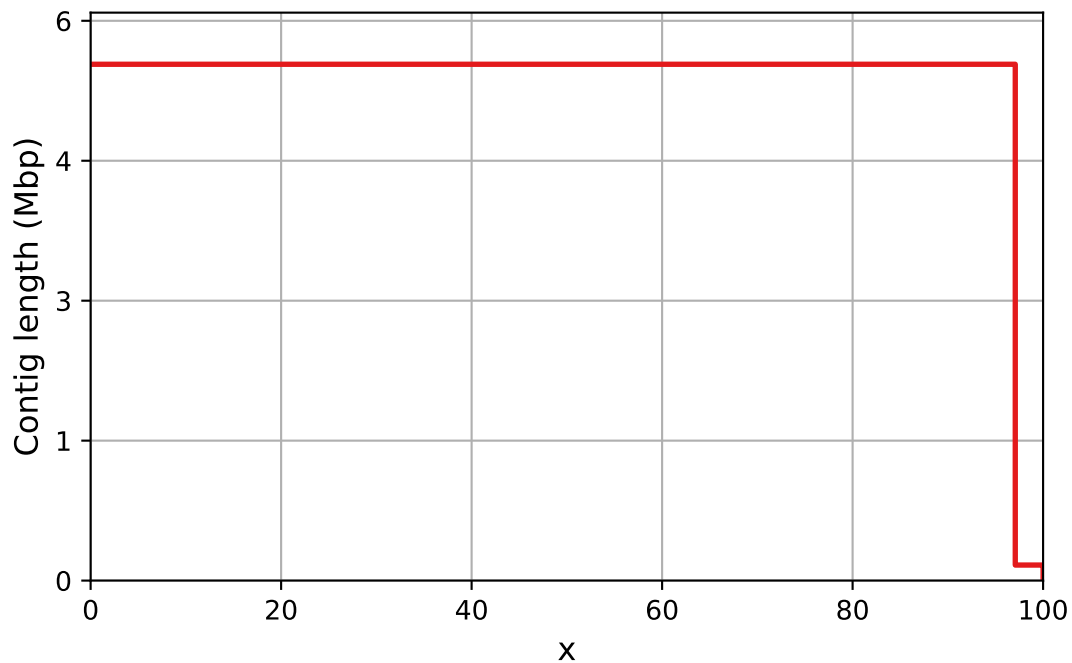
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.MiniH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	170176
# N's	0

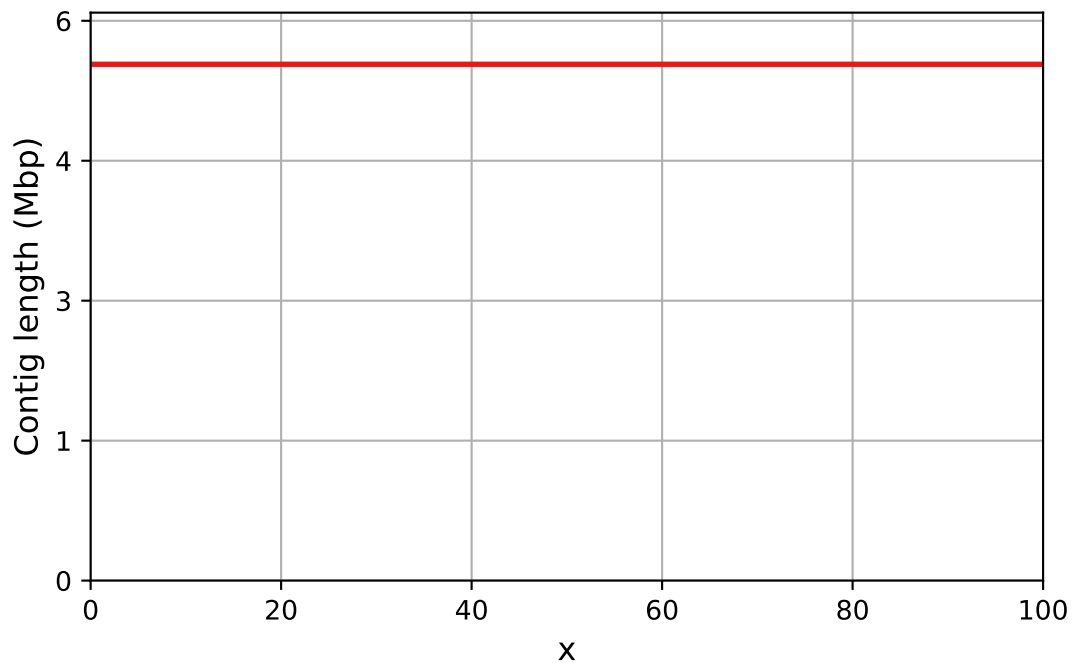
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



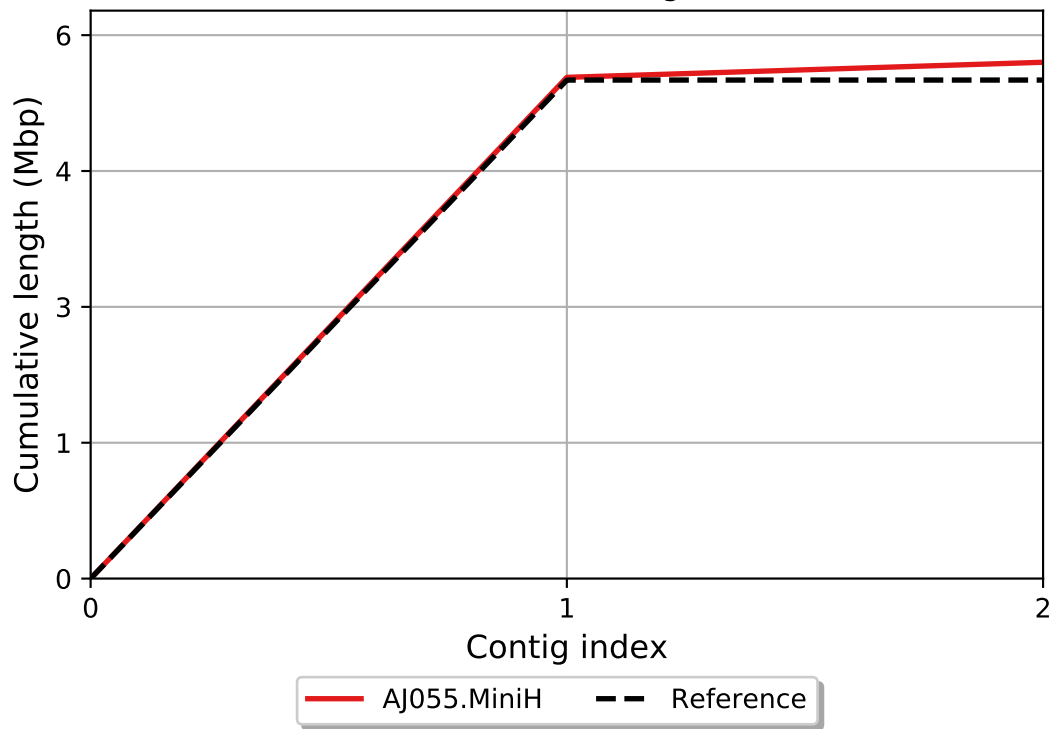
Aj055.MiniH

NGx

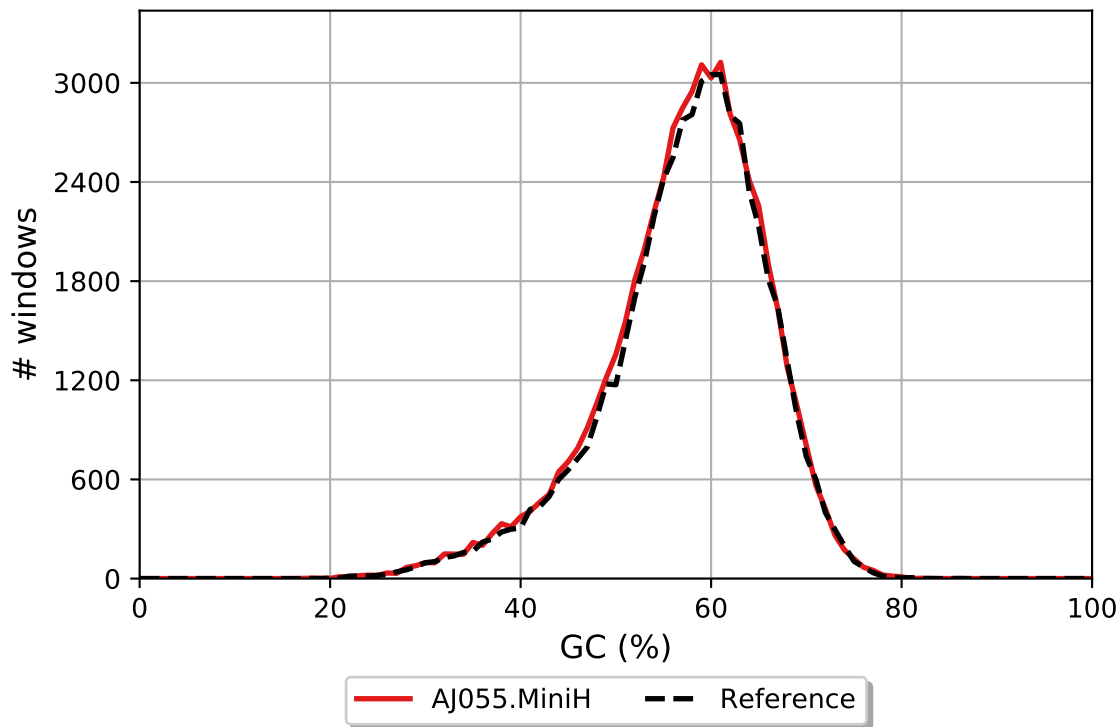


Aj055.MiniH

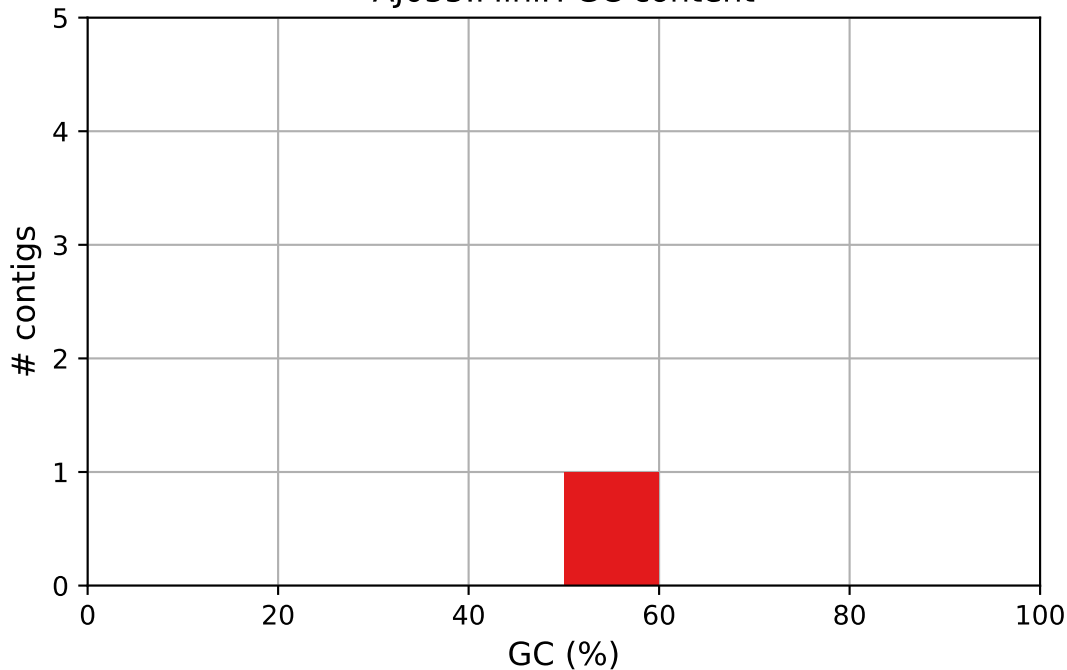
Cumulative length



GC content



AJ055.MiniH GC content

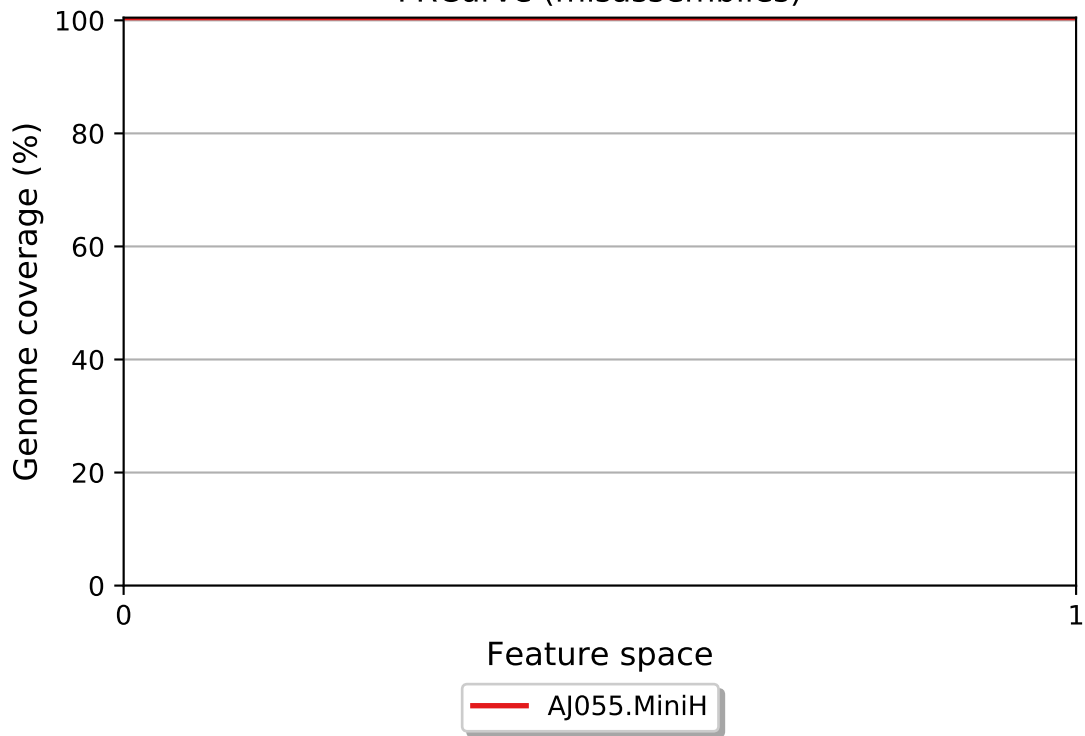


AJ055.MiniH

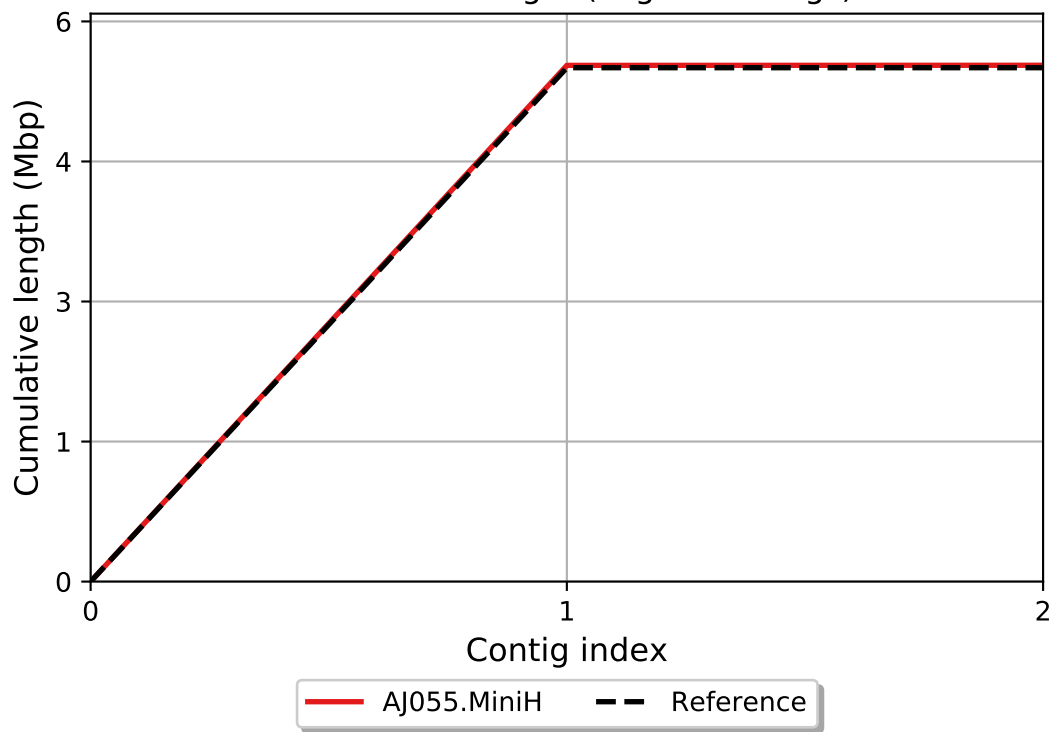
Misassemblies



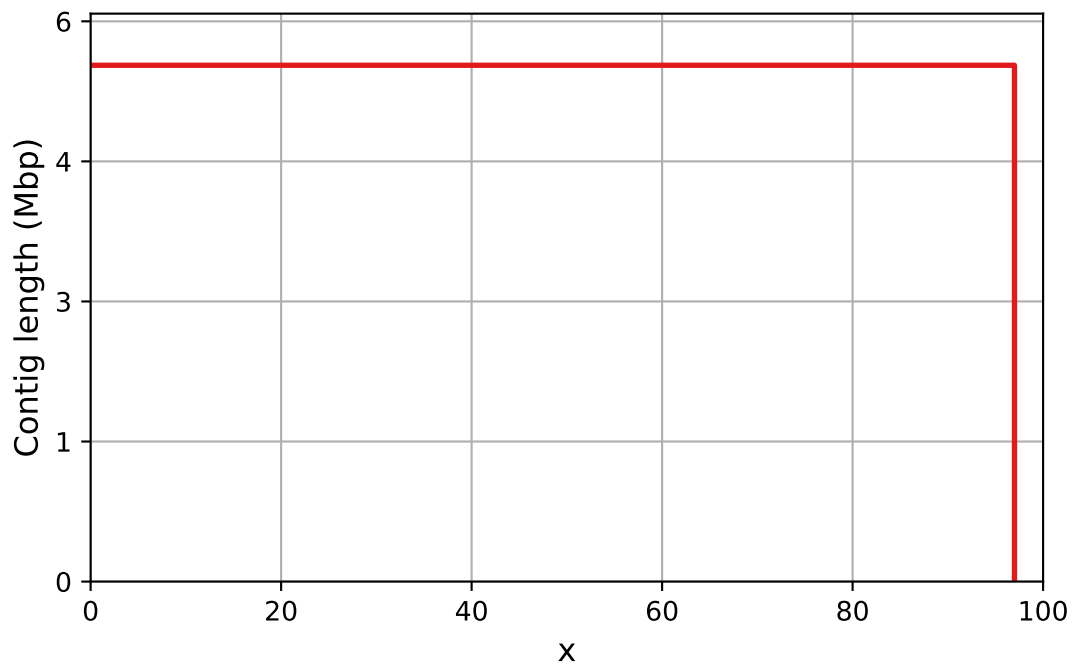
FRCurve (misassemblies)



Cumulative length (aligned contigs)

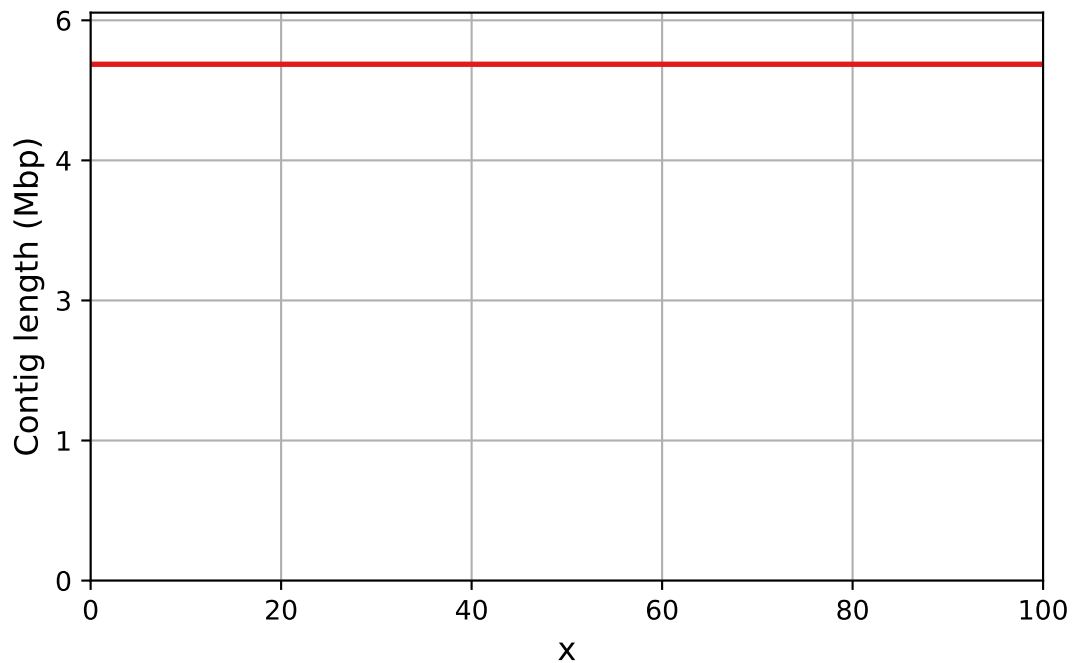


NAx



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NGAx



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