

Report

	AJ292.CanuL
# contigs (>= 0 bp)	7
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	6
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	5490581
Total length (>= 1000 bp)	5490581
Total length (>= 5000 bp)	5488607
Total length (>= 10000 bp)	5488607
Total length (>= 25000 bp)	5444101
Total length (>= 50000 bp)	5412730
# contigs	7
Largest contig	5055382
Total length	5490581
Reference length	5445112
GC (%)	57.57
Reference GC (%)	57.62
N50	5055382
NG50	5055382
N75	5055382
NG75	5055382
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	1 + 0 part
Unaligned length	1974
Genome fraction (%)	99.692
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.84
# indels per 100 kbp	80.39
Largest alignment	5055382
Total aligned length	5488607
NA50	5055382
NGA50	5055382
NA75	5055382
NGA75	5055382
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

	AJ292.CanuL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	100
# indels	4364
# indels (≤ 5 bp)	4359
# indels (> 5 bp)	5
Indels length	4530

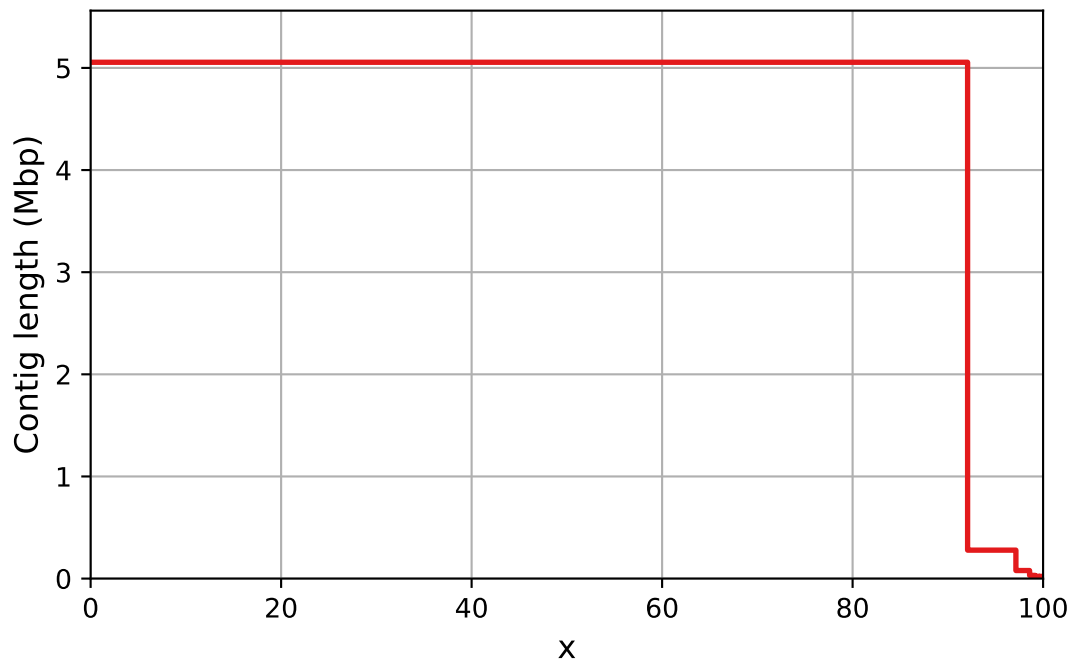
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ292.CanuL
# fully unaligned contigs	1
Fully unaligned length	1974
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

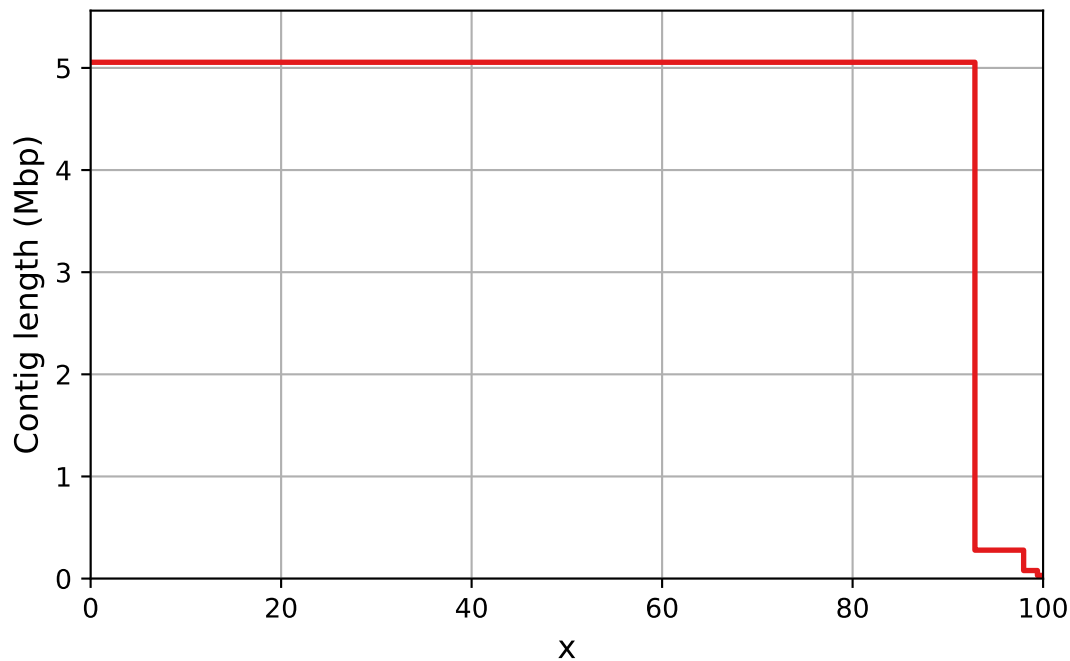
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

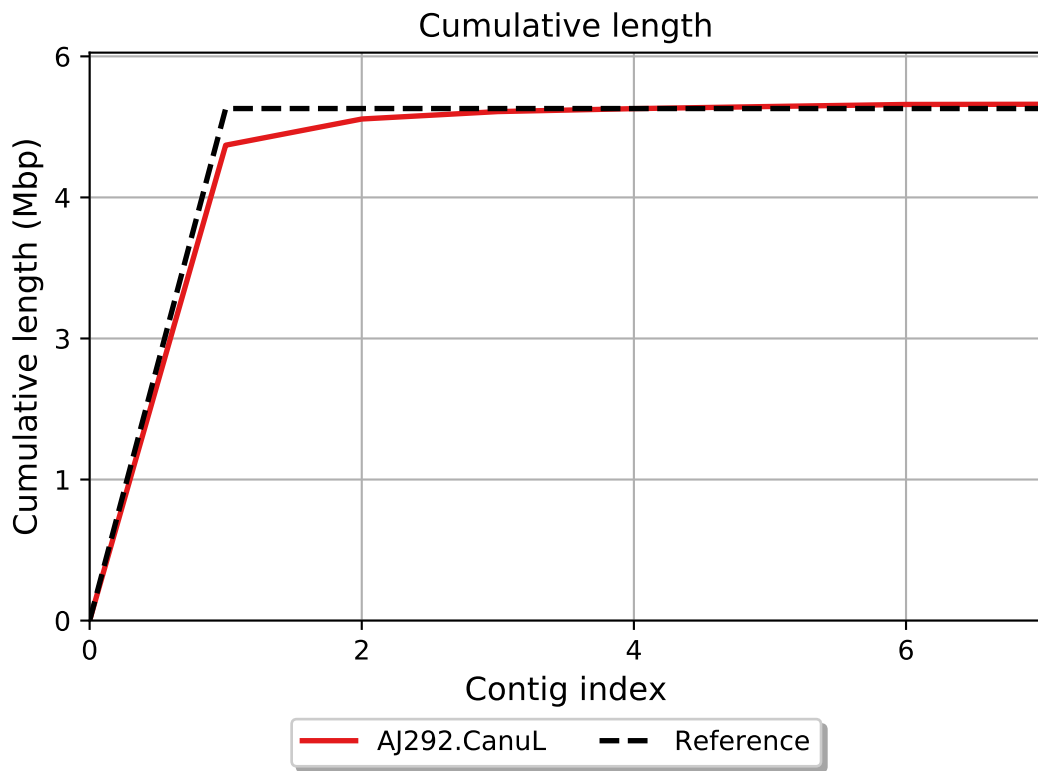


AJ292.CanuL

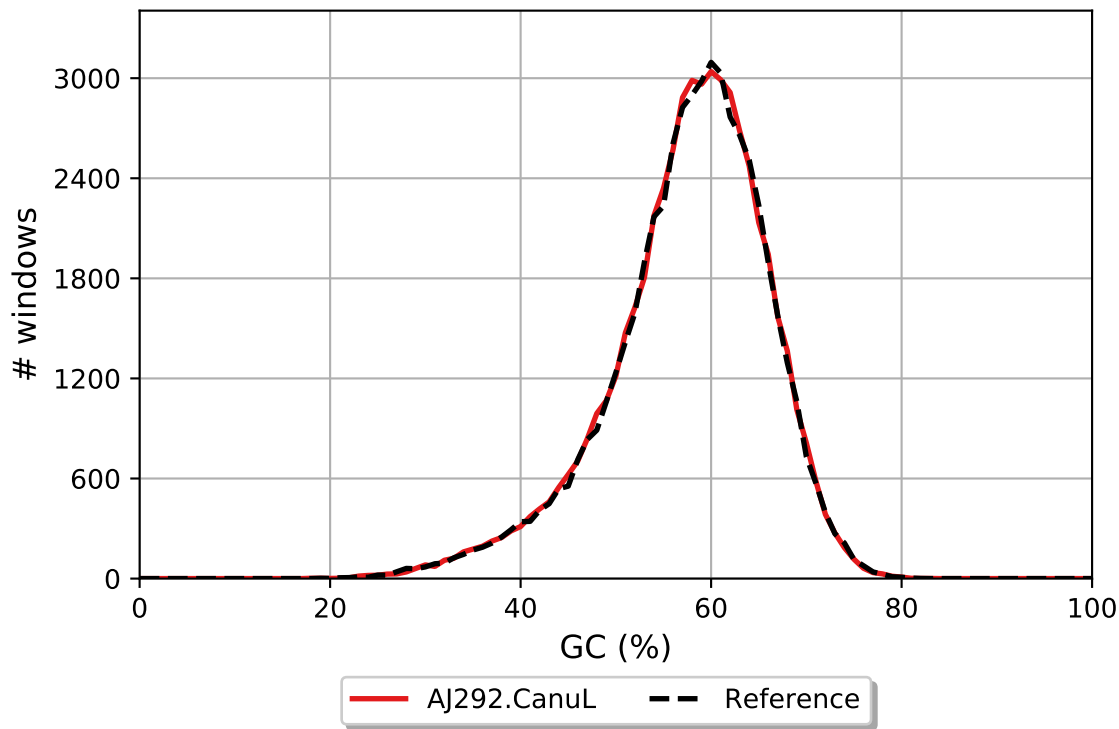
NGx



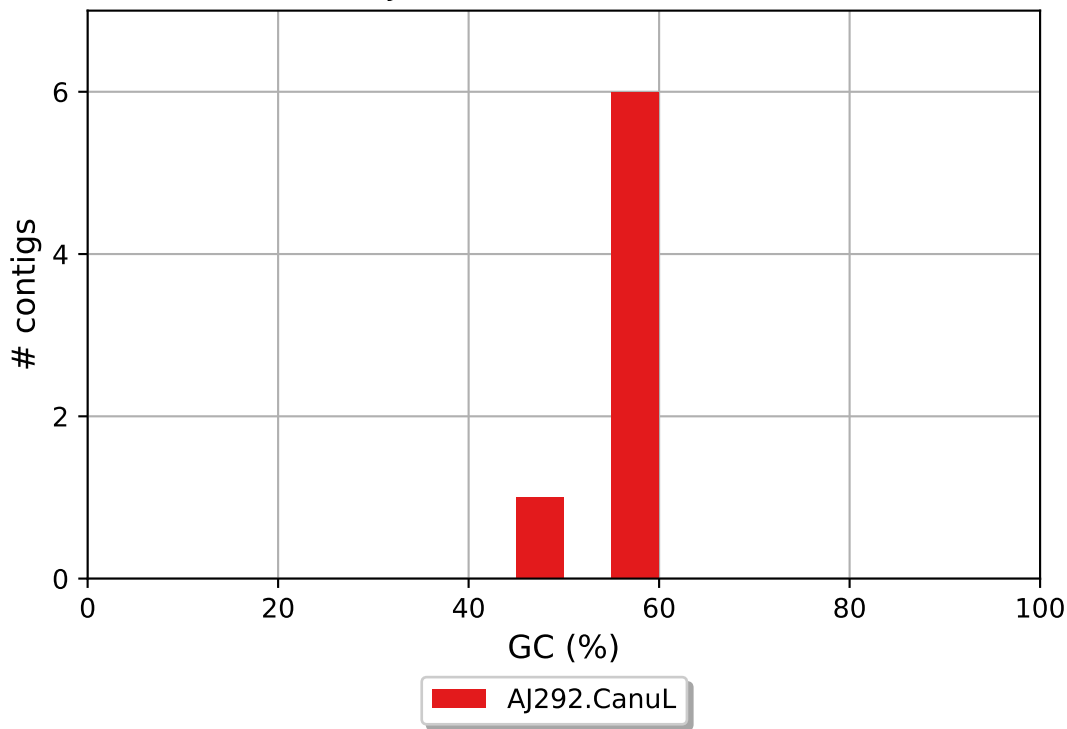
AJ292.CanuL



GC content



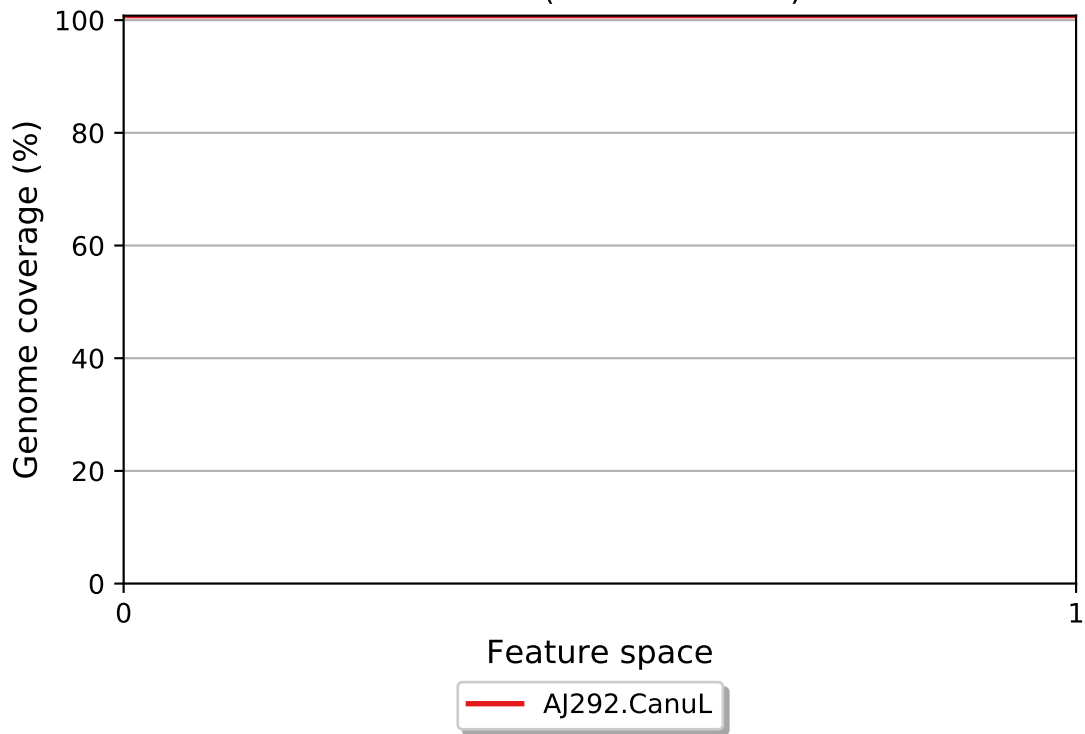
AJ292.CanuL GC content



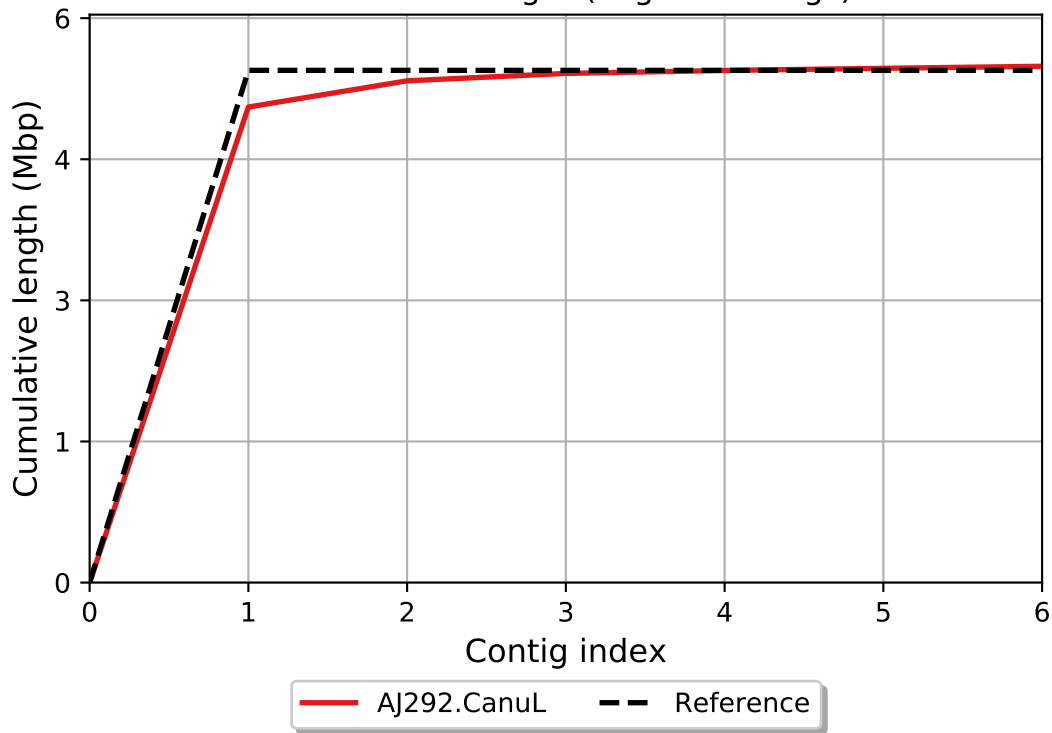
Misassemblies



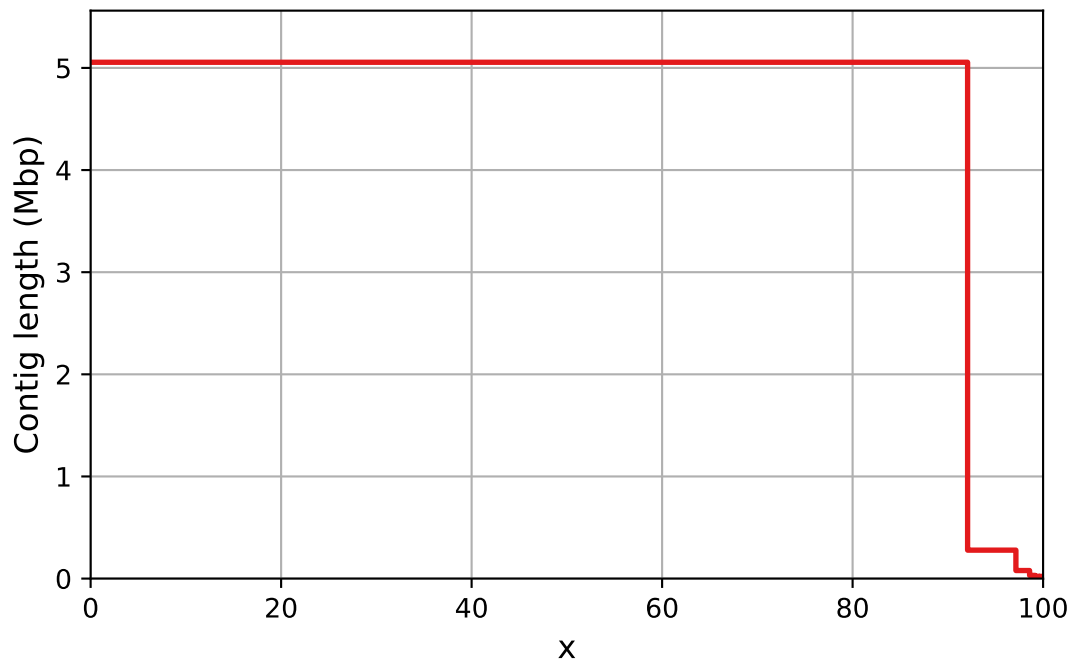
FRCurve (misassemblies)



Cumulative length (aligned contigs)

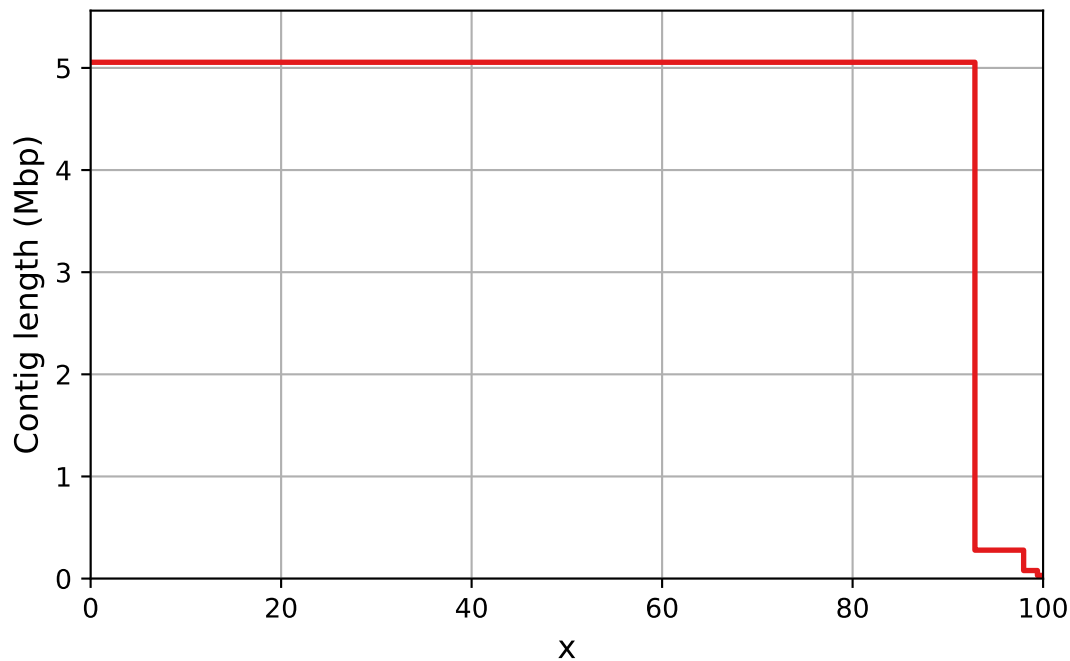


NAx



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NGAx



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