Report

	AJ292.CanuH
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5516556
Total length (>= 1000 bp)	5516556
Total length (>= 5000 bp)	5516556
Total length (>= 10000 bp)	5516556
Total length (>= 25000 bp)	5478302
Total length (>= 50000 bp)	5442094
# contigs	4
Largest contig	5442094
Total length	5516556
Reference length	5445112
GC (%)	57.63
Reference GC (%)	57.62
N50	5442094
NG50	5442094
N75	5442094
NG75	5442094
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	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	15.10
Largest alignment	5442094
Total aligned length	5516556
NA50	5442094
NGA50	5442094
NA75	5442094
NGA75	5442094
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).
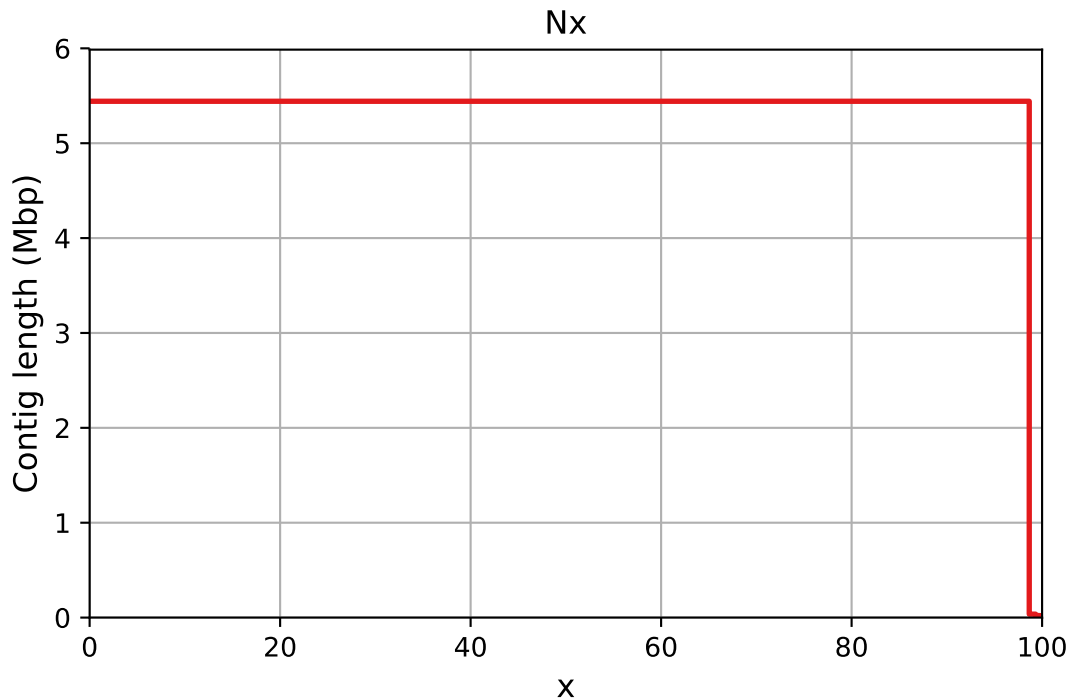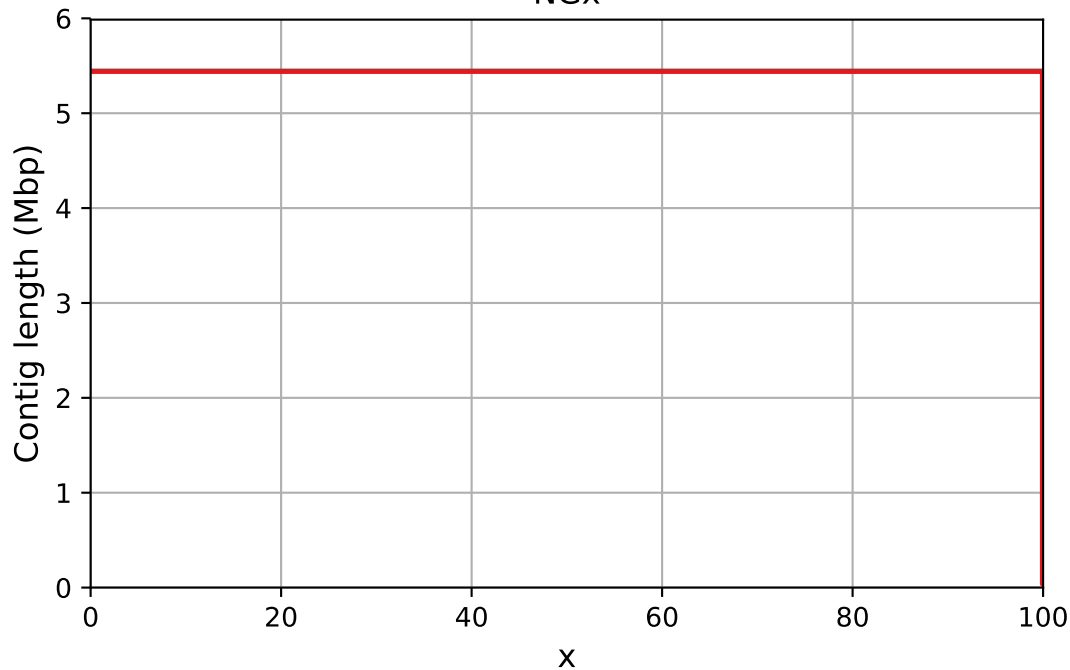
Misassemblies report

	AJ292.CanuH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	10
# indels	822
# indels (<= 5 bp)	822
# indels (> 5 bp)	0
Indels length	825

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).

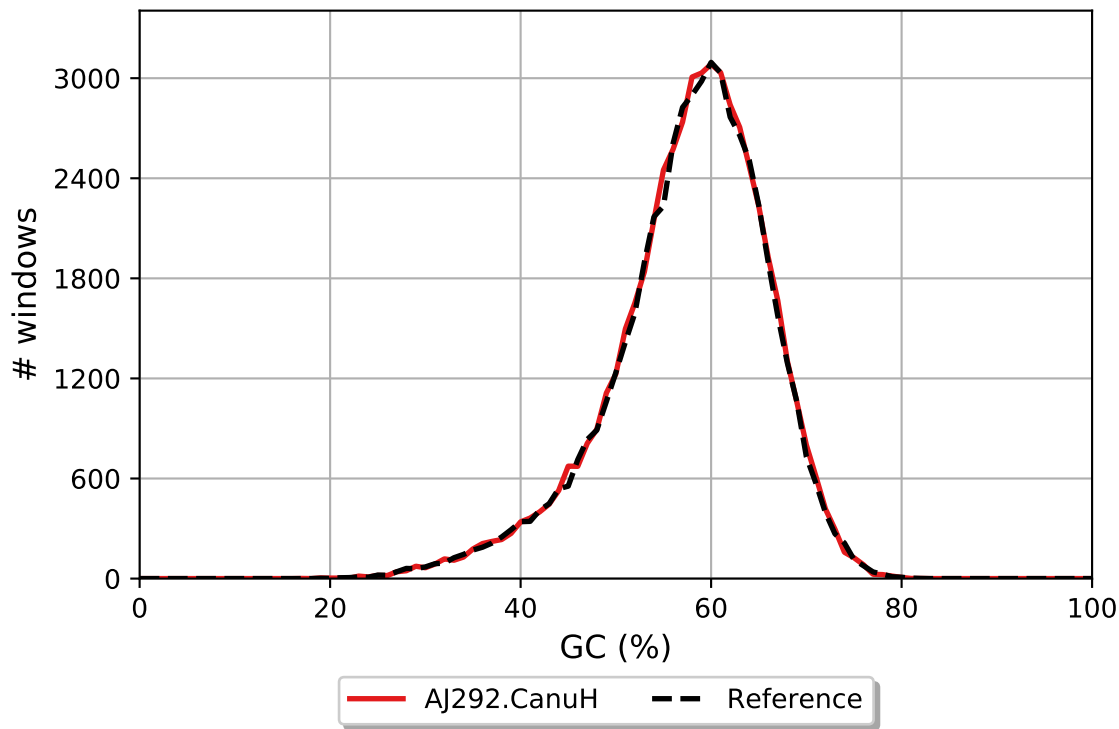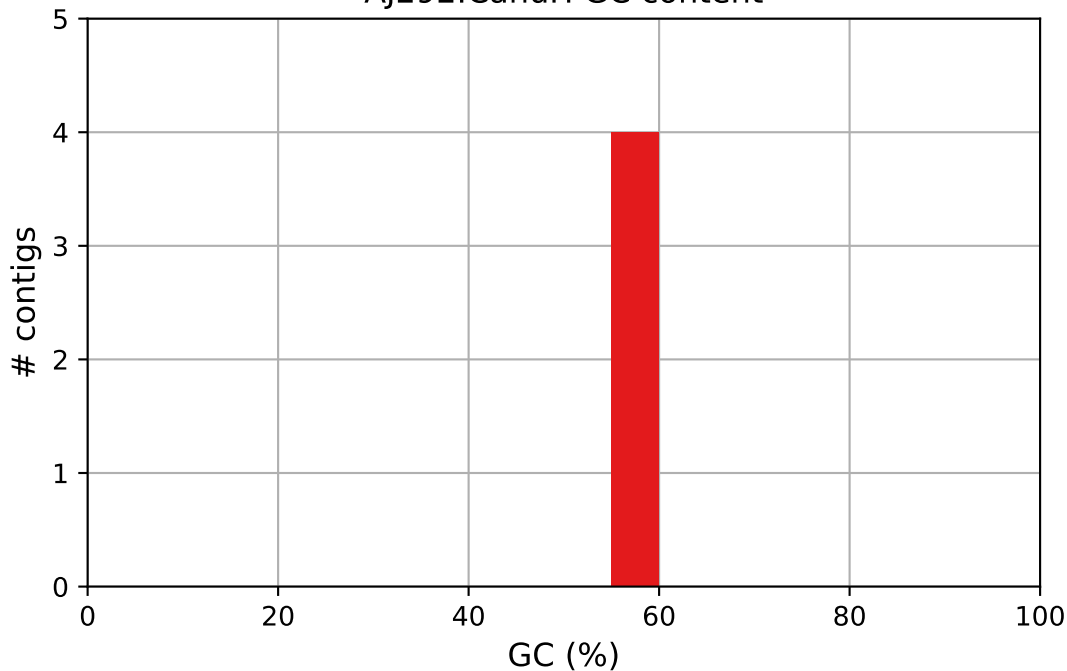# Unaligned report

	AJ292.CanuH
# 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

NGx

Contig length (Mbp) vs x

AJ292.CanuH
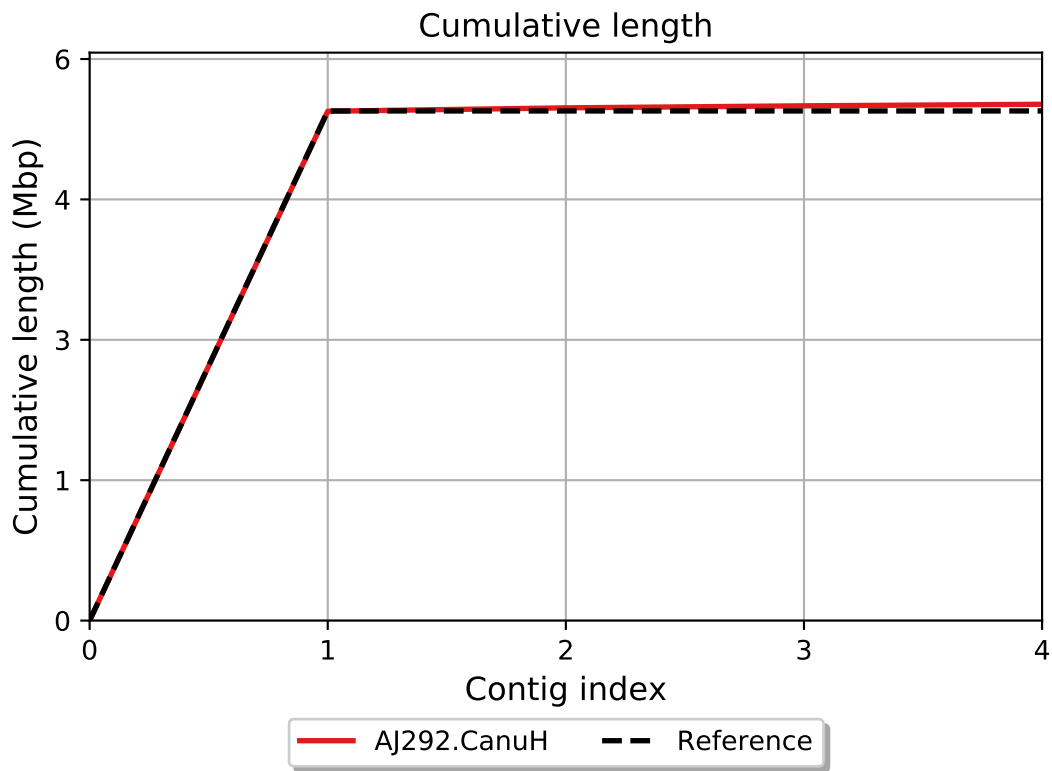
Cumulative length

GC content

AJ292.CanuH GC content

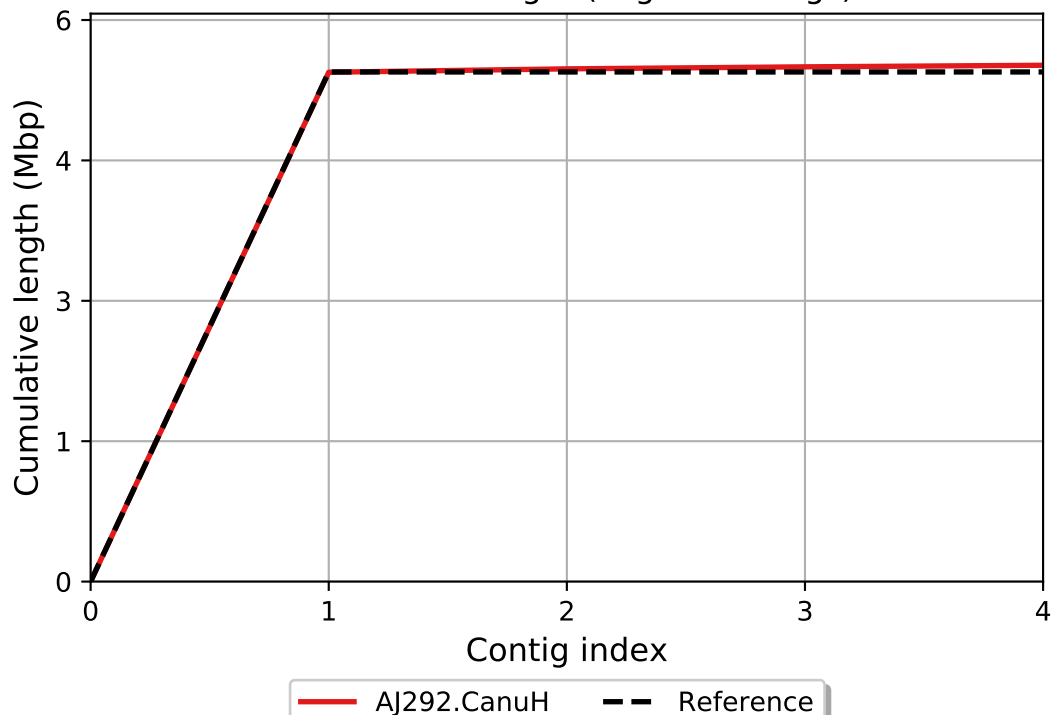# Misassemblies

AJ292.CanuH

FRCurve (misassemblies)
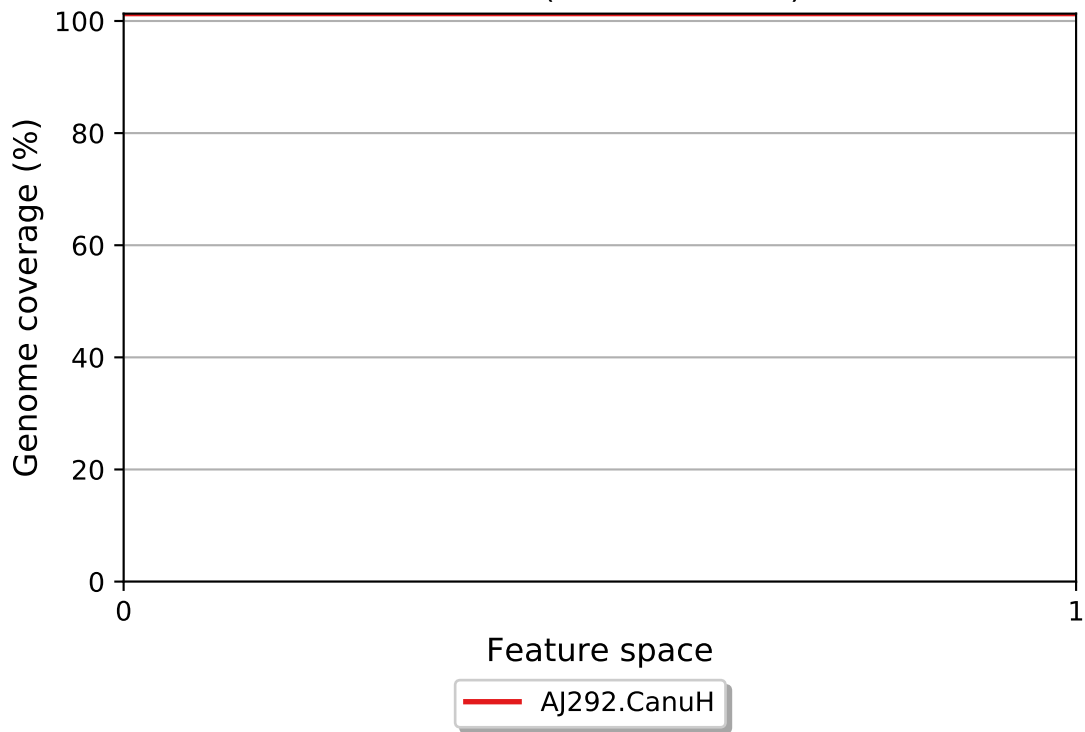
AJ292.CanuH

Cumulative length (aligned contigs)

NAx

NGAx