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Figure S1. Packaged read depth across the *de novo* CA-11.2A genome assembly. *De novo* assembly
of packaged reads >5kb produced the indicated contigs. Read coverage was then mapped to each contig.
(A–H) Read coverage across the CA-11.2A chromosome or indicated plasmids are shown. Coverage maps
for the cp32s and lp54 are shown in Figures 6 and 9, respectively.

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195 Figure S2. Whole genome sequencing of the CA-11.2A genome reveals that plasmid lp36/lp28-4 196 resolves into two separate episomes. (A) The CA-11.2A genome was sequenced using long-read 197 technology. Reads were aligned to the lp36/lp28-4 reference sequence (NC 012202.1) and read depth 198 plotted. (B) Schematic of PCR design. Primers 1 and 2 flank the lp36/lp28-4 junction, with primer 1 199 annealing to Ip36 and primer 2 annealing to Ip28-4, creating a 620 bp product if joined. Primers 3 and 4 200 anneal to Ip36 DNA, creating an 813 bp product if present. Primers 5 and 6 anneal to Ip28-4 DNA, creating 201 a 1,115-bp product if present. (C) The presence or absence of lp36, lp28-4, or lp36/lp28-4 was confirmed 202 by PCR.