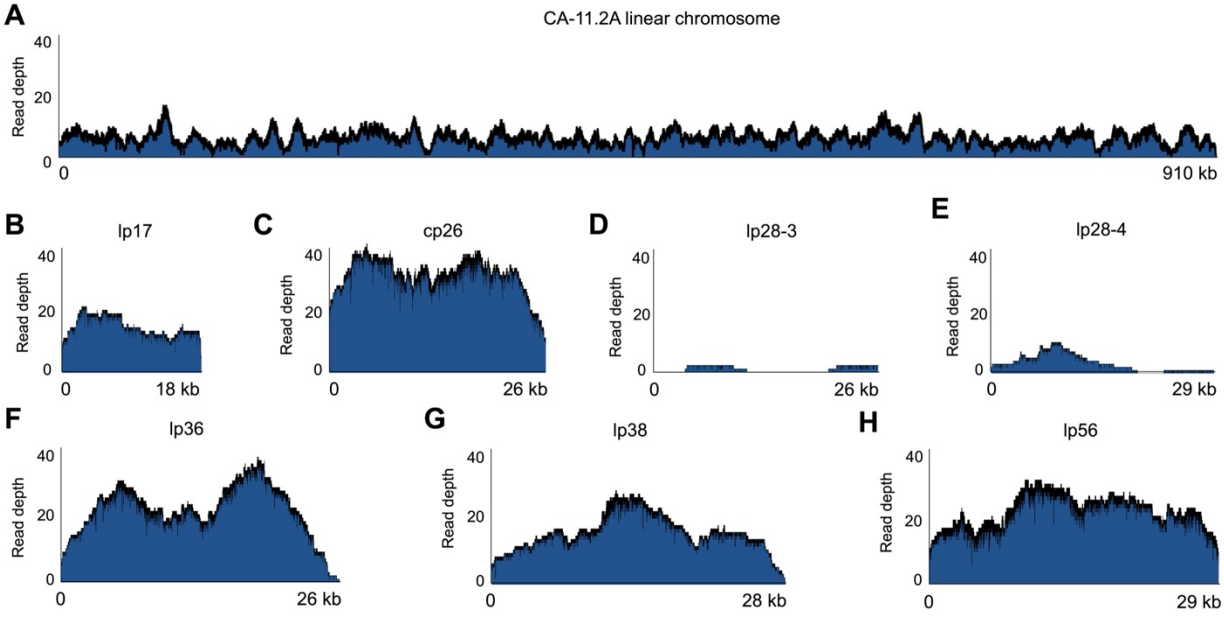

Figure S1. Packaged read depth across the *de novo* CA-11.2A genome assembly. *De novo* assembly of packaged reads >5kb produced the indicated contigs. Read coverage was then mapped to each contig. **(A–H)** Read coverage across the CA-11.2A chromosome or indicated plasmids are shown. Coverage maps for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

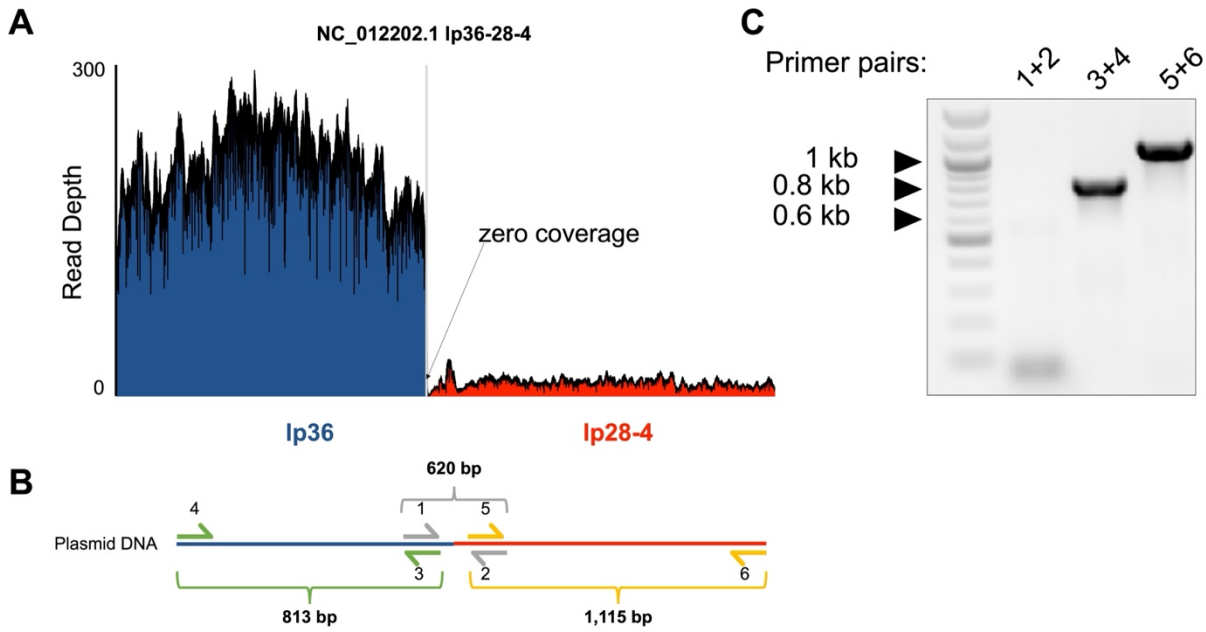

Figure S2. Whole genome sequencing of the CA-11.2A genome reveals that plasmid lp36/lp28-4 resolves into two separate episomes. (A) The CA-11.2A genome was sequenced using long-read technology. Reads were aligned to the lp36/lp28-4 reference sequence (NC_012202.1) and read depth plotted. **(B)** Schematic of PCR design. Primers 1 and 2 flank the lp36/lp28-4 junction, with primer 1 annealing to lp36 and primer 2 annealing to lp28-4, creating a 620 bp product if joined. Primers 3 and 4 anneal to lp36 DNA, creating an 813 bp product if present. Primers 5 and 6 anneal to lp28-4 DNA, creating a 1,115-bp product if present. **(C)** The presence or absence of lp36, lp28-4, or lp36/lp28-4 was confirmed by PCR.