

***PirAB^{vp}*-bearing *Vibrio parahaemolyticus* and *Vibrio campbellii* pathogens isolated from the same AHPND-affected pond possess highly similar pathogenic plasmids**

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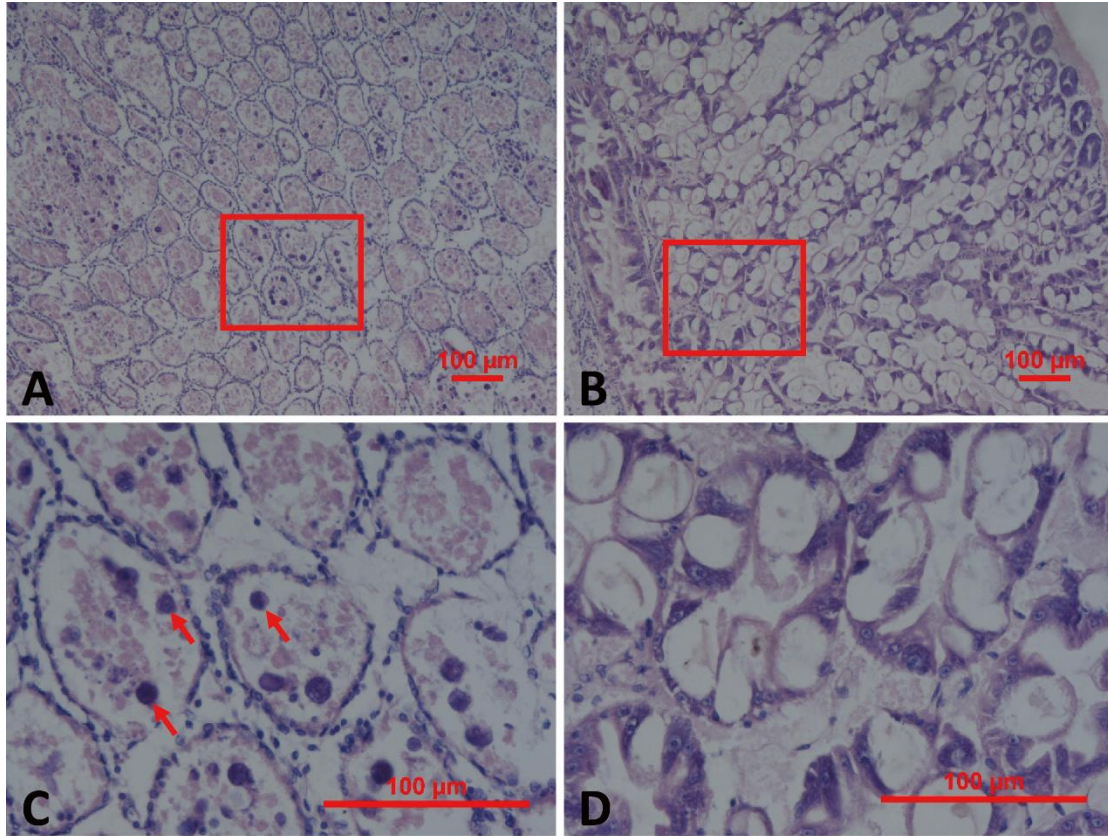
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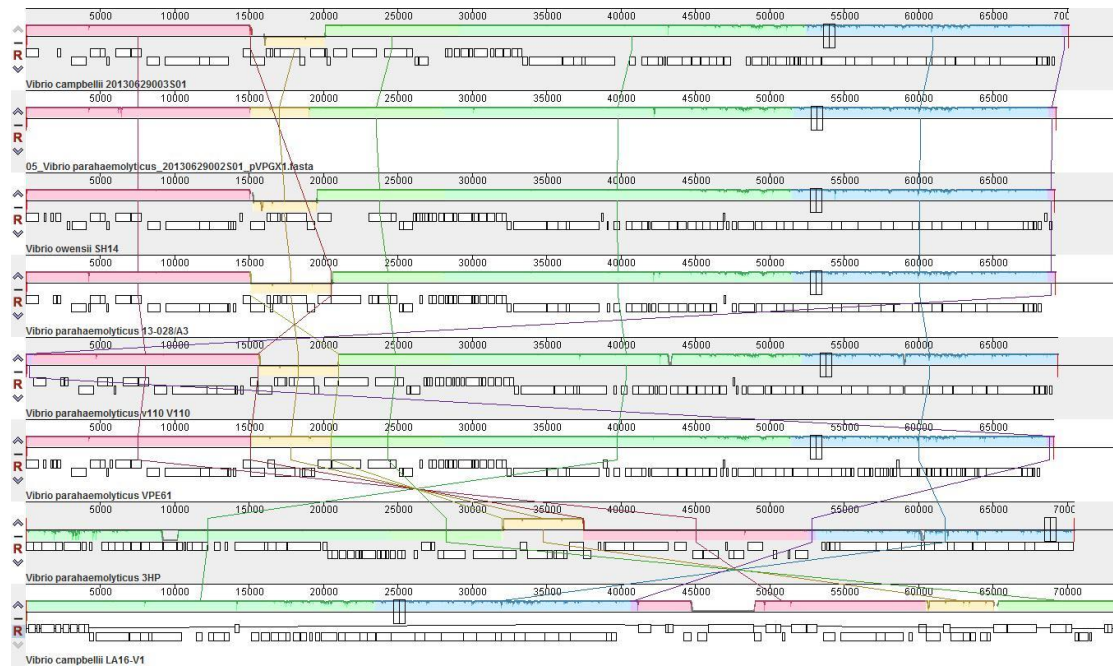
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Supplementary Figure S1. H&E stained histological sections of the hepatopancreas of *Litopenaeus vannamei* from the challenge tests. A-B, 100× view field. C-D, Zoom-in view (400×) of the corresponding areas in the red blocks in A-B. A and C: *Vp* 2S01-infected group; B and D, Negative-control group; A and C: AHPND pathology characterized by sloughing of hepatopancreatic tubule epithelial cells (arrows); B and D: Normal shrimp hepatopancreatic histology. Scale bars = 100 μm.



Supplementary Figure S2. Complete sequences comparison of *pirAB^{vp}*-bearing plasmids.

The complete reference sequences of *pirAB^{vp}*-bearing plasmids (pLA16-2, pVHvo, pVPA3-1, pVA1, pVPE61a, pV110) were downloaded from NCBI. Multiple plasmid sequences alignment among *pirAB^{vp}*-bearing plasmids from *Vp* 2S01, *Vc* 3S01 and reference strains was calculated using mauve (Darling et al., 2004).

Colored blocks in the first genome are connected by lines to similarly colored blocks in other genomes. These lines indicate which regions in each genome are homologous.

Darling, A.C., Mau, B., Blattner, F.R., and Perna, N.T. (2004). Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res* 14(7), 1394-1403. doi: 10.1101/gr.2289704.