

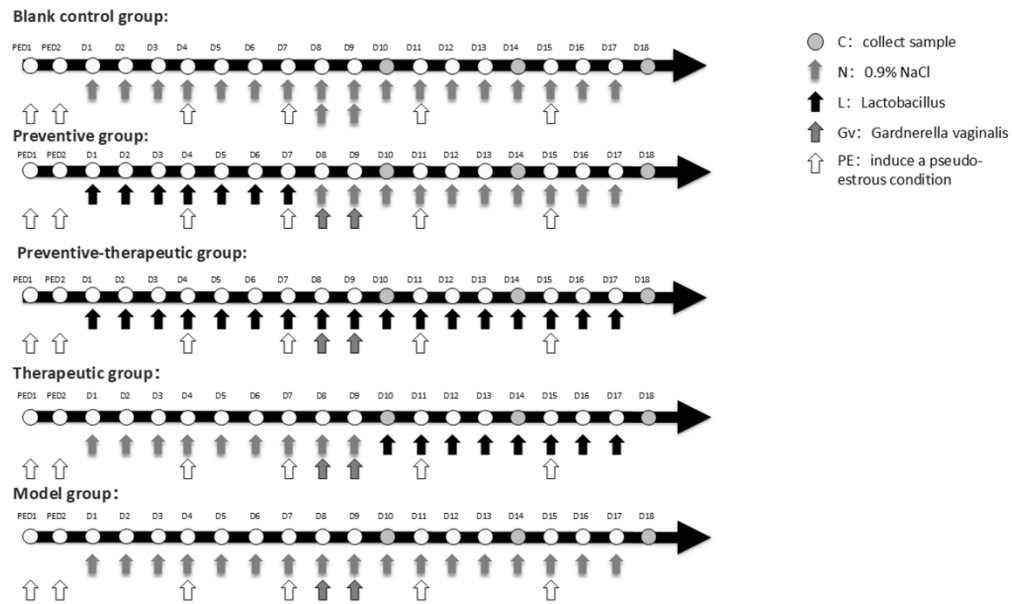


Fig. S1. Experimental design for the BV mouse model. Eight-week-old female BALB/c mice were randomly assigned to five experimental groups: blank control (BC), model (M), preventive (P), preventive-therapeutic (PT), and therapeutic (T).

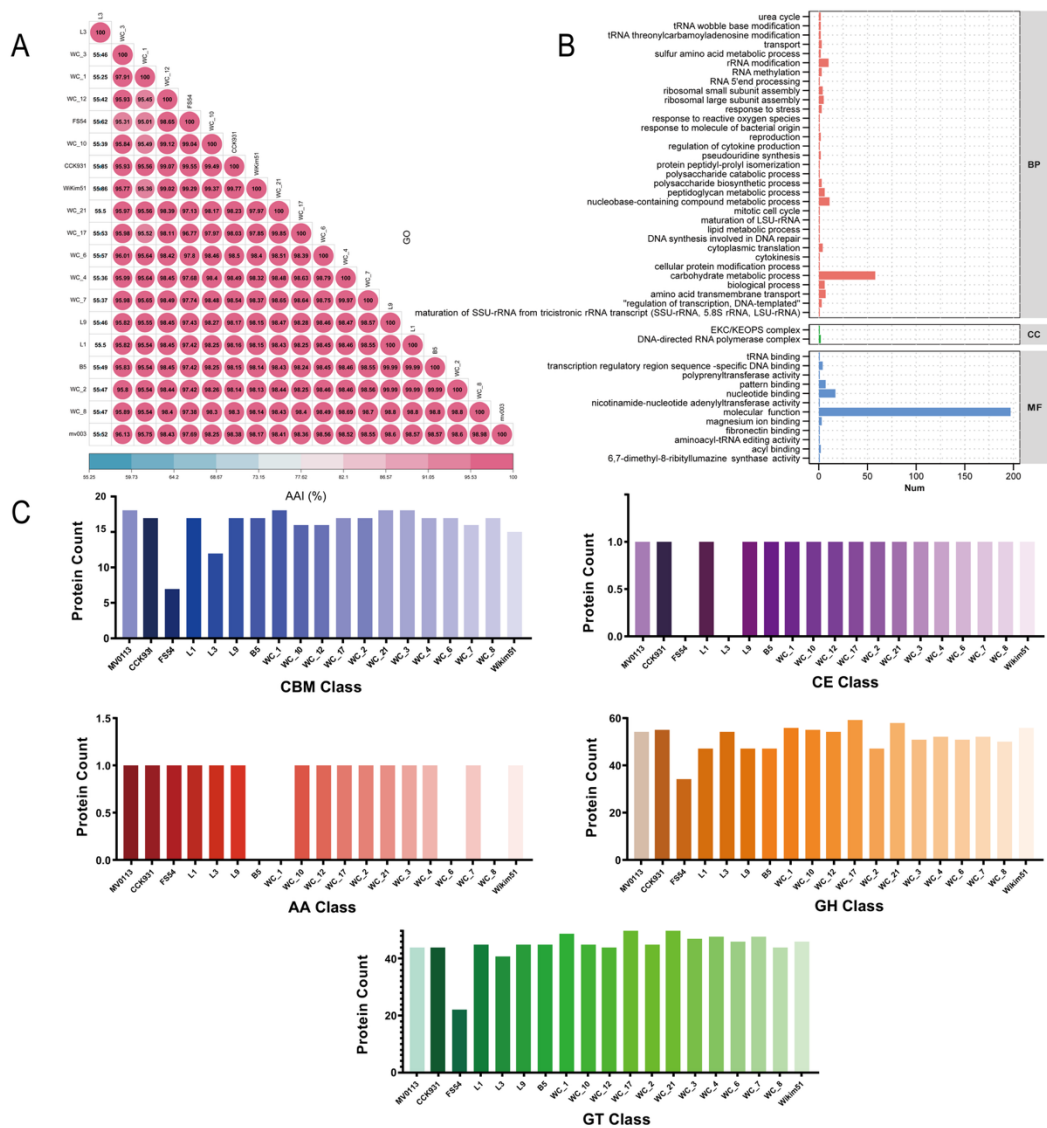


Fig. S2 Additional genomic analyses of *W. confusa* MV0113.

(A) Average amino acid identity (AAI) matrix confirming close relatedness to other *W. confusa* strains. (B) Gene Ontology (GO) annotation categorized into biological process (BP), cellular component (CC), and molecular function (MF). (C) Detailed distribution of CAZy families including GH, CE, AA, and CBM subclasses.

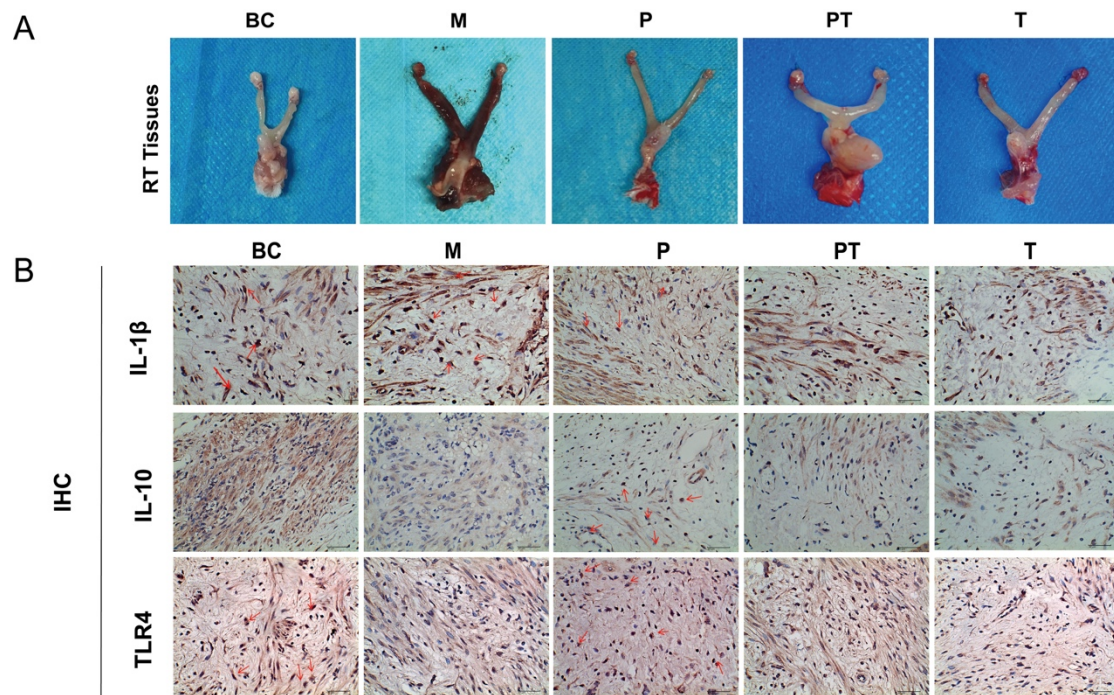


Fig. S3. Gross and immunohistochemical evaluation in the murine BV model.

(A) Representative gross images of reproductive tract (RT) tissues from each group. (B) Representative IHC of vaginal tissues stained for IL-1 β , IL-10, and TLR4 (day 9 post-infection; objective $\times 40$; scale bar = 10 μ m). Red arrows indicate positive staining.

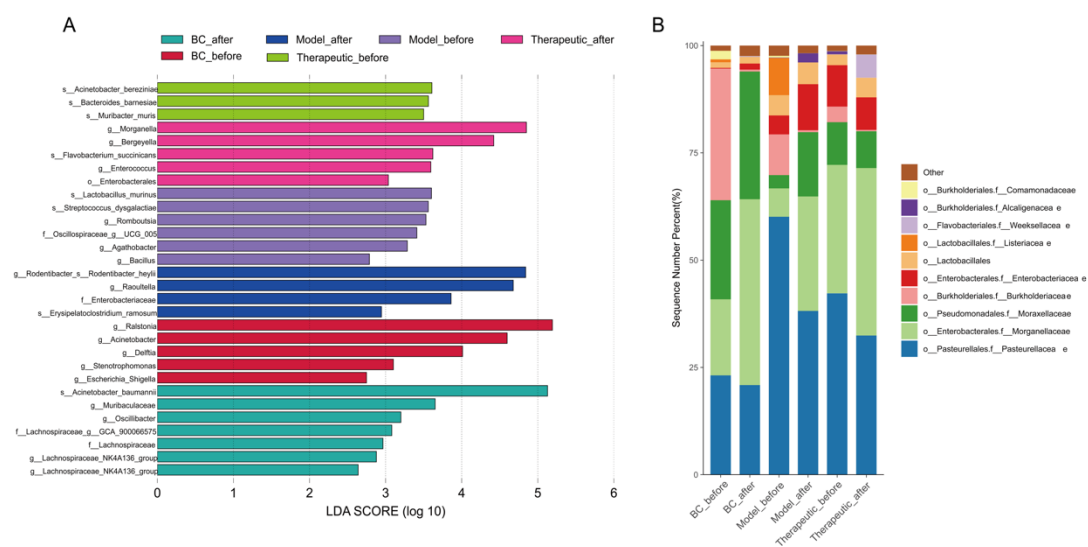


Fig. S4. Differential taxa associated with BV and MV0113 treatment.

(A) Differentially enriched taxa identified by LEfSe (LDA > 3.0, $P < 0.05$). (B) Family-level relative abundance highlighting Enterobacteriaceae and Lactobacillaceae.