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Correction: Hydrolyzed protein formula improves the nutritional tolerance by increasing intestinal development and altering cecal microbiota in low-birth-weight piglets

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A Correction on

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There was a mistake in Figure 3 as published. The image of RB41 was duplicated with the image of Rubrobacter. The corrected Figure 3 appears below.

The original version of this article has been updated.

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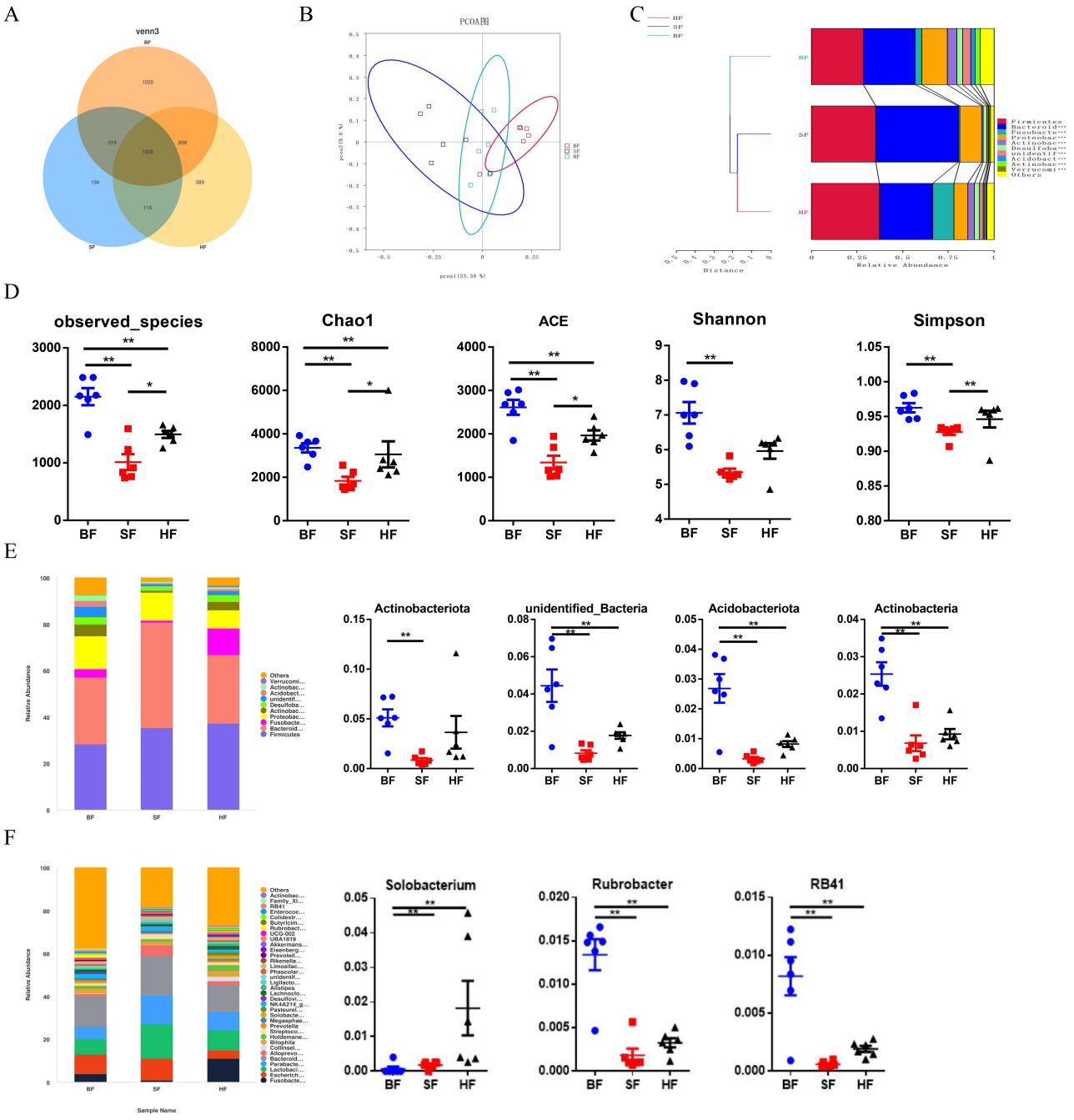

FIGURE 3
Effect of different formula treatments on colonic microbiota diversity and composition in pigs. **(A)** A Venn diagram illustrating the overlaps of OTUs in the gut microbiota. **(B)** Principal coordinate analysis (PCoA). **(D)** Non-metric multidimensional scaling (NMDS) analysis. **(C)** Unweighted unifrac cluster tree based on Unweighted Pair-group Method with Arithmetic Mean (UPGMA) analysis. **(D)** The microbial alpha diversity index (Observed-species, Chao1, Shannon, Simpson, ACE) were calculated using the mother program. **(E)** Relative contribution of the top 10 phylum in each group (left) and the relative abundance of significantly different microorganisms (right). **(F)** The relative contribution of the top 35 genera in each group (left) and the relative abundance of significantly different microorganisms (right). BF, basal infant formula; SF, standard premature infant formula; HF, hydrolyzed protein formula. Data are expressed as means ± SEM ($n = 6$). $^{*}p < 0.05$, $^{**}p < 0.01$, and $^{***}p < 0.001$.