Fig S1. Difference in diversity of microbial communities between Gut (G) and Vagina (V) in AB (A) and in NoAB (B) mice in the discovery cohort

Fig. S2. Changes in diversity of bacterial communities after AB treatment in the gut (A) and in the vagina (B) in the validation cohort of mice

Fig. S3. Difference in diversity of microbial communities between Gut (G) and Vagina (V) in AB (A) and in NoAB (B) mice in the validation cohort

Fig. S4. Changes in distribution of species with different abundances in the gut and in the vagina after AB treatment in the validation cohort

Fig. S5. Differentially abundant taxa between AB (A) and NoAB mice in the gut and vagina of mice in the validation cohort

Fig. S6. Opposite effect of AB treatment (A -treated, N-not treated mice) on relative abundance of some bacterial phyla in the gut and vagina in the validation cohort

Fig. S7. Association network of bacterial species in terms of similarity of co-occurrence profiles of the OTUs in the studied samples and their heatmap in NoAB (A) and AB (B) mice in the validation cohort.

Fig. S8. Association of the gut bacterial diversity with the tumor growth in AB mice

Fig. S9. Association of diversity in the gut and in the vaginal with the tumor growth in NoAB mice