Figure S3. Phylogenetic tree of fecal and vaginal microbiota during cancer development. Results are given with phylogenetic distances by hierarchically clustering samples using logarithmic abundance values of OTUs with maximal abundance cut < 1%. Numbers, clades; F, fecal sample; L, vaginal lavage sample; A, antibiotic treated; C, control; 00 to 54, sampling point (week); XL number, sample ID; OTU number and bacteria name, the most abundant OTU. All samples used here are the same as those used to generate Figure 3.