



Figure S4. Specific bacteria are associated with tumor development and post-antibiotic treatment microbiota transition. A) OTUs with abundances that were highly associated with overall tumor scores at the end point Week 54 were screened by Spearman Ranking coefficient $p < 0.05$. Negatively and positively associated OTUs in fecal microbiota are shown with Spearman Ranking coefficients at Week 54 and early time points with p value cut 0.05. B) High correlations were found between OTU abundances estimated by Illumina sequencing and qPCR methods. qPCR analysis for three representative OTUs that showed significant associations with tumor scores was performed with OTU-specific primers shown in Table S1 and normalized by universal 16S rRNA copies. Ovarian cancer-associated OTUs ($p < 0.05$) in C) fecal and D) vaginal microbiota are shown with Spearman Ranking coefficients with overall tumor scores including metastasis evaluation (Overall+meta), the tumor scores of left and right oviducts that exclude metastatic effects at Week 54. In the case of positively associated bacteria, shown is the top 8 of 56. E) and F), OTUs and higher taxons that have different abundances in Abx-treated and control samples (LEfSe $p < 0.05$, FDR $q < 0.05$) are shown with polarized LDA (plus, control-rich; minus Abx group-rich). t, detection threshold for OTUs (the minimal 1/2 inverse value of total reads).