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Supplemental information

Bifidobacterium affects antitumor efficacy

of oncolytic adenovirus in a mouse

model of melanoma

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Treatment	Phylum	Timepoints	Z	Un p-value	Ad p-value
Mock	Tenericutes	-10 to 20	-3.527848	0.00041895	0.00251371
		0 to 20	-2.244994	0.02476849	0.04953698
	Actinobacteria	-10 to 18	-3.3140394	0.00091959	0.00275876
		0 to 18	-3.3674917	0.00075855	0.00455132
Bifidus	Actinobacteria	0 to 20	-3.3140394	0.00091959	0.00551751
	Proteobacteria	-10 to 0	2.7260647	0.00640944	0.03845666
		-10 to 18	2.5657079	0.01029655	0.03088965
	Cyanobacteria	-10 to 0	2.3518989	0.01867785	0.05603355
Ad-CpG	Actinobacteria	-10 to 18	-3.3674916	0.00075855	0.00455132
	Firmicutes	0 to 18	2.6191602	0.00881466	0.02644396
		18 to 20	-3.1002304	0.0019337	0.01160221
Ad-CpG + Bifidus	Actinobacteria	-10 to 18	2.8864214	0.0038965	0.023379
	Firmicutes	-10 to 20	-2.4053512	0.01615693	0.04847079
	Deferribacteres	-10 to 18	2.93987366	0.00328346	0.01970077
		0 to 18	2.88642141	0.0038965	0.0116895
	Cyanobacteria	-10 to 0	2.7805624	0.00542648	0.03255889
		-10 to 18	2.4597283	0.01390422	0.04171267
	Tenericutes	-10 to 18	2.4053512	0.01615693	0.04847079
		0 to 18	2.6726124	0.00752632	0.04515789

Table S1. Abundance of phyla obtained by Dunn's test, Related to Figure 4

Table S1. Results of Dunn's test, applied to the Kruskal-Wallis significant amplicon sequence variants (ASVs) shown in Figure 4 panel A; the phyla shown in the table for each treatment, were obtained from significant comparisons between time pairs, according to the Benjamini and Hochberg's false discovery rate (FDR) correction (BH) adjusted p-value<0.05.

Figure S1. Perturbation of gut microbiome reduced the efficacy of Ad-CpG in a syngeneic mouse model of melanoma, Related to Figure 1







Figure S1. The panel below represents the quadrant gating strategy that has been used for all samples. **A)** The lymphocytes gate was obtained by selecting CD45+ lymphocytes (red color population indicated as LYM) **B)** T lymphocytes CD3+ were gated on CD45+ lymphocytes el). B220 was used to select B lymphocytes among CD45+ lymphocytes. For each treatment, we report the gating strategy of CD8+ CD3+ CD45+ T-lymphocytes and of CD4+ CD3+ CD45+ T lymphocytes.

Figure S2. Flow cytometry representative plots of analysis of Foxp3+ CD4+ CD45+ T lymphocytes collected from Ad-CpG-treated tumors, Related to Figure 3



Lymphocytes (LYM)

В





Ad-CpG + Bifidus

Figure S2. The panels represent the quadrant gating strategy that has been used for all tumor samples collected from both OAd- treated mice, indicated as Ad-CpG and Ad-CpG + Bifidus. **A)** Lymphocytes were gated on CD45+ cells. **B)** For each treatment, we report the flow cytometry representative plots of CD4+ CD45+ T-lymphocytes and Foxp3+ CD4+ CD45+ T lymphocytes.





Figure S3. Flow cytometry representative plots of analysis of Foxp3+ CD4+ CD3+ T lymphocytes. **A)** The panels represent the quadrant gating strategy that has been used for all tumor samples collected from untreated mice (Mock) and **B)** from Bifidus-treated group (Bifidus). Lymphocytes were gated on CD45+ cells. For each treatment, we report the flow cytometry representative plots of CD4+ CD45+ T-lymphocytes and Foxp3+ CD4+ CD45+ T lymphocytes.

Α В Ad-CpG Ad-CpG + Bifidus LY B220+ °0 ŝ LY B220+ B220 APC-H7-A 10³ 10⁴ B220 APC-H7-A è LY CD3+ LY CD3+ -1,377 -1,004 10⁵ -10²0 10² 10³ 10³ 10 CD3 PerCP-Cy5-5-A 10³ 10⁴ CD3 PerCP-Cy5-5-A -537 -816 ŝ ŝ CD3 PerCP-Cy5-5-A CD3 PerCP-Cy5-5-A 40 LYCD4+ LYCD4+ ŝ 818 233 10⁵ 105 105 -1,198 -1,301 102 ŝ CD4+FOXP3+ CD4+FOXP3+ FOXP3 PE-A 10³ 10¹ FOXP3 PE-A ~__ 0 5 ŝ 10⁵ 10⁵ 10³ 10¹ CD4 PE-Cy7-A 104 -1,301

-1,198

Figure S4. Flow cytometry representative plots of analysis of Foxp3+ CD4+ CD3+ T lymphocytes collected from Ad-CpG-treated groups, Related to Figure 3

Figure S4. A) The panels represent the quadrant gating strategy that has been used for all spleen samples collected from OAd-treated mice, indicated as Ad-CpG and **B)** from combined regimen-treated mice, indicated as Ad-CpG + Bifidus. B220 was used to select B lymphocytes. For each treatment, we report the flow cytometry representative plots of CD4+CD3+ T lymphocytes and Foxp3+ CD4+ CD3+ T lymphocytes.

Figure S5. Flow cytometry representative plots of analysis of Foxp3+ CD4+ CD3+ T lymphocytes collected from untreated and Bifidus-treated groups, Related to Figure 3



Figure S5. A) The panels represent the quadrant gating strategy that has been used for all spleen samples collected from untreated mice (Mock) **B**) and from Bifidus-treated mice (Bifidus). B220 was used to select B lymphocytes. For each treatment, we report the flow cytometry representative plots of CD4+CD3+ T lymphocytes and Foxp3+ CD4+ CD3+ T lymphocytes.

Figure S6. Co-culture experiment of melanoma cells with splenocytes pre-immunized, Related to Figure 3



Figure S6. Representative images of B16-OVA cells co-cultured with splenocytes preimmunized, as indicated (Mock, Bifidus, Ad-CpG and Ad-CpG+Bifidus) were acquired before and after splenocytes removal.



Figure S7. Alpha diversity of microbial communities, Related to Figure 4

Figure S7. The microbial richness measured by Observed OTU, Chao1 and Shannon indices do not highlight any differences between treatments indicated as: Mock, Bifidus (BIF), Ad-CpG and Ad-CpG+BIF or time points (Day-10; Day 0; Day 18; Day 20)





Figure S8. A) Principal coordinates analysis (PCoA) plot of the four groups. The plots show the first two principal coordinates (axes) for PCoA using unweighted UniFrac distances **B)** and weighted UniFrac distances. The treatments are indicated as: Mock, Bifidus (BIF), Ad-CpG and Ad-CpG+BIF and time points as (Day-10; Day 0; Day 18; Day 20). On the top of the plots, the results of *PERMANOVA* statistical test are reported in terms of R2, F statistic and p-value.

Figure S9. Evaluation of immunogenicity of Bifidobacterium-derived peptide B1, and tumor peptides T3 and T4, Related to Figure 7



Figure S9. A) IFN- γ ELISpot was performed on harvested splenocytes from mice preimmunized with PBS, adjuvant poly (I:C) and with *Bifidobacterium* peptide B1 and individual response to T3 stimulus and T4 for each group of mice (n=3) is reported as number of spots (IFN- γ). **B)** Comparison of the number of spots IFN- γ detected between splenocytes from mice preimmunized with B1 and pulsed with B1, T3 and T4 stimulus with relative means. All data are depicted as bar plots and mean ± SEM is shown. The statistical analysis was performed with ordinary one-way ANOVA (*p<0.05; **p<0.01; ***p<0.001; ****p<0.0001).