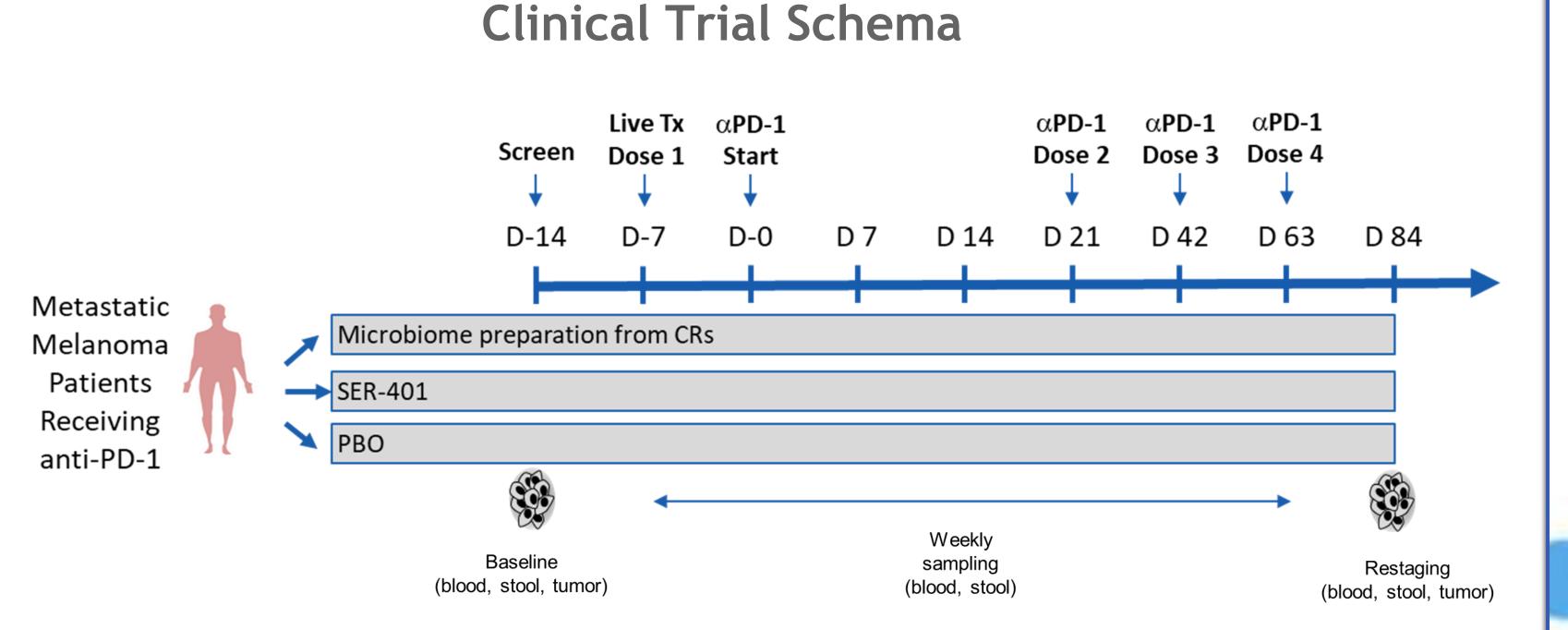
LB-283

Abstract

Background: The human gut microbiome is a diverse, dynamic and complex ecosystem that modulates numerous host processes including metabolism, inflammation and cellular and humoral immune responses. Recent publications have suggested that the gut microbiota of cancer patients is predictive of response to immune checkpoint inhibitors (ICI). To better understand how the microbiome may impact response to ICI, we have developed and validated robust tumor models using both conventional mice treated with antibiotics as well as germ free mice. **Results:** We show that germ-free mice lacking a microbiome, as well as antibiotics-treated mice fail to mount an effective anti-tumor immune response following treatment with anti-PD-1. The response to anti-PD-1 can be restored in germ free mice by introduction of a microbiome using fecal material prepared from healthy donor stool, and is driven by increased entry of tumor-infiltrating lymphocytes (TILs) into the tumor; specifically CD8+ T cells. Importantly, for the first time, we show that the bacterial spore fraction from healthy donor stool can restore response to anti-PD-1 and increase CD8+ TILs in both conventional mice treated with antibiotics as well as germ free mice. Based on these encouraging animal model data we plan to initiate a

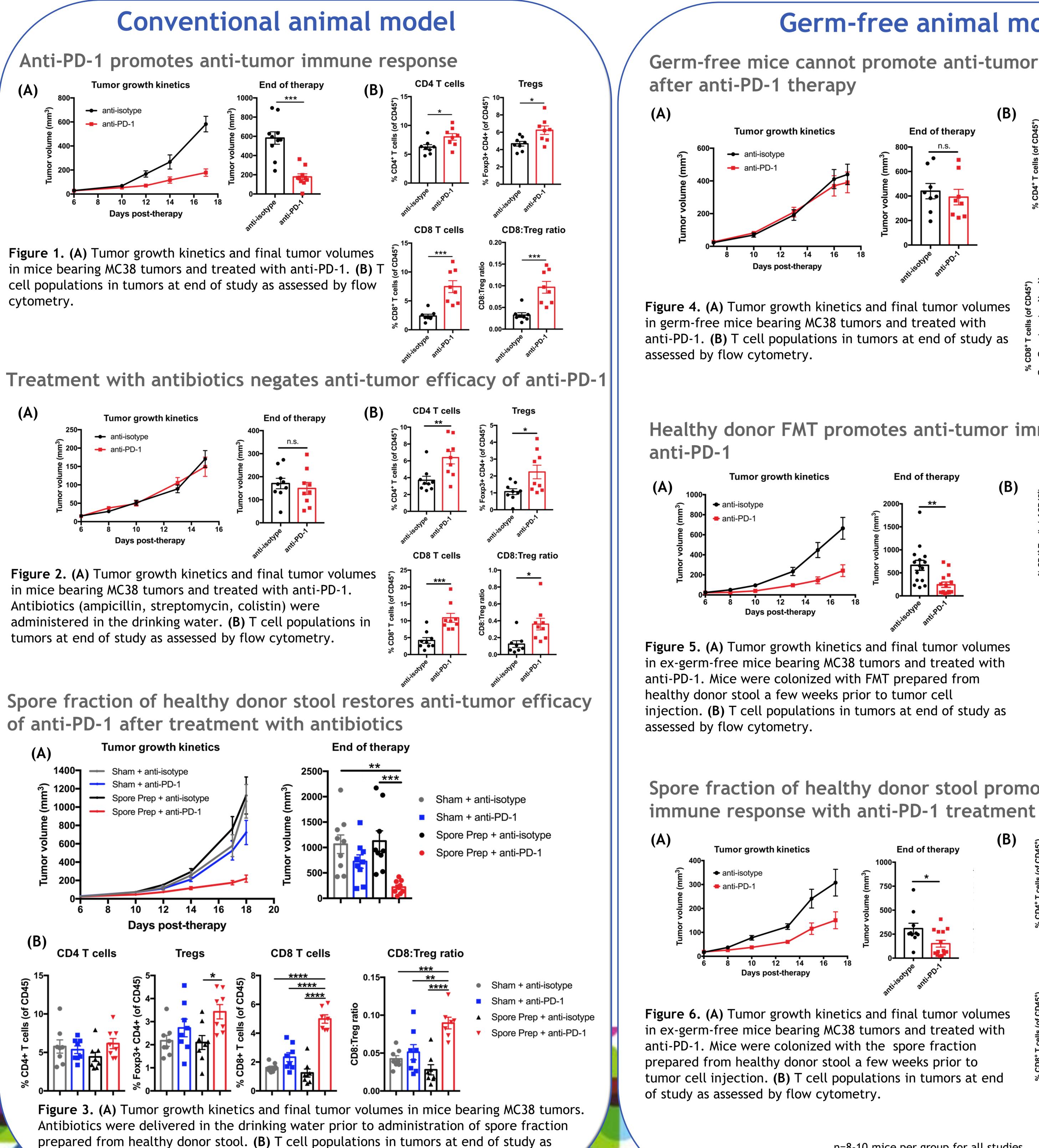
randomized, placebo-controlled clinical study at MD Anderson Cancer Center in 2018, sponsored by the Parker Institute for Cancer Immunotherapy, in patients with advanced metastatic melanoma. The clinical trial will evaluate the impact of an anti-PD-1 checkpoint inhibitor with adjunctive microbiome therapy on patient outcomes. Seres is developing SER-401, a preclinical stage oral microbiome therapy to improve the efficacy and safety of immunotherapy. Our drug discovery strategy iterates computational analyses with machine learning approaches, as well as empirical *in vitro*, *in vivo* and *ex-vivo* screening of strains and consortia to inform selection and drive microbiome drug design. Data from such a comprehensive approach is invaluable for designing compositions of bacteria that form "functional ecological networks" that can impact response to ICI therapy. We believe these data will provide insight into how microbiome drugs can be discovered and developed in the setting of immunotherapy to augment the efficacy of ICIs by altering the cancer-immune set point.



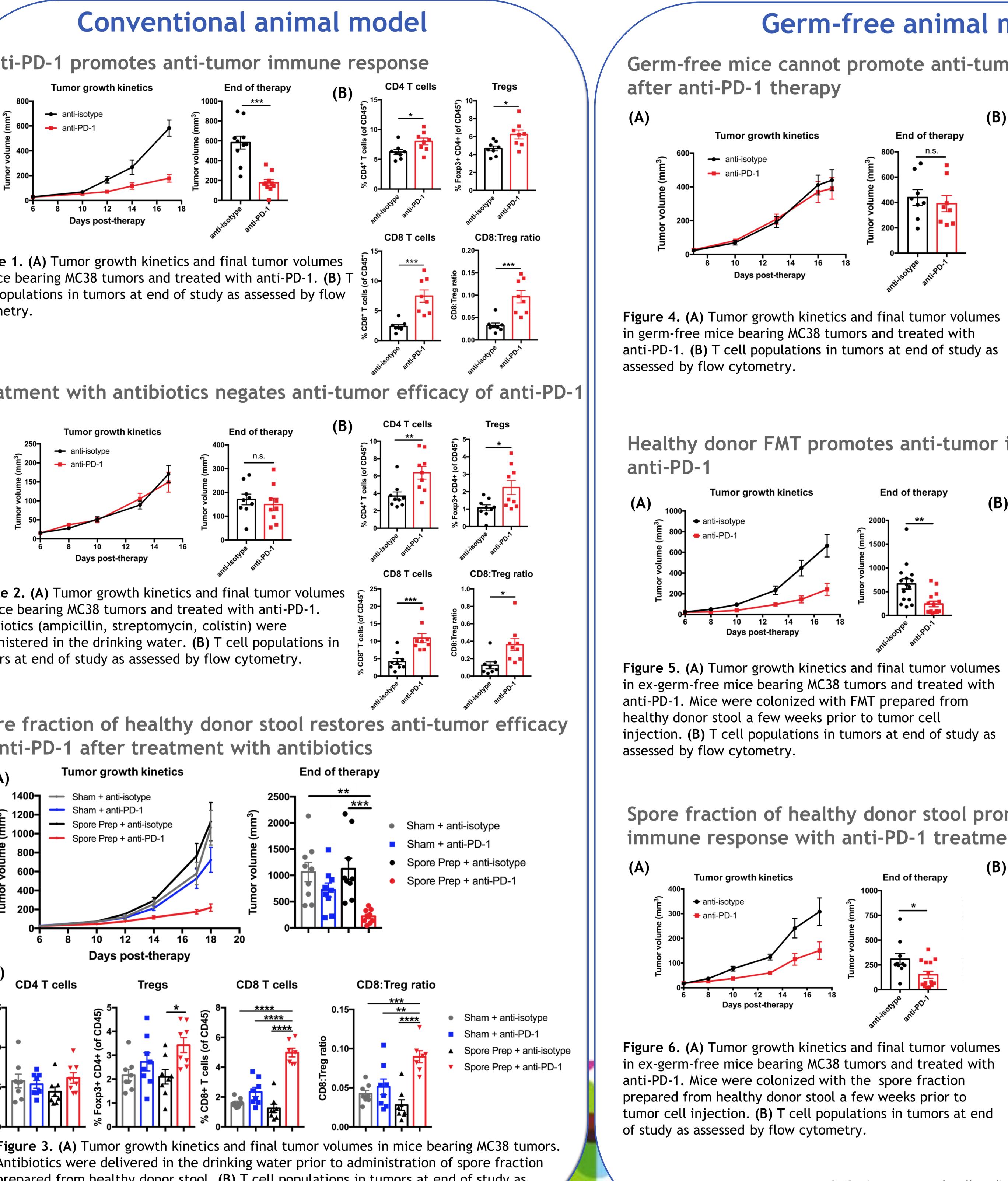
• Primary readouts: (i) safety/ tolerability (ii) tumor response and T cell infiltration vs. baseline Exploratory readouts: microbiome and metabolome correlates of clinical measures

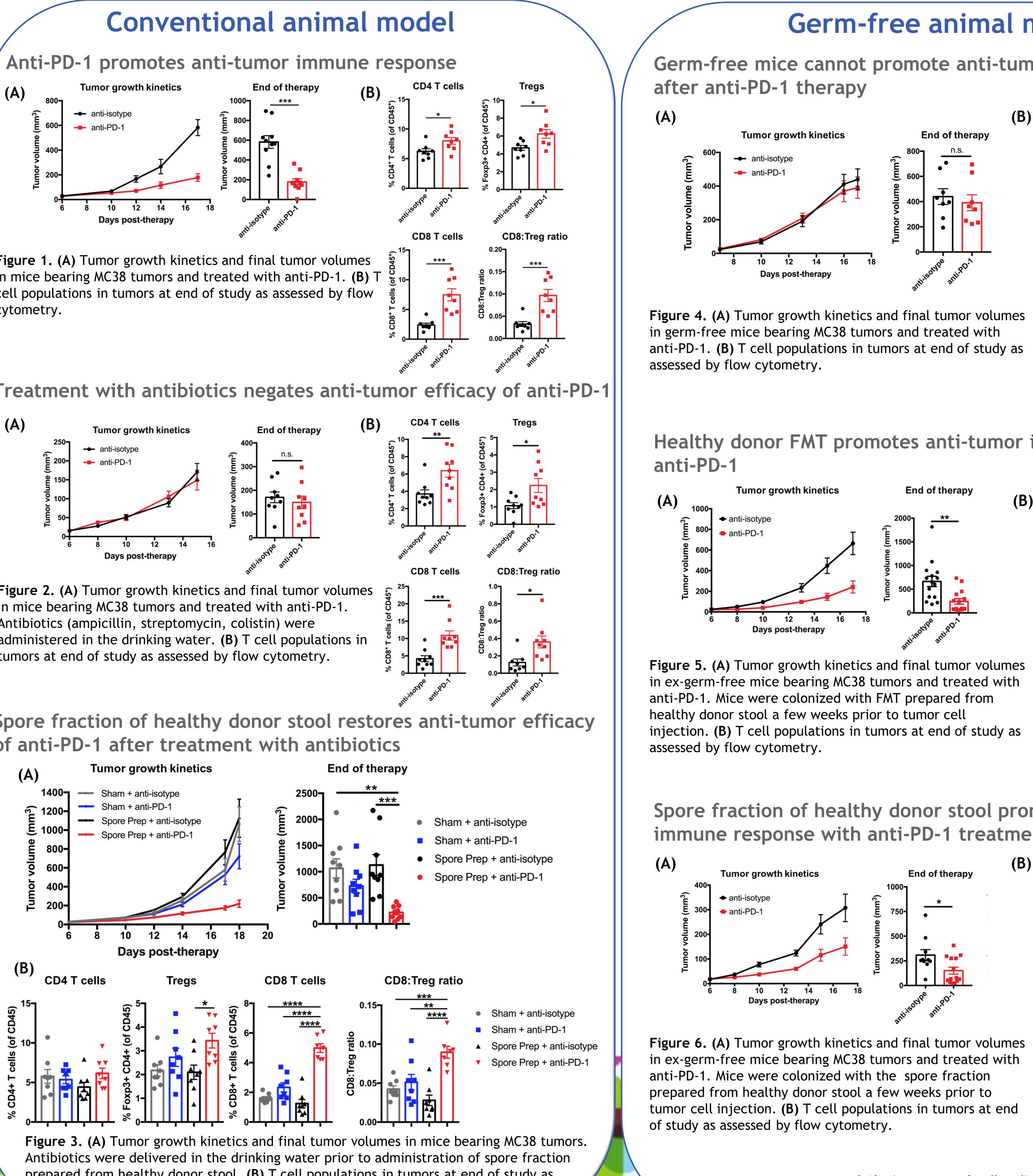
Leveraging gut microbiota to impact tumor immunotherapy

Jaclyn Sceneay, Srimathi Srinivasan, Keith Halley, George Marnellos, Jennifer Wortman, Matthew Henn, Elura Fink, Kevin Litcofsky, David Cook and Lata Jayaraman SERES THERAPEUTICS, 200 Sidney St., Cambridge, MA, www.serestherapeutics.com



cytometry.





assessed by flow cytometry.

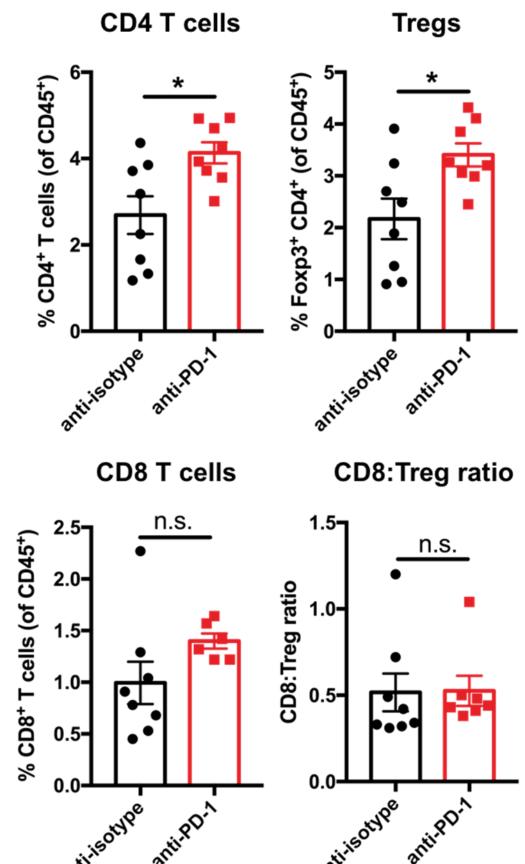
Statistical analysis was performed using two-tailed Student's T test or one-way ANOVA with p<0.05 considered significant (*p<0.05; **p<0.01, ***p<0.001, ****p<0.0001).



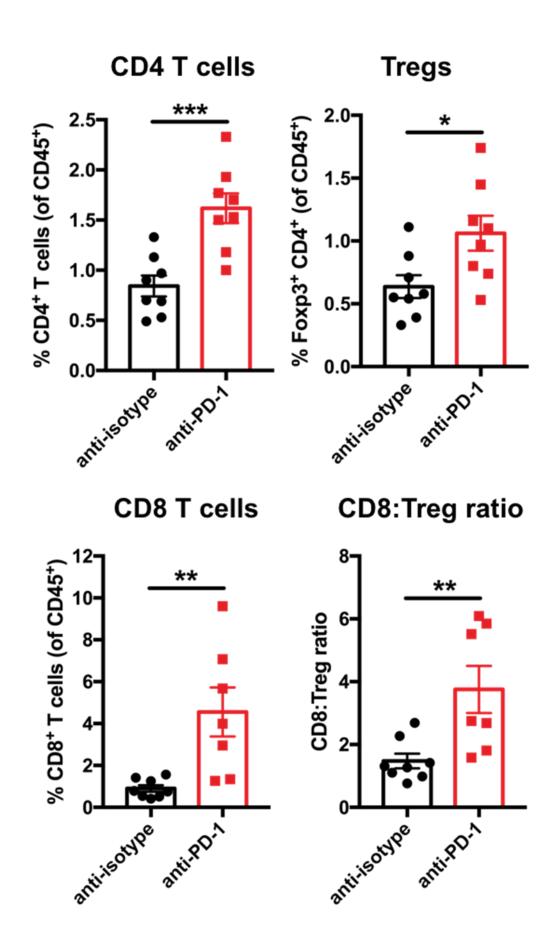


Germ-free animal model

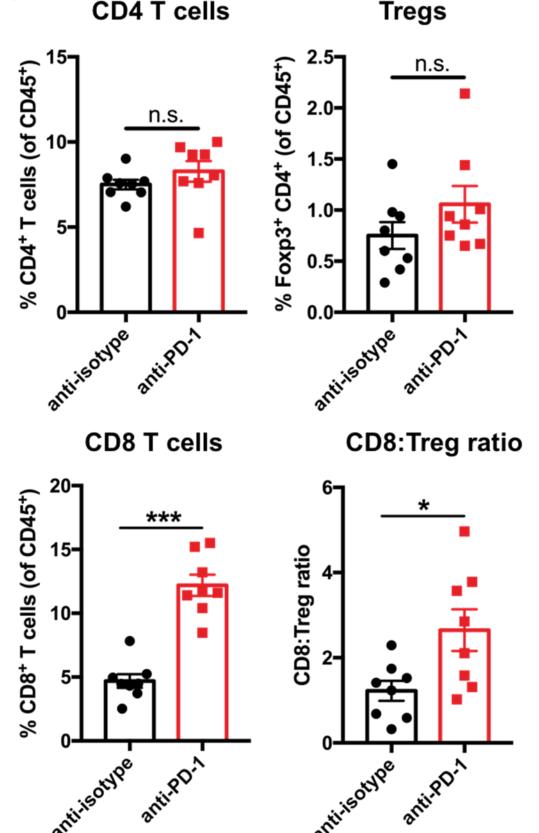
Germ-free mice cannot promote anti-tumor immune response



Healthy donor FMT promotes anti-tumor immune response to



Spore fraction of healthy donor stool promotes anti-tumor



n=8-10 mice per group for all studies