Additional data tables S1 through S24 are included in separate Excel (.xlsx) files.

Table S1. Domain names and corresponding InterPro (IPR) IDs used to search the proteomes of *Enterococcus* strains and species for peptidoglycan remodeling peptidases and UniProt proteome IDs, NCBI organism IDs, and alternative designations of *Enterococcus* strains and species used herein.

Table S2. Putative peptidoglycan remodeling peptidases of Efm Com15, Efm 7171, Efm DO, Eds 23C2, Ehe R, Emi 2375, Efs OG1RF, Efs 775, Efs V583, and Egm 2313. Table data contain the UniProt proteome entry ID, alternative entry ID(s), gene and protein names (if annotated), InterPro domain IDs, and primary sequence of every protein with a matching InterPro domain ID within the corresponding UniProt proteomes from Table S1.

Table S3. Quantification of Efm genome coverage in clinical samples from patients prior to treatment with checkpoint inhibitors.

Table S4. TBLASTN results for SagA-like orthologs from all RefSeq genomes annotated as strains of Efm, Eds, Ehe, or Emi.

Table S5. BLASTP results for SagA-like orthologs from all reference genomes within the Human Microbiome Project regardless of strain identification.

Table S6. Differential operational taxonomic unit (OTU) abundance analysis for the antibiotic pretreatment mouse model.

Table S7. Differential operational taxonomic unit (OTU) abundance analysis for the Taconic supplementation mouse model.

Table S8-S24. Differential gene expression and gene set enrichment analyses for all (S8) and each individual cluster (S9-S24) within the scRNA-seq dataset comparing CD45$^+$ cells from tumors treated with anti–PD-L1 and either MDP diastereomer. Clusters are numbered in order as described in Fig. 4. Each table contains separate sheets for differential gene expression and analyses from hallmark (H), curated (C2:CP), and biological process gene ontology gene sets (C5:BP). Positive values correlate with upregulation in the MDP-L,D sample.