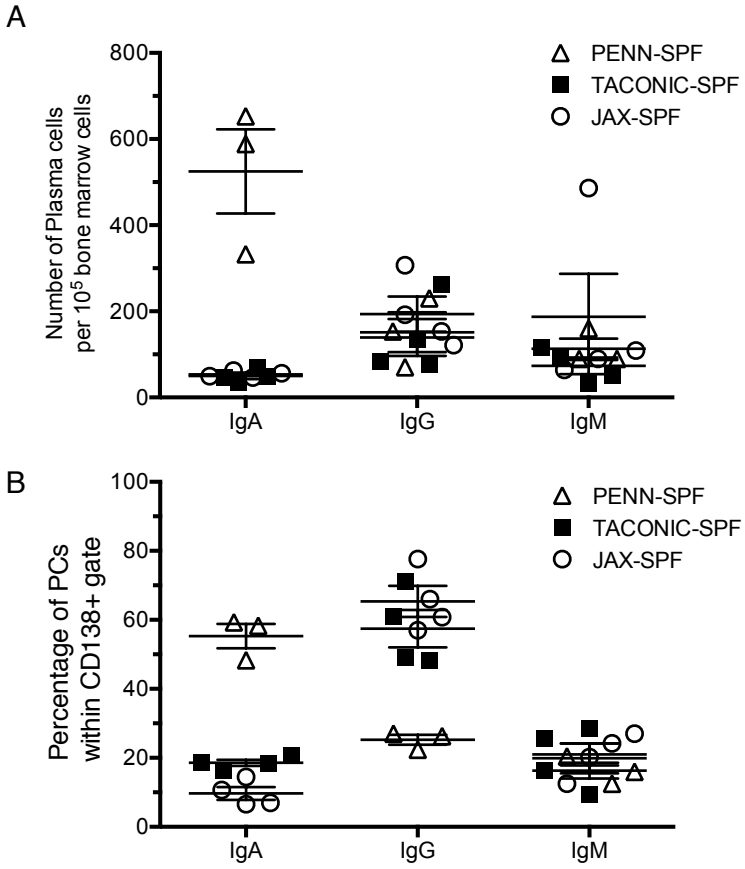
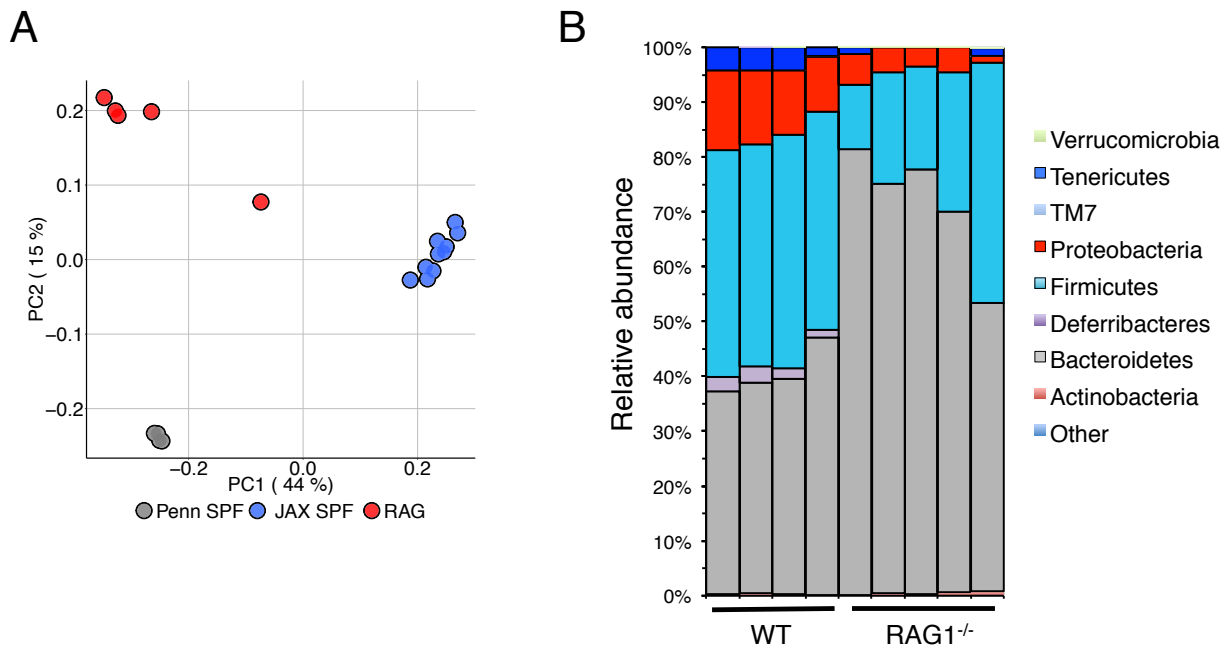
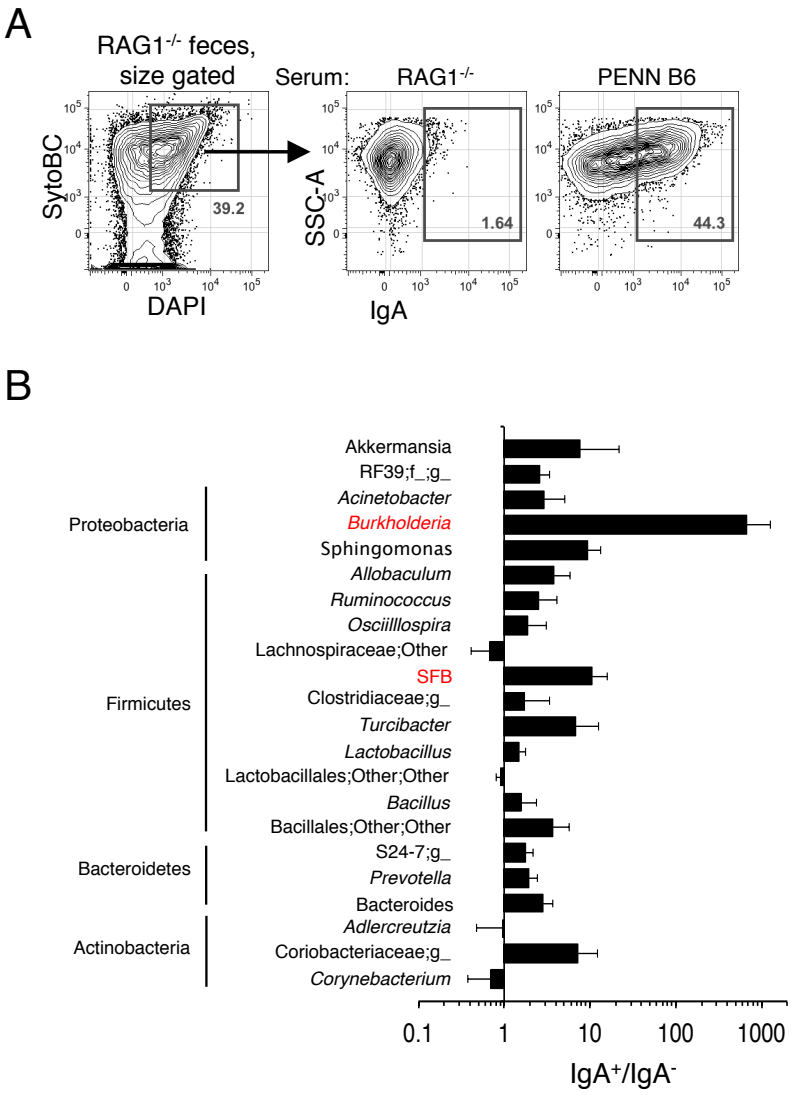
SUPPLEMENTAL INFORMATION



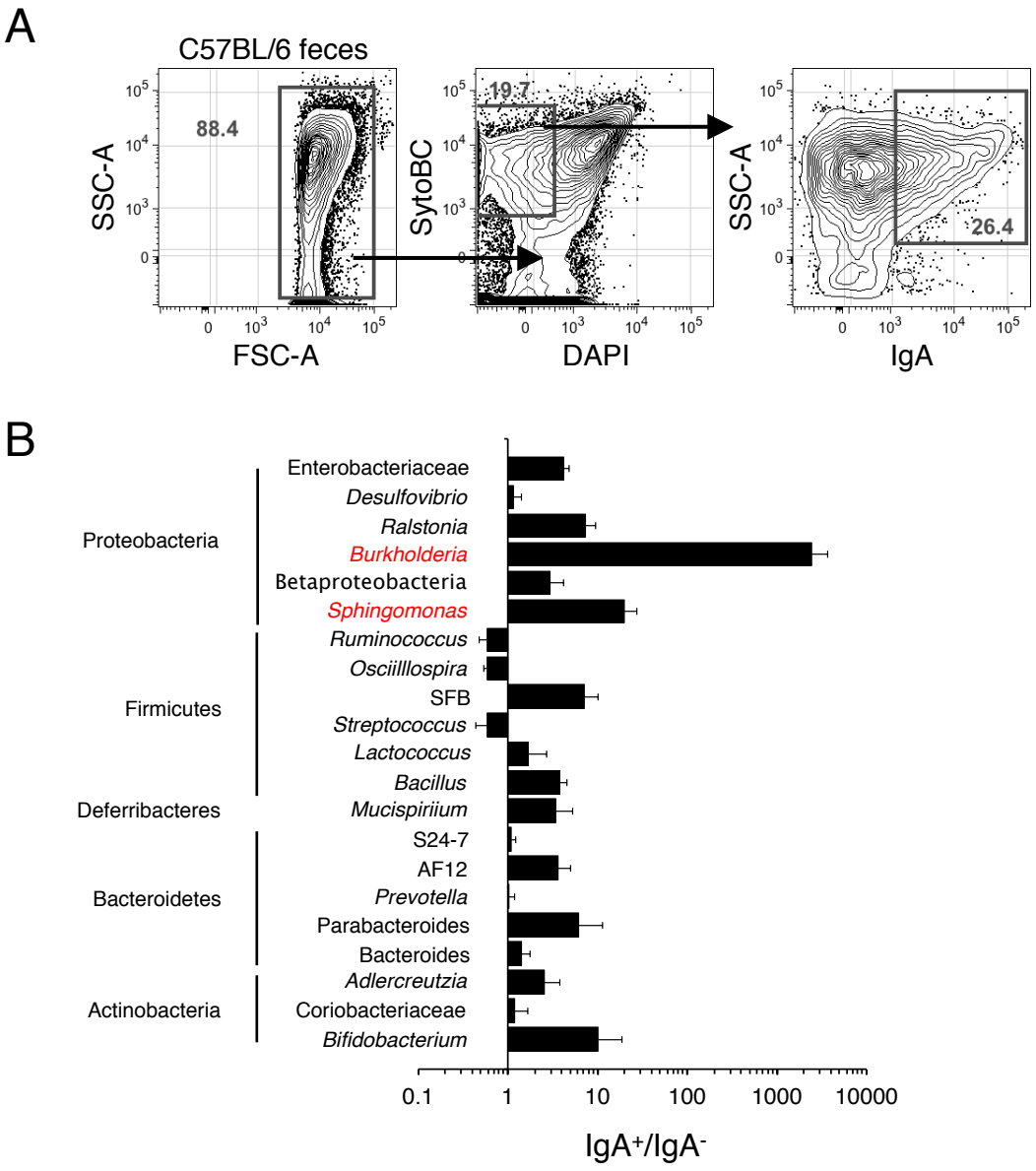
Supplemental Figure 1. Frequencies of IgA$^+$ bone marrow plasma cells in B6 mice from Taconic Farms, related to Figure 1. 16-week old B6 mice were purchased from Jackson Labs, Taconic farms, or bred in house. (**A**) Total number of IgA, IgG, and IgM secreting PCs per 10^5 BM cells determined by ELISpot. (**B**) Frequencies of the indicated plasma cell subset among all BM plasma cells were determined by flow cytometry focusing on Dump$^-$ IgD$^-$ Thy1.2$^-$ CD138^{high} cells as illustrated in Figure 1. Horizontal lines indicate means and error bars SEMs for each group.



Supplemental Figure 2. Fecal microbiota in B6 and B6.RAG$^{-/-}$ mice, related to Figure 4. Taxonomy for fecal bacteria in stool samples from individuals in the indicated group was determined by 16S V4 rDNA gene sequencing. (**A**) Principal coordinate analysis of the resulting data. (**B**) Relative abundance of the indicated phyla is shown.



Supplemental Figure 3. Select taxa among serum IgA-bound bacteria, related to Figure 4. (**A**) Fecal bacteria from B6.RAG1$^{-/-}$ mice were stained with sera from the indicated mice, and IgA^{+} bacteria identified with PE-anti-IgA antibodies. (**B**) Fecal bacteria from RAG1$^{-/-}$ mice were stained with sera from PENN-B6 adults and both IgA^{+} and IgA^{-} fraction within the DAPI^{+} SytoBC^{+} gate as shown in (A) sorted twice. DNA from these samples was then used for16S V4 sequencing. The ratio of the relative abundance for each taxa in each fraction (IgA^{+}, IgA^{-}) was used to identify taxa enriched for IgA binding. Bacterial genera that were highly enriched (IgA^{+}/IgA^{-} $\geq$ 10) are highlighted in red. Genera shown were selected because they possessed ICI scores above or below 3, or because of potential relevance based on previous studies.



Supplemental Figure 4. Select taxa bound by IgA in B6 mice, related to Figure 4. (**A**) Representative flow cytometric data of fecal bacteria stained with DAPI, Syto BC, and PE-anti-IgA from a Penn-SPF B6 adult. (**B**) Twice sorted bacteria from (A) were sequenced for the 16S V4 region to identify bacterial taxa in each population. As in Figure 5, highly coated bacteria ($IgA^+/IgA^- \geq 10$) are in red and the remaining groups were among the most enriched across all taxa.