Supplemental Figure 1

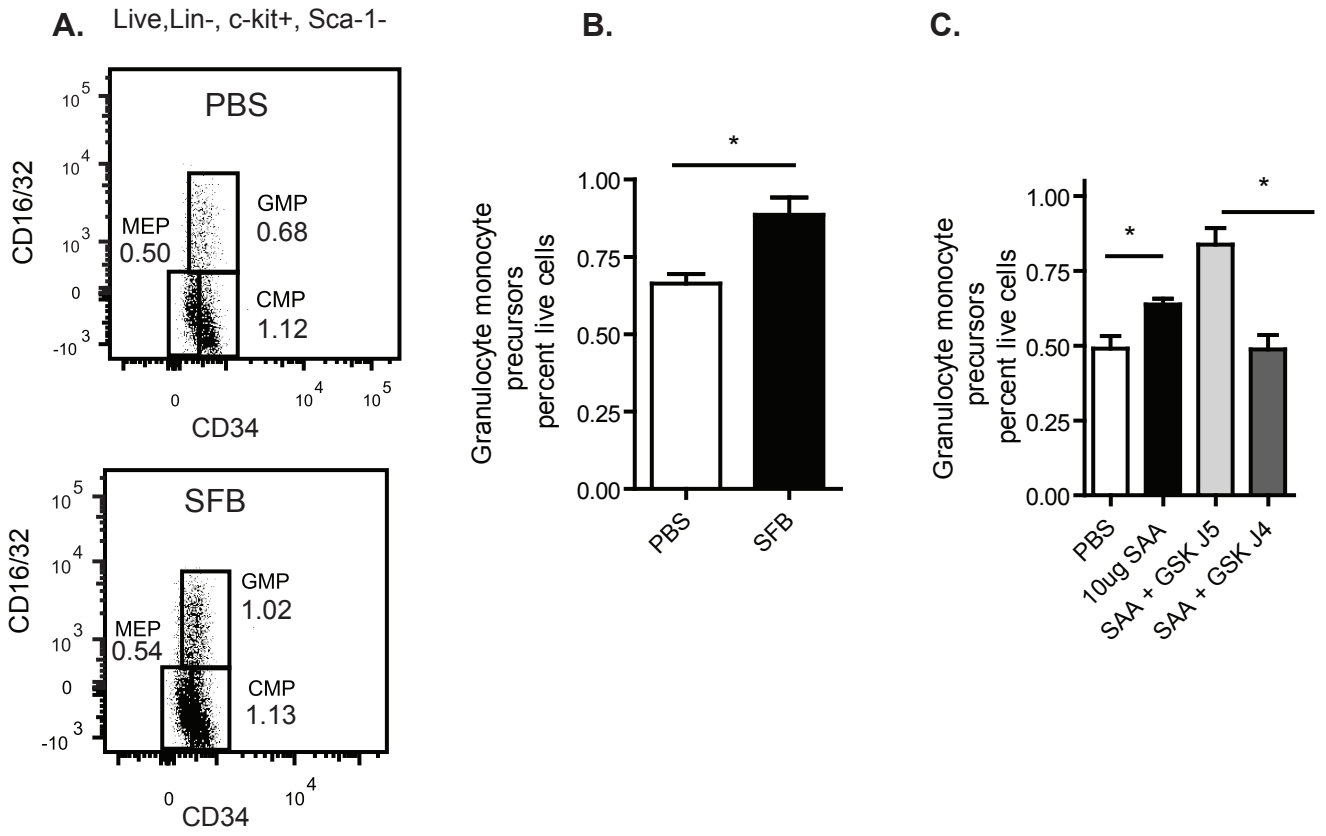

Figure S1. Granulocyte monocyte precursors were increased both by alteration of microbiota and by SAA treatment. Flow cytometry was utilized to assay expansion of GMPs in the bone marrow of mice colonized with SFB (A,B) or treated with SAA (Peprotech) with or without an inhibitor of Jmjd3 (H3K27 demethylase), GSK-J4, or its inactive control GSK-J5 (C). A representative flow cytometry plot of two mice is shown in A. All gates were set based on fluorescence minus one (FMO) controls. Values shown are percent of live cells. Bone marrow cells were stained with PerCP-Cy5.5-labeled lineage (Lin) markers (CD4,CD8,NK1.1,B220, CD11b,CD11c),anti-MHCII-Brilliant Violet 510, anti CD34 Brilliant Violet 421, c-Kit Brilliant Violet 605, CD127 PE-Cy7, CD16/CD32-APC-Cy7, and Sca-1 APC. Flow cytometric analysis was performed on an LSR Fortessa (BD Biosciences) and data analyzed via FlowJo (Tree Star Inc.).Common myeloid progenitors (CMP) are Lin-,c-Kit+,Sca-1-,CD34+ CD16/CD32-;Granulocyte monocyte progenitors (GMP) are Lin-,c-Kit+,Sca-1-,CD34+, CD16/CD32+; megakaryocyte–erythroid progenitors (MEP) are Lin-,c-Kit+Sca-1-CD34-, CD16/CD32 -. Mean +/- SEM of a representative experiments is shown; *P<0.05.