

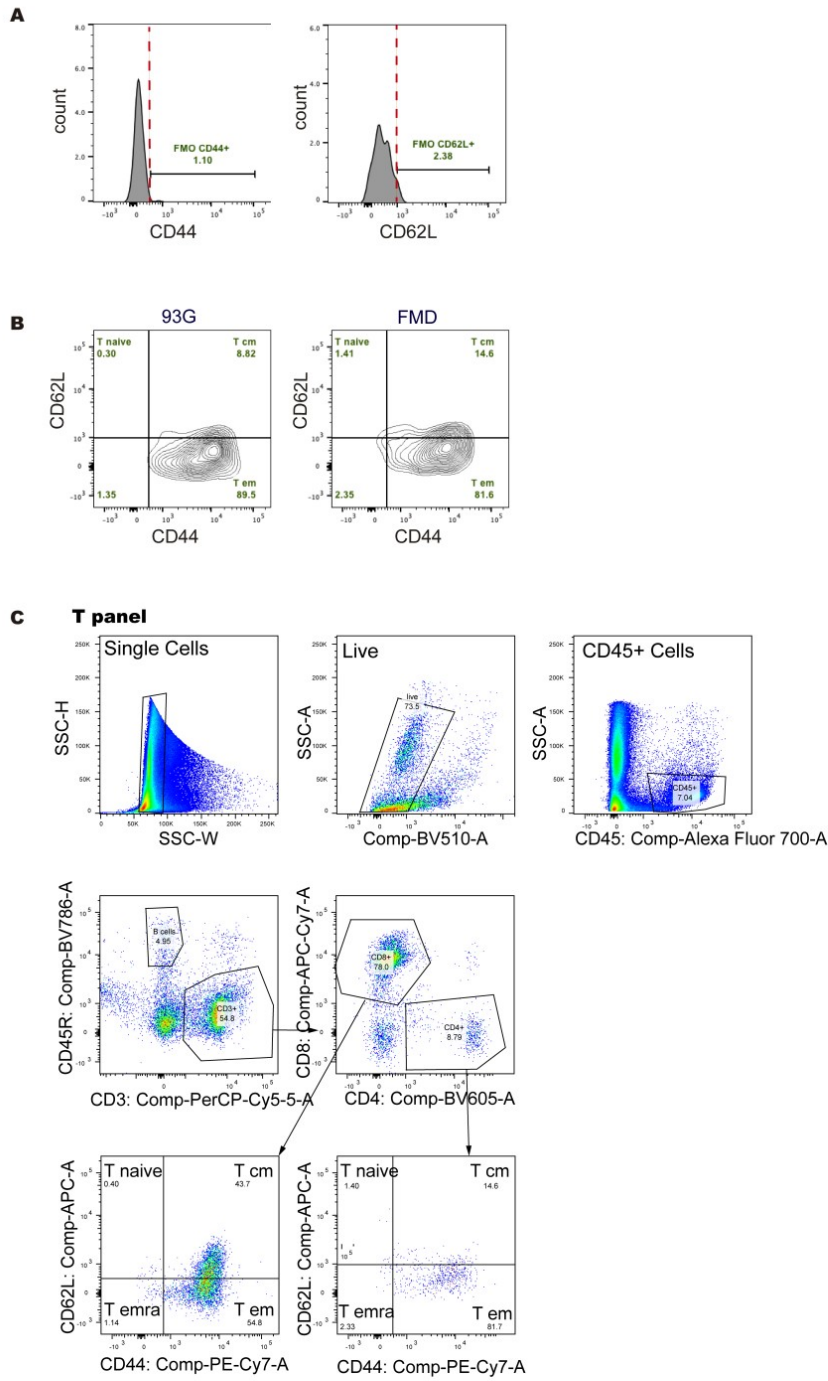
Supplement Information

Supplement table 1. List of primers used in the manuscript.

Primer	Forward 5'→3'	Reverse 5'→3'
<i>P53</i>	CTGGTTAGTCCTGAGACAGAGG	AGATGCAGCCAAACACAGGCAC
<i>H2ax</i>	CCCTTTTAAGGGCCACCACC	GTCGTCCACAACCGAGAACG
<i>Muc2</i>	ATGCCCACCTCCTCAAAGAC	GTAGTTTCCGTTGGAACAGTGAA
<i>Occludin</i>	TCCACGTAGAGACCAGTACCT	TACTGGTCTCTACGTGGATCAAT
<i>Zo1</i>	GCCGCTAAGAGCACAGCAA	TCCCCACTCTGAAAATGAGGA
<i>Claudin1</i>	AGCACCGGGCAGATACAGT	GCCAATTACCATCAAGGCTCG
<i>Ifng</i>	ATGAACGCTACACACTGCATC	CCATCCTTTTGCCAGTTCCTC
<i>Tnfa</i>	CTGAACTTCGGGGTGATCGG	GGCTTGTCACCTCGAATTTTGAGA
<i>Il6</i>	TAGTCCTTCCTACCCCAATTTCC	TTGGTCCTTAGCCACTCCTTC
<i>Cxcl15</i>	GGTGATATTCGAGACCATTACTG	GCCAACAGTAGCCTTCACCCAT
<i>Mmp3</i>	CTCTGGAACCTGAGACATCACC	AGGAGTCCTGAGAGATTTGCGC
<i>Il1β</i>	TGGACCTTCCAGGATGAGGACA	GTTTCATCTCGGAGCCTGTAGTG
<i>L.johnsonii</i>	TCGAGCGAGCTTGCCTAGATGA	TCCGGACAACGCTTGCCACC
<i>Universal Eubacteria 16S</i>	CGGCAACGAGCGCAACCC	CCATTGTAGCACGTGTGTAGCC

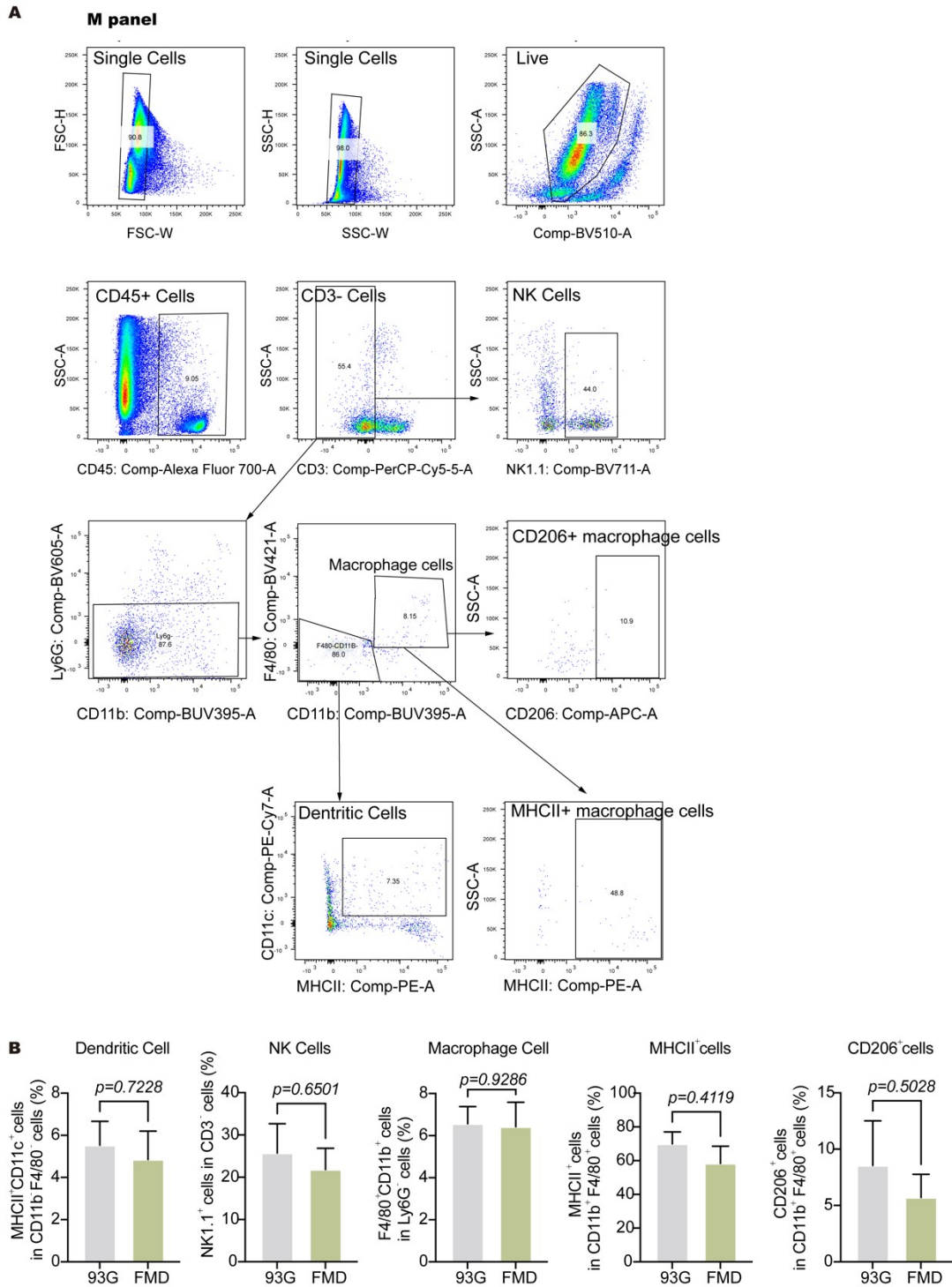
Supplement Figures

Figure S1



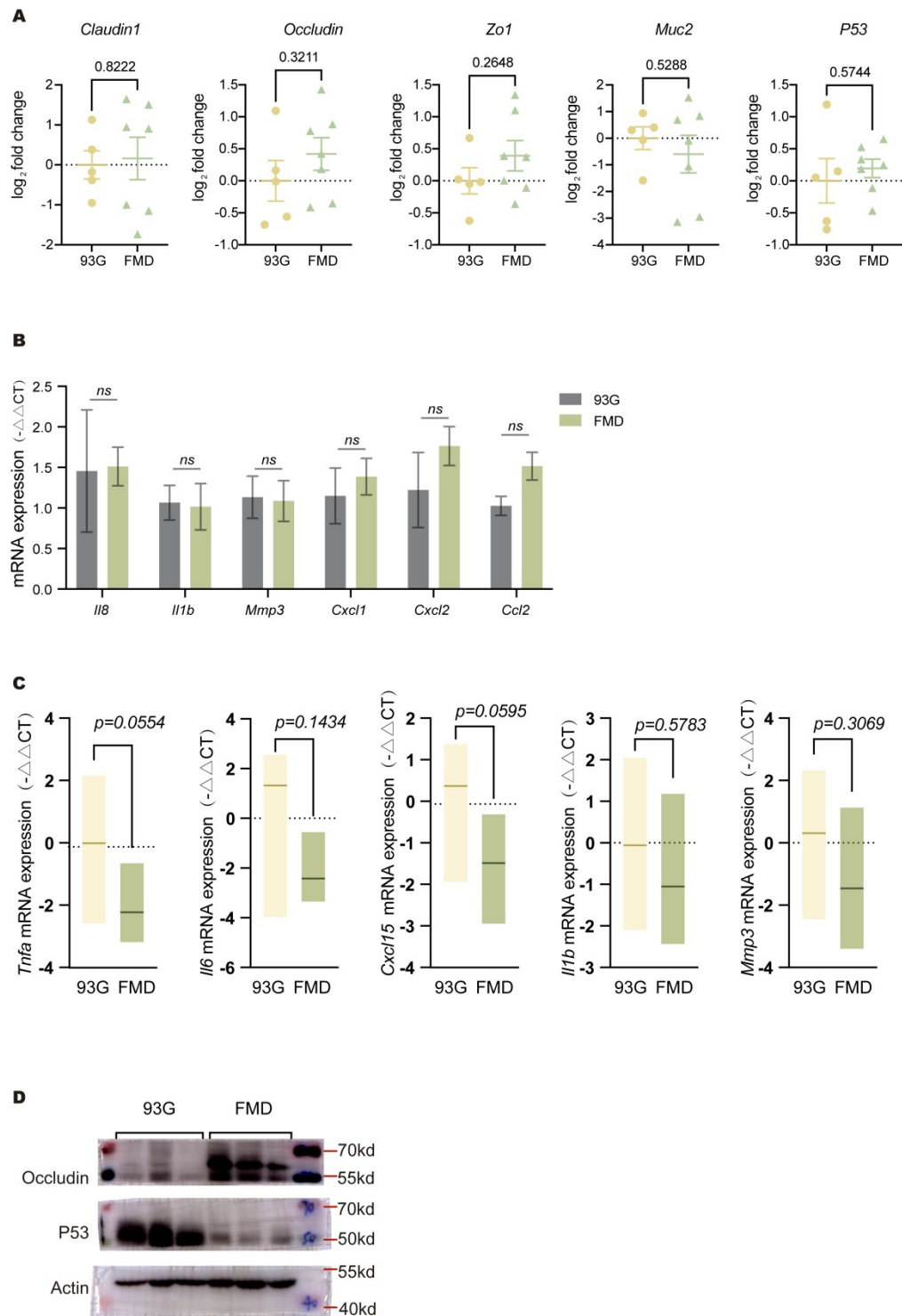
FigS1 A. Flow cytometry images of Fluorescence minus one (FMO) control; B. Representative flow cytometry images of gating T naive, Tcm, and Tem; C. Flow cytometry gating strategies of T panel

Figure S2



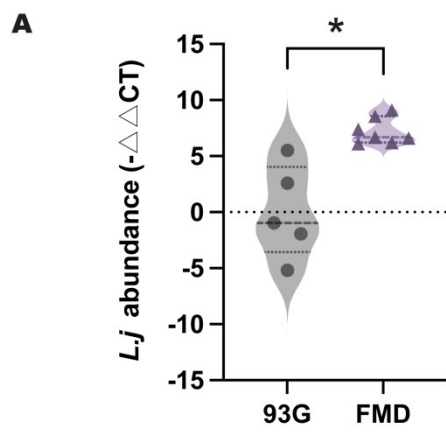
FigS2 A.Flow cytometry gating strategies of M panel B.Flow cytometry data showing frequencies of dendritic cells, NK cells, Macrophage cells, MHCII+ macrophage cells and CD206+ macrophage cells.

Figure S3



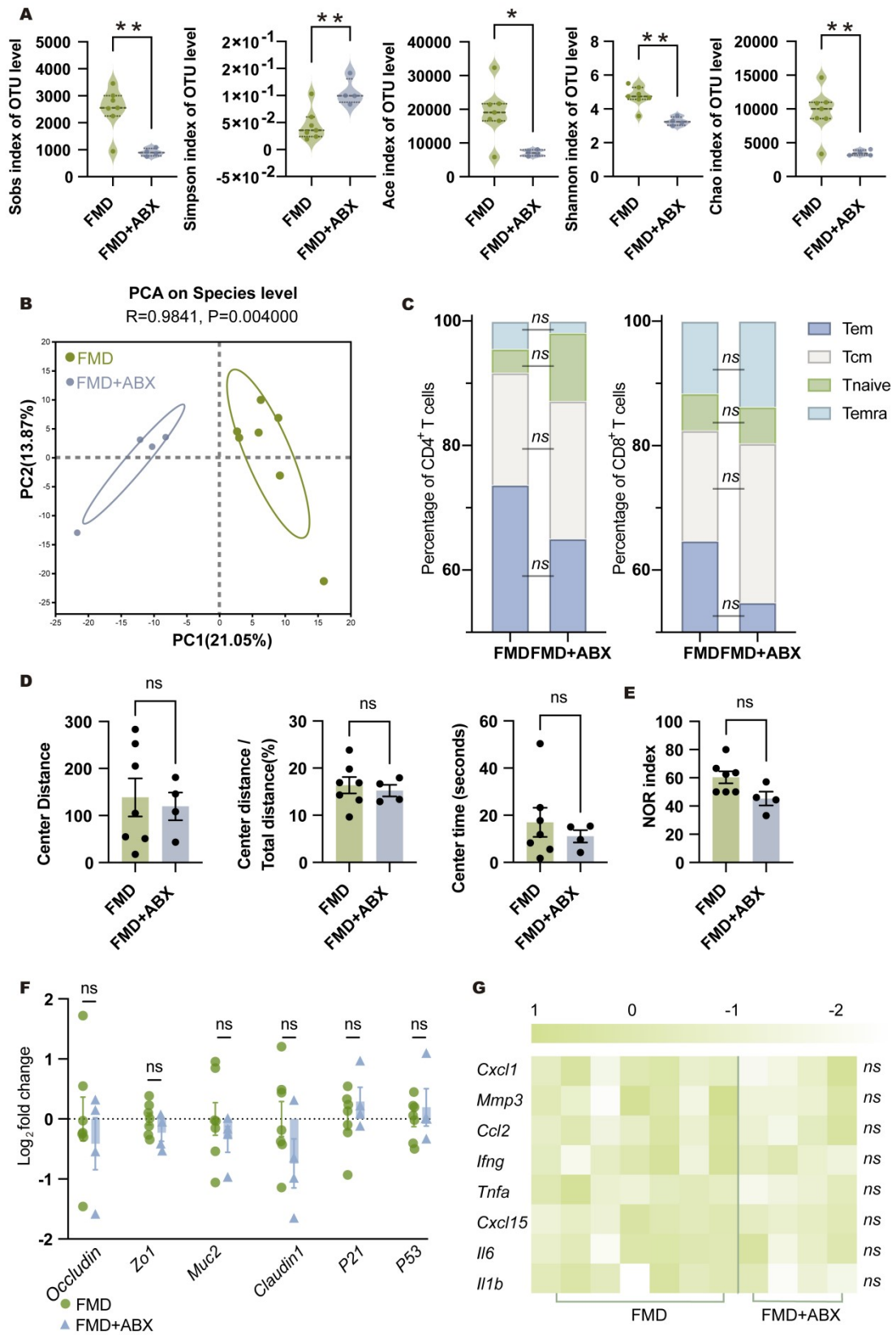
FigS3 A. Relative mRNA expression levels of genes associated with barrier and senescence in colon tissue; B. Relative mRNA expression levels of SASP genes in colon tissue. C. Relative mRNA expression levels of genes associated with barrier and senescence in the intestines. D. original graphs of western blots with a clear marker.

Figure S4



FigS4 A. Stool *Lactobacillus johnsonii* abundance verified by qPCR.

Figure S5



FigS5 A. α diversity of the gut microbiome; Sobs, Simpson, Ace, Shannon, Chao indices; B. β diversity of the gut microbiome, visualized by the principal coordinate analysis (PCA) plot; C. Flow cytometry data

showing effector memory, central memory, and naïve memory subsets from both CD4+T cells and CD8+T cells; D. In the open field test, the movement distance in the center area, its percentage in the total distance and time in the center; E. In the novel object recognition test, the NOR index; F. Comparison of relative mRNA levels for senescence-related genes and intestinal barrier-related genes; G. Heat map of relative mRNA expression levels of pro-inflammatory genes in the intestine tissues