# SUPPLEMENTARY DATA

## REFERENCES

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**Supplementary Figure S1: A bar chart of the relative abundance of bacterial genera in the individual mice of different treatment groups.**
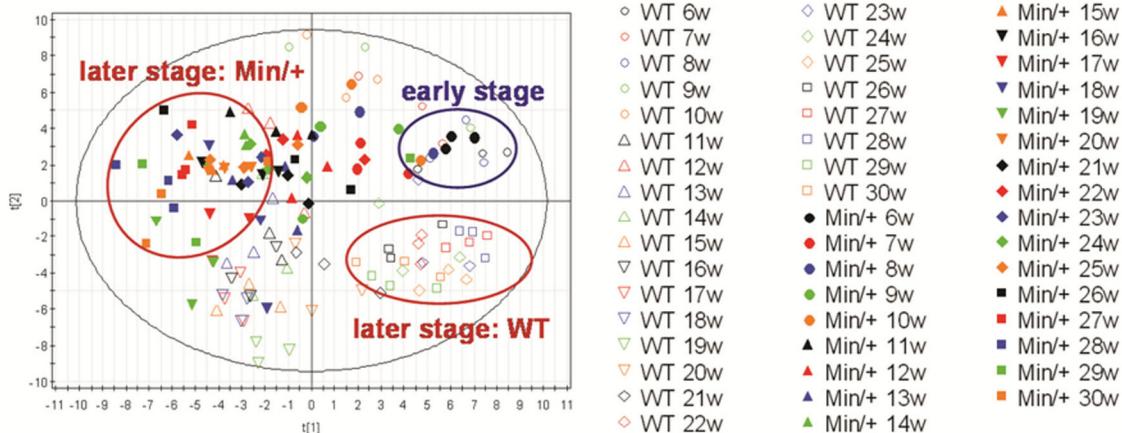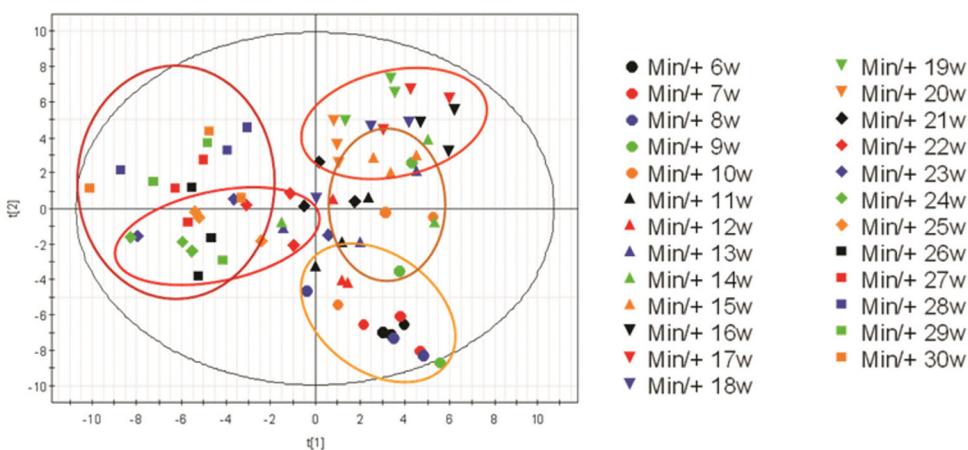
**Supplementary Figure S2: The time course PLS-DA plots of ERIC-PCR DNA profile. A.** $Apc^{Min/+}$ mice versus WT. Open symbols: WT; Solid symbols: $Apc^{Min/+}$ mice. **B.** $Apc^{Min/+}$ mice at different disease stages. Different symbol shapes represented for different disease stages. The microbial profiles of $Apc^{Min/+}$ mice and their WT littermates were characterized from 6 weeks to 30 weeks of age for 25 consecutive weeks. The fecal samples were prepared for genomic DNA and subjected for ERIC-PCR. Gel pictures were digitized by Image Lab 3.0 system (Bio-Rad). Based on the distance and the intensity of each DNA band, SIMCA-P 12.0 tool was applied to obtain the PLS-DA score plots. WT: n=3; $Apc^{Min/+}$ mice: n=3.
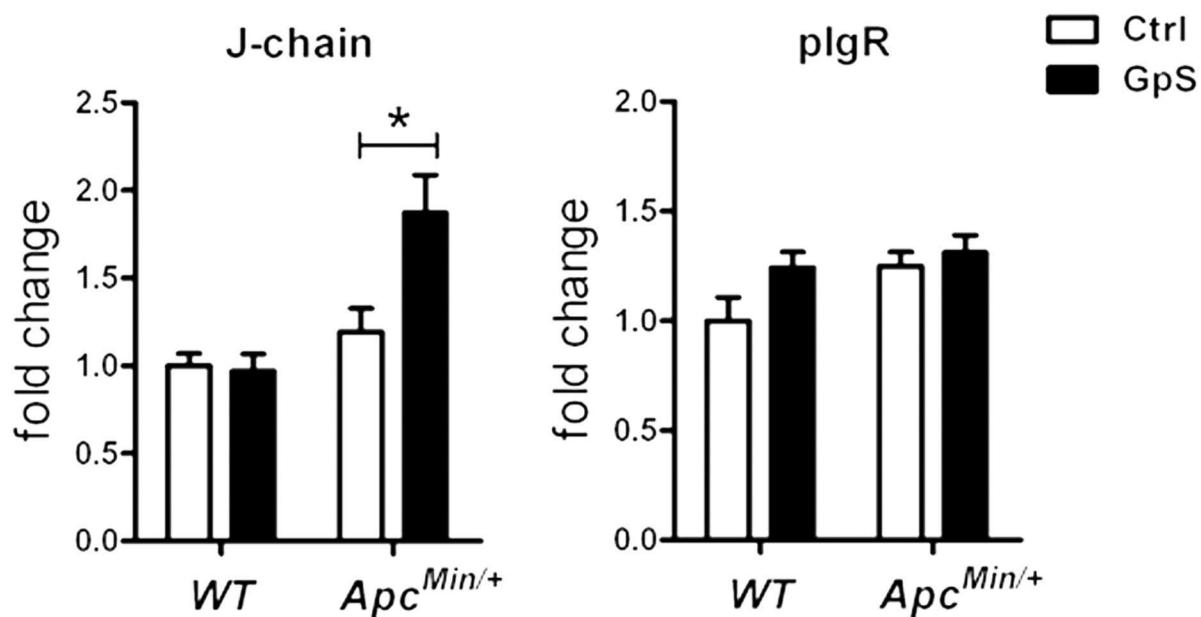
**Supplementary Figure S3: The relative mRNA expression of J-chain and pIgR.** J-chain is known to be critical for polymeric immunoglobulin receptor (pIgR)-mediated epithelial transport of IgA. Data were normalized to the expression of reference gene, and expressed as fold change of the WT control group. Data is presented as the mean ± SEM (* $P < 0.05$, GpS versus control samples); n=6/ group.

**Supplementary Table S1: Primers for Quantitative Real-Time PCR**

| Target gene | Nucleotide sequence of primers (5' to 3') | | References |
|---|---|---|---|
| | **Forward** | **Reverse** | |
| *β-actin* | TGTTACCAACTGGGACGACA | CTGGGTCATCTTTTCACGGT | [1] |
| *Hprt1* | TCAGTCAACGGGGGACATAAA | GGGGCTGTACTGCTTAACCAG | [2] |
| *dsrA* | CTGCGAATATGCCTGCTACA | TGGTCGARCTTGATGTCGTC | [3] |
| *PanCrp* | GGTGATCATCAGACCCCAGCATCAGT | AAGAGACTAAAACTGAGGAGCAGC | [4] |
| *Lyz 1 (P-lysozyme)* | GCCAAGGTCTACAATCGTTGTGAGTTG | CAGTCAGCCAGCTTGACACCACG | [5] |
| *Lyz 2 (M-lysozyme)* | GGCTGGCTACTATGGAGTCAGCCTG | GCATTCACAGCTCTTGGGGTTTTG | [5] |
| *MUC2* | CCCAGAAGGGACTGTGTATG | TTGTGTTCGCTCTTGGTCAG | [6] |
| *MUC4* | GTCTCCCATCACGGTTCAGT | TGTCATTCCACACTCCCAGA | [6] |
| *J-chain* | GAACTTTGTATACCATTTGTCAGACG | CTGGGTGGCAGTAACAACCT | [6] |
| *pIgR* | AGTAACCGAGGCCTGTCCTT | GTCACTCGGCAACTCAGGA | [6] |
| *iNOS* | GTTCTCAGCCCAACAATACAAGA | GTGGACGGGTCGATGTCAC | [7] |
| *CXCL10* | CCAAGTGCTGCCGTCATTTTC | GGCTCGCAGGGATGATTTCAA | [7] |
| *Arginase 1* | TGGCTTGCGAGACGTAGAC | GCTCAGGTGAATCGGCCTTTT | [7] |
| *Ym1* | TTATCCTGAGTGACCCTTCTAAG | TCATTACCCTGATAGGCATAGG | [7] |
| *Trem2* | CTGGAACCGTCACCATCACTC | CGAAACTCGATGACTCCTCGG | [7] |
| *MR* | GCTGAATCCCAGAAATTCCGC | ATCACAGGCATACAGGGTGAC | [7] |
| *IFN-γ* | ATGAACGCTACACACTGCATC | CCATCCTTTTGCCAGTTCCTC | [7] |
| *TNF-α* | CAAATGGCCTCCCTCTCAT | CTCCTCCACTTGGTGGTTTG | [8] |
| *IL-12* | ACTCTGCGCCAGAAACCTC | CACCCTGTTGATGGTCACGAC | [7] |
| *IL-4* | GGTCTCAACCCCCAGCTAGT | GCCGATGATCTCTCTCAAGTGAT | [7] |
| *IL-10* | GCTCTTACTGACTGGCATGAG | CGCAGCTCTAGGAGCATGTG | [7] |
| *IL-13* | GGATATTGCATGGCCTCTGTAAC | AACAGTTGCTTTGTGTAGCTGA | [7] |
| *IL-1β* | GCTGAAAGCTCTCCACCTCA | GGCCACAGGTATTTTGTCGT | [8] |
| *IL-6* | CTTCCATCCAGTTGCCTTCTTG | AATTAAGCCTCCGACTTGTGAAG | [9] |
| *IL-18* | CCTGACATCTTCTGCAACCT | TTCCGTATTACTGCGGTTGT | [10] |
| *IL-23* | GCACCTGCTTGACTCTGACA | ATCCTCTGGCTGGAGGAGTT | [8] |
| *Foxp3* | CCCATCCCCAGGAGTCTTG | ACCATGACTAGGGGCACTGTA | [11] |
| *IL-17* | TTTAACTCCCTTGGCGCAAAA | CTTTCCCTCCGCATTGACAC | [11] |