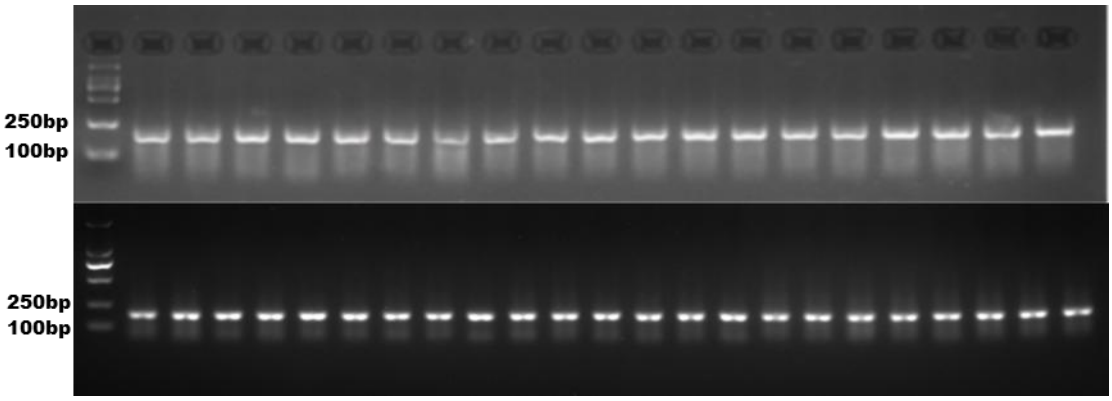



**Figure S1. Mouse tail identification of α7 nicotinic acetylcholine receptor (α7nAChR)-pure knockout mice.** Heterozygote = 187 bp and 390 bp, Wild type = 390 bp, Mutant = 187 bp.

**Table S1 Primers used for genotyping of α7 nicotinic acetylcholine receptor (α7nAChR)-pure knockout mice.**

| Primer name | Primer (5′-3′) |
|---|---|
| Common | TTC CTG GTC CTG CTG TGT TA |
| Wild type Reverse | ATC AGA TGT TGC TGG CAT GA |
| Mutant Reverse | CCC TTT ATA GAT TCG CCC TTG |

**Table S2 Disease activity index scoring.**

| Score | Weight loss (%) | Stool consistency | Blood stool |
|---|---|---|---|
| 0 | No less | Normal | No blood |
| 1 | 1-5 | Fluffy and still formed | |
| 2 | 5-10 | Very soft | Blood visible in the stool |
| 3 | 10-20 | Loose and unmolded | |
| 4 | > 20 | Watery diarrhea | Gross bleeding |

**Table S3 Reaction mixture for RT-qPCR.**

| Component | Per reaction |
|---|---|
| ChamQ SYBR Color qPCR Master Mix | 5 μL |
| Forward primer (10 pmol/μL)* | 0.2 μL |
| Reverse primer (10 pmol/μL)* | 0.2 μL |
| Nuclease-free water | 3.6 μL |
| cDNA template (8 ng/μL) | 1 μL |

The asterisk (*) indicates that the primers used in this reaction correspond to the specific primer sequences listed in Table S5.

## Table S4 Temperature program used for RT-qPCR.

| Operation | Temperature (℃) | Duration | Cycles |
|---|---|---|---|
| Initial activation | 95 | 30 sec | 1 |
| Denaturation | 95 | 10 sec | 40 |
| Annealing | * | 30 sec | |
| Melting curve | 95 | 1 min | 1 |
| | 60 | 30 sec | |
| | 60-95 (+0.2/sec) | 1 min | |

The asterisk (*) indicates that the annealing temperature corresponds to the Tm value listed for each primer pair in Table S5.

## Table S5 Primers sequence and annealing temperatures for RT-qPCR.

| Gene | Forward Primer (5′-3′) | Reverse Primer (5′-3′) | Annealing temperature Tm (℃) |
|---|---|---|---|
| IL-6 | GAGGATACCACTCCCAACAGACC | AAGTGCATCATCGTTGTTCATACA | 61 |
| TNF-α | CTGTCTACTGAACTTCGGGGTGAT | GGTCTGGGCCATAGAACTGATG | 60 |
| IL-1β | GCTGAAAGCTCTCCACCTCA | AGGCCACAGGTATTTTGTCG | 59 |
| MCP-1 | CGGAACCAAATGAGATCAGAA | TGTGGAAAAGGTAGTGGATGC | 61 |
| iNOS | GACATTACGACCCCTCCCAC | ACTCTGAGGGCTGACACAAG | 60 |
| Occludin | GAGCTTACAGGCAGAACTAGAC | CAGCCATGTACTCTTCACTCTC | 62 |
| ZO-1 | CATCTCCAGTCCCTTACCTTTC | CCTCCAGGCTGACATTAGTTAC | 60 |
| GAPDH | TGTAGACCATGTAGTTGAGGTCA | AGGTCGGTGTGAACGGATTTG | 60 |

**Abbreviations:** IL-6, interleukin-6; TNF-α, tumor necrosis factor-alpha; IL-1β, interleukin-1β; MCP-1, monocyte chemoattractant protein-1; iNOS, inducible nitric oxide synthase; ZO-1, zonula occludens-1; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

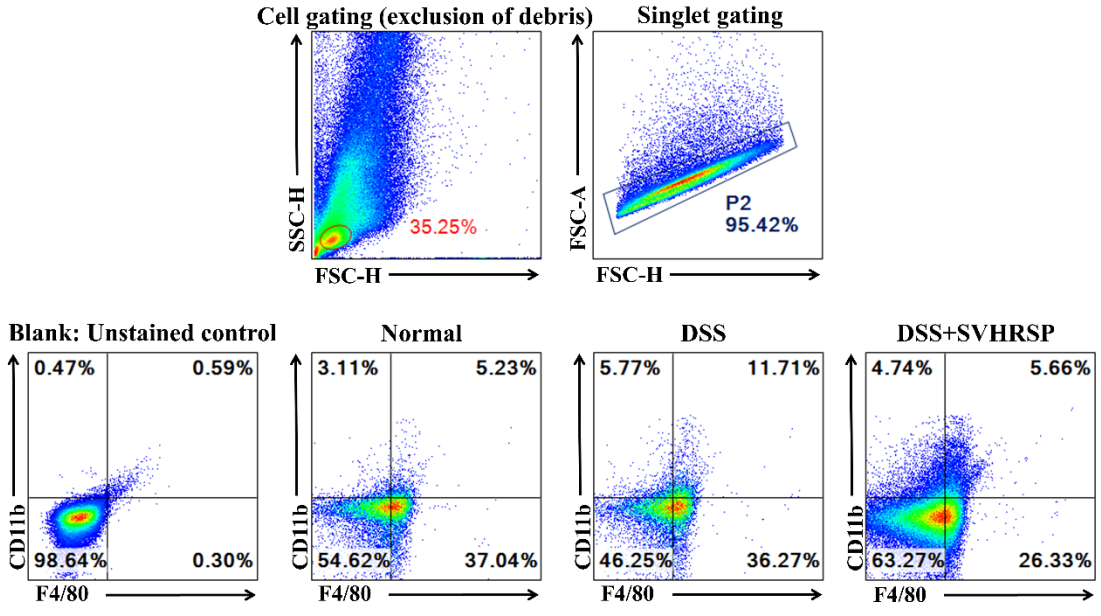


**Figure S2. Gating strategy and unstained control for macrophage analysis (corresponding to Main Figure 3C).** Cells were first gated on FSC-H vs SSC-H to exclude debris, followed by FSC-H vs FSC-A to select singlets. Representative dot plots show unstained control (Blank) and experimental groups (Normal, DSS, DSS+SVHRSP). Percentages indicate the proportion of F4/80$^{+}$CD11b$^{+}$ macrophages. **Abbreviations:** DSS, dextran sodium sulfate; SVHRSP, synthetic peptide-scorpion venom heat-resistant synthetic peptide; FSC-H, forward scatter-height; FSC-A, forward scatter-area; SSC-H, side scatter-height.

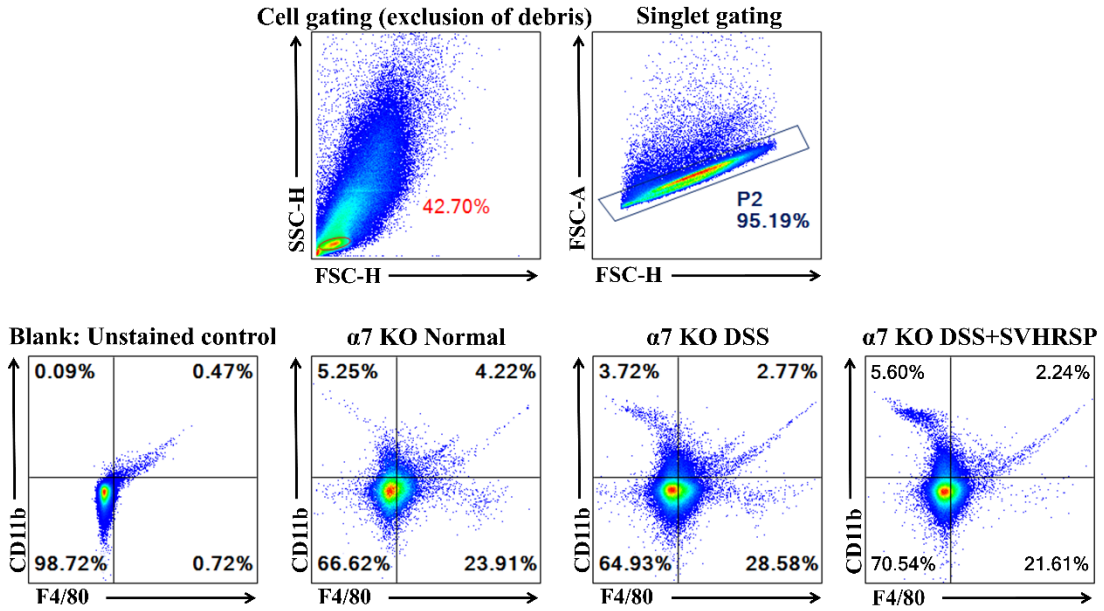



**Figure S3. Gating strategy and unstained control for macrophage analysis (corresponding to Main Figure 6H).** Cells were first gated on FSC-H vs SSC-H to exclude debris, followed by FSC-H vs FSC-A to select singlets. Representative dot plots show unstained control (Blank) and experimental groups (α7 KO Normal, α7 KO DSS, α7 KO DSS+SVHRSP). Percentages indicate the proportion of F4/80$^{+}$CD11b$^{+}$ macrophages. **Abbreviations:** α7 KO, α7 nicotinic acetylcholine receptor-pure knockout; DSS, dextran sodium sulfate; SVHRSP, synthetic peptide-scorpion venom heat-resistant synthetic peptide; FSC-H, forward scatter-height; FSC-A, forward scatter-area; SSC-H, side scatter-height.

**Table S6 Complete blood count (CBC) analysis was performed after 14 days of subcutaneous administration of SVHRSP in male Sprague-Dawley rats ($n$ = 5).**

| Parameter | 0 mg/kg/day | 20 mg/kg/day | 60 mg/kg/day | 200 mg/kg/day |
|---|---|---|---|---|
| Red Blood Cell Count (×10$^{12}$/L) | 7.418 ± 0.17 | 7.310 ± 0.15 | 7.472 ± 0.11 | 7.520 ± 0.19 |
| Hematocrit (%) | 50.42 ± 0.99 | 48.86 ± 0.95 | 50.48 ± 0.68 | 51.08 ± 0.93 |
| Hemoglobin (g/dL) | 14.80 ± 0.28 | 14.20 ± 0.27 | 14.56 ± 0.19 | 14.62 ± 0.21 |
| Mean Corpuscular Volume | 68.02 ± 0.72 | 66.86 ± 0.74 | 67.58 ± 0.68 | 67.98 ± 0.72 |

| | | | | |
|---|---|---|---|---|
| (fL) | | | | |
| Mean Corpuscular Hemoglobin (pg) | 19.98 ± 0.19 | 19.48 ± 0.30 | 19.44 ± 0.22 | 19.44 ± 0.24 |
| Mean Corpuscular Hemoglobin Concentration (g/dL) | 29.34 ± 0.13 | 29.10 ± 0.34 | 28.80 ± 0.03 | 28.62 ± 0.13* |
| Reticulocyte Count (×10⁹/L) | 281.20 ± 23.61 | 248.04 ± 12.35 | 274.84 ± 10.83 | 285.84 ± 23.15 |
| White Blood Cell Count (×10⁹L) | 8.018 ± 0.56 | 7.906 ± 0.67 | 8.342 ± 0.69 | 8.106 ± 0.42 |
| Neutrophil Count (×10⁹/L) | 0.836 ± 0.14 | 0.808 ± 0.04 | 0.846 ± 0.12 | 1.004 ± 0.13 |
| Lymphocyte Count (×10⁹/L) | 6.680 ± 0.47 | 6.740 ± 0.63 | 7.024 ± 0.61 | 6.584 ± 0.49 |
| Monocyte Count (×10⁹/L) | 0.244 ± 0.03 | 0.152 ± 0.02 | 0.202 ± 0.04 | 0.252 ± 0.04 |
| Basophil Count (×10⁹/L) | 0.010 ± 0.00 | 0.004 ± 0.00 | 0.008 ± 0.00 | 0.008 ± 0.00 |
| Eosinophil Count (×10⁹/L) | 0.054 ± 0.01 | 0.070 ± 0.01 | 0.114 ± 0.02* | 0.104 ± 0.02 |
| Platelet Count (×10⁹/L) | 1091.2 ± 40.6 | 1182.6 ± 58.9 | 1150.6 ± 106.3 | 1161.4 ± 34.5 |
| Mean Platelet Volume (fL) | 12.04 ± 0.12 | 12.22 ± 0.21 | 12.14 ± 0.20 | 12.44 ± 0.21 |

Data were presented as mean ± standard error of the mean (SEM). *$p<0.05$ versus 0 mg/kg/day group.