Supplementary materials

Table S1. Primer sequences for qPCR.

Gene name	Forward primer sequences (5'-3')	Reverse primer sequences (5'-3')
IFN-γ	GGTCAACAACCCACAGGTCCA	GCGACTCCTTTTCCGCTTCCT
IL-4	CGGAGATGGGATGTGCCAAACG	TGGAAGCCCTACAGACGAGC
Hes-1	ATGTGGAGACCGTGGCGGAA	CGTCAGAAGAGAGAGGTGGGC
Gata-3	TATCCGCCCTATGTGCCCGA	AGGTTGCCCCGCAGTTCAC
T-bet	TCAACTGCTTGGGGGAGACC	GGGGTAGAAACGGCTGGGAAC
NF-κB	GGTGTGGAGACATCCTTCCGC	CCTTCCTGCCCATAACCGTGG
GAPDH	AGGAGCGAGACCCCACTAAC	CGGAGATGATGACCCTTTTGGCT

Table S2. R values of the Spearman Correlation between the top 20 bacteria with significantly differential abundances and SCFAs concentrations.

	Acetate	Propionate	Isobutyrate	Butyrate	Isovalerate	Pentanoate	Isohexylate	Hexanoate
g__Enterococcus	-0.6176	-0.7055	-0.5912	-0.5736	-0.6967	-0.5956	-0.1824	-0.6909
g__norank_f__Muribaculaceae	-0.4637	-0.2703	0.0813	-0.4813	0.1165	-0.3934	-0.0418	-0.3542
g__Lactobacillus	0.6352	0.4945	0.3451	0.6615	0.4769	0.5736	0.1956	0.6733
g__Escherichia-Shigella	-0.5667	-0.6800	-0.6712	-0.5867	-0.6912	-0.6756	0.2489	-0.7375
g__Bacteroides	-0.2088	-0.2835	0.0725	-0.4154	0.0198	-0.3451	0.2747	-0.4114
g__Candidatus_Saccharimonas	0.6336	0.5982	0.5673	0.7660	0.6954	0.7572	-0.0596	0.7713
g__norank_f__norank_o__Clostridia_ UCG-014	0.6336	0.6821	0.6071	0.7086	0.6601	0.7263	-0.2671	0.7204
g__Enterorhabdus	0.7187	0.6527	0.7275	0.7582	0.8286	0.7846	0.0549	0.8031
g__Alistipes	0.3319	0.3055	0.7099	0.3890	0.7407	0.5165	-0.1297	0.5413
g__Romboutsia	-0.7890	-0.6676	-0.5013	-0.5462	-0.4383	-0.6002	-0.0787	-0.4523
g__norank_f__norank_o__RF39	0.6512	0.6556	0.6027	0.7395	0.7351	0.8190	-0.1965	0.8022
g__Rikenellaceae_RC9_gut_group	-0.0155	0.0817	0.2406	-0.0993	0.3068	0.0949	-0.2009	-0.0751
g__Desulfovibrio	0.7768	0.6736	0.4905	0.7252	0.5093	0.8144	-0.1948	0.7260
g__unclassified_f__Lachnospiraceae	0.7613	0.8625	0.6645	0.6755	0.7437	0.7833	-0.0506	0.7885
g__Lachnospiraceae_NK4A136_group	0.8190	0.8057	0.7837	0.8278	0.8720	0.8896	0.1038	0.8950
g__Odoribacter	0.4884	0.5282	0.7647	0.5414	0.8221	0.6475	-0.2387	0.6261
g__Clostridium_sensu_stricto_1	-0.6823	-0.6223	-0.5800	-0.5178	-0.5000	-0.5623	0.0156	-0.4272
g__Alloprevotella	0.2133	0.2778	0.4134	-0.0178	0.3289	0.0356	0.2778	-0.0845
g__Parabacteroides	-0.2356	-0.1467	-0.0667	-0.5423	-0.0689	-0.4378	0.1045	-0.5028
g__Paraprevotella	-0.1760	0.1432	0.1479	-0.2511	0.1009	-0.0962	-0.1103	-0.1504

Table S3. R values of the Spearman Correlation between the top 10 bacteria with significantly differential abundances and allergic indices in different groups (*n* = 5).

	sIgE	sIgG1	His	mMCP1
g__Enterococcus	0.6396	0.5780	0.3275	0.5516
g__norank_f__Muribaculaceae	0.1736	0.5297	0.1516	-0.2571
g__Lactobacillus	-0.6571	-0.8418	-0.3714	-0.3538
g__Escherichia-Shigella	0.7245	0.3822	0.4711	0.7089
g__Bacteroides	0.1385	0.3538	0.0681	-0.2615
g__Candidatus_Saccharimonas	-0.7395	-0.7660	-0.5453	-0.5099
g__norank_f__norank_o__Clostridia_UCG-014	-0.7572	-0.7174	-0.4305	-0.5320
g__Enterorhabdus	-0.8110	-0.6879	-0.6747	-0.6352

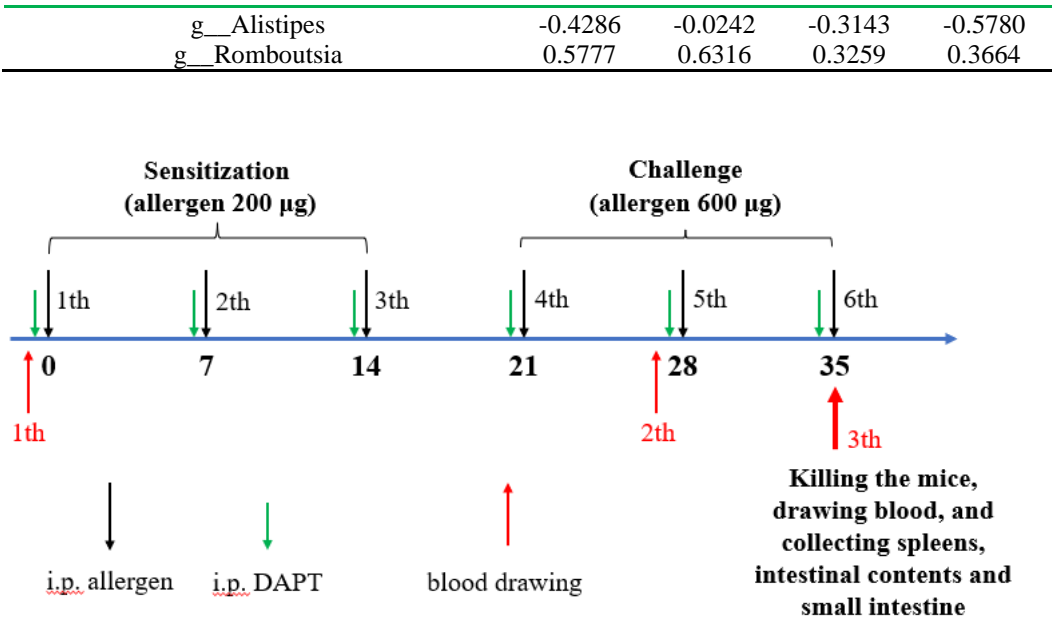|				
g__Alistipes	-0.4286	-0.0242	-0.3143	-0.5780
g__Romboutsia	0.5777	0.6316	0.3259	0.3664

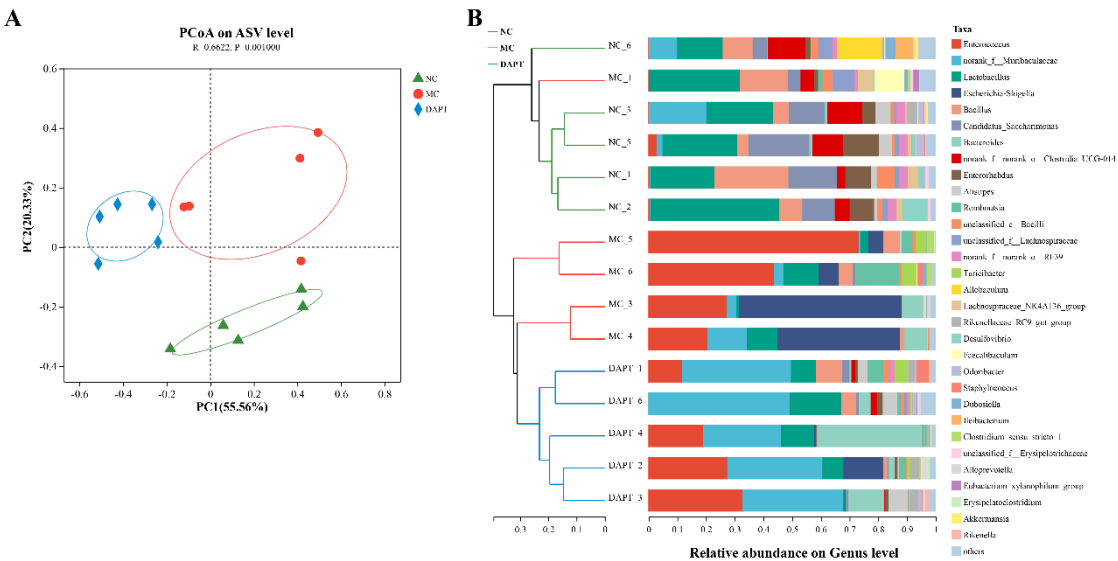**Figure S1.** Protocol for the AkTM-sensitized and DAPT-treated mice model.

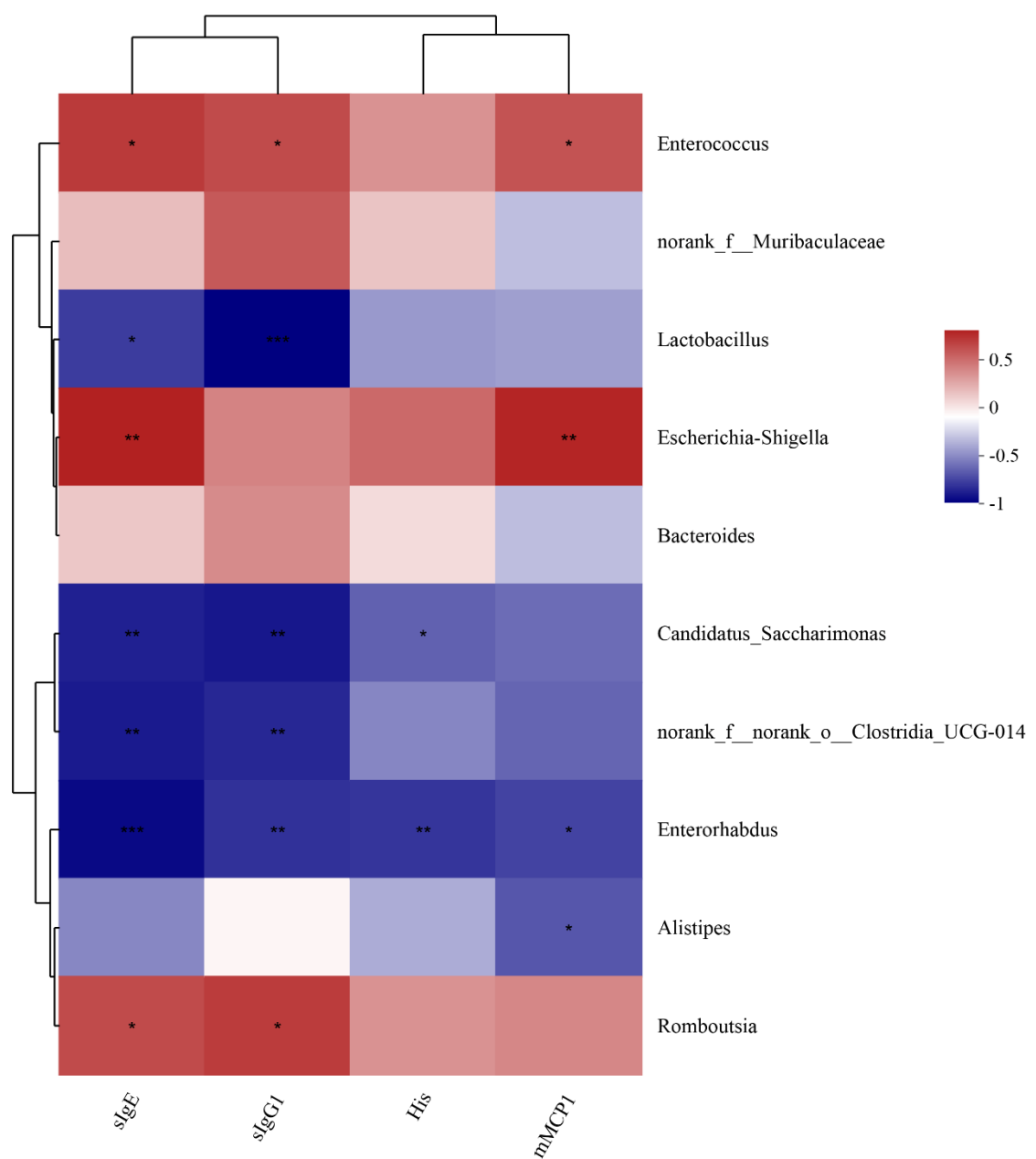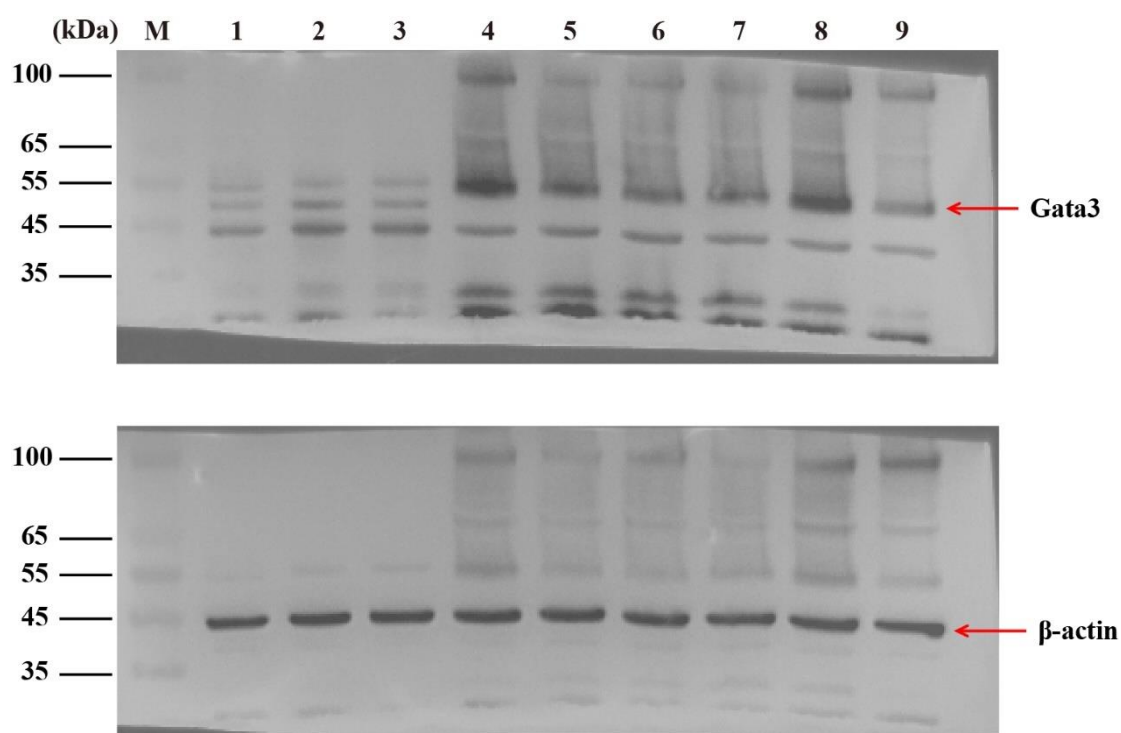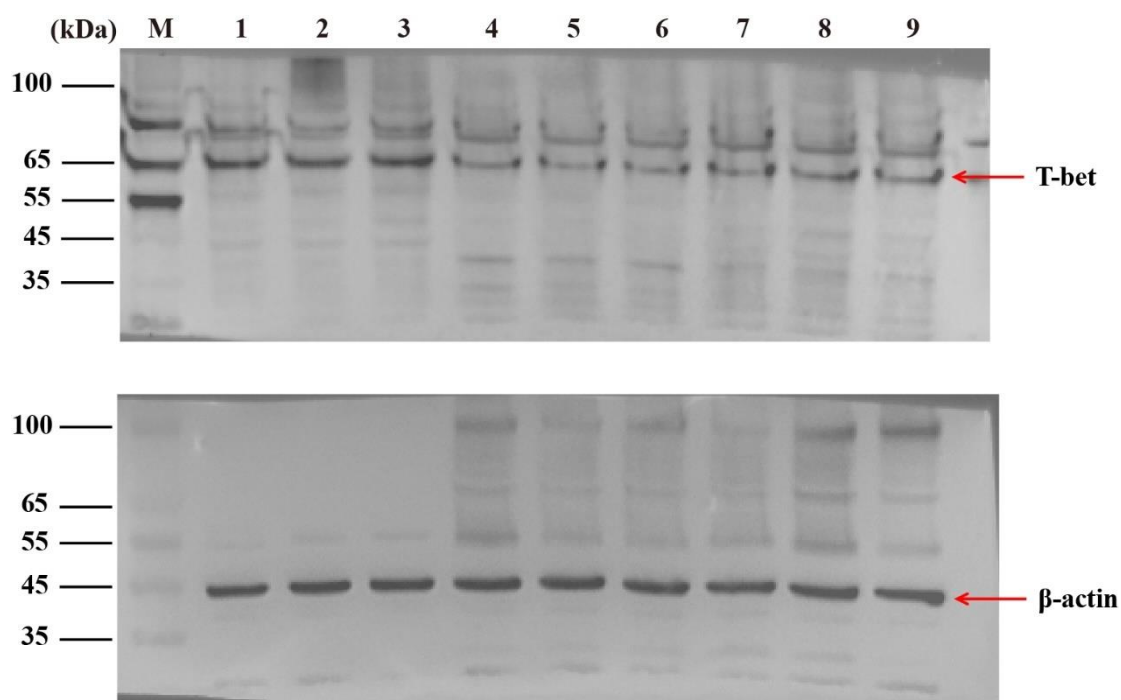**Figure S2.** The β-diversity analysis of gut microbiota in mice (n = 5 for each group). (A) PCoA analysis based on weighted unifrac distances; (B) Hierarchical clustering tree on genus level based on Bray-curtis distance.
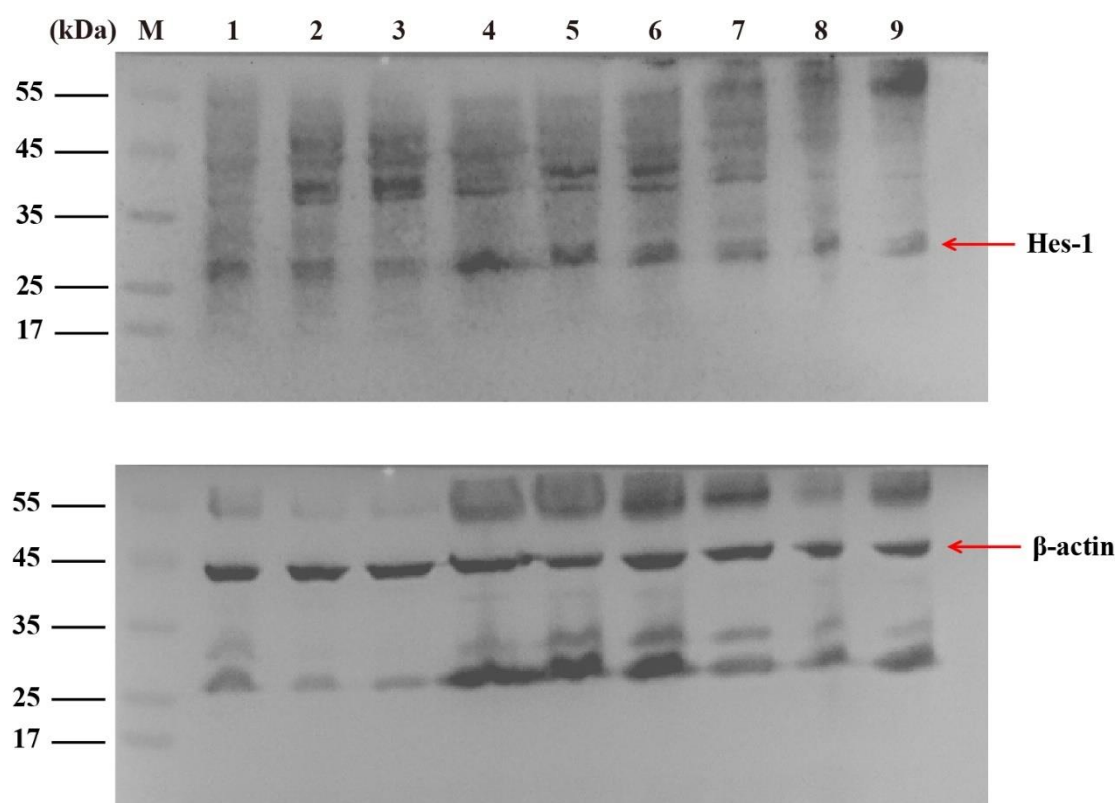
Figure S3. Heatmap of spearman correlation between the top 10 bacteria with significantly differential abundances and allergic indices in different groups (*n* = 5). * *p* < 0.05, ** *p* < 0.01, and *** *p* < 0.001.
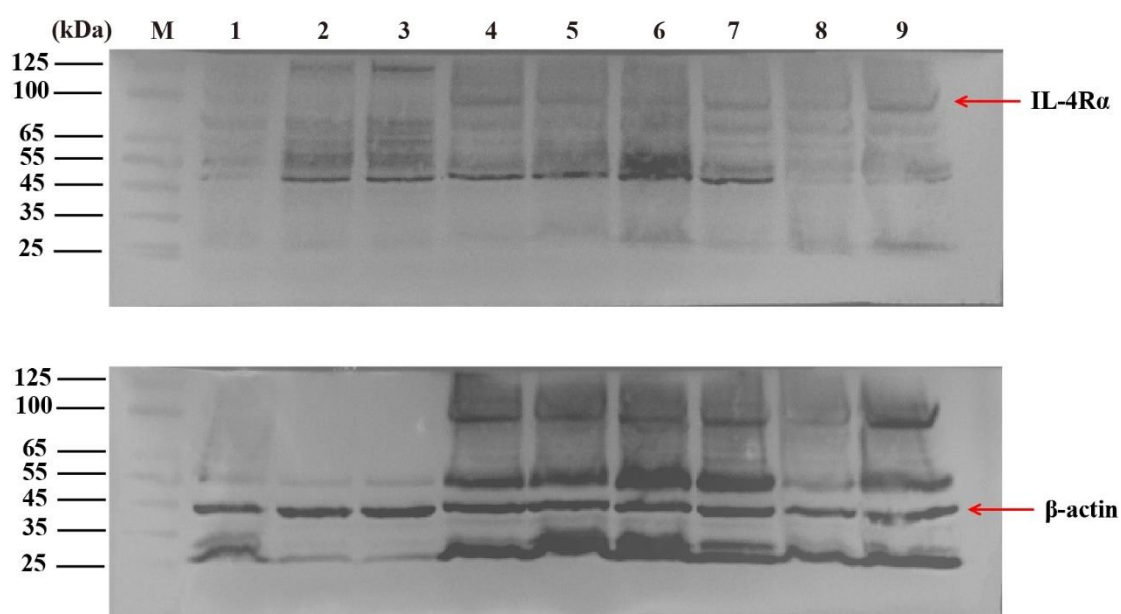
Figure S4. Western blotting raw images of Gata3 and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. Gata3 bands of lanes 3, 4, 7, and β-actin bands of lanes 3, 4, 7, were used in Figure 2C in the manuscript.
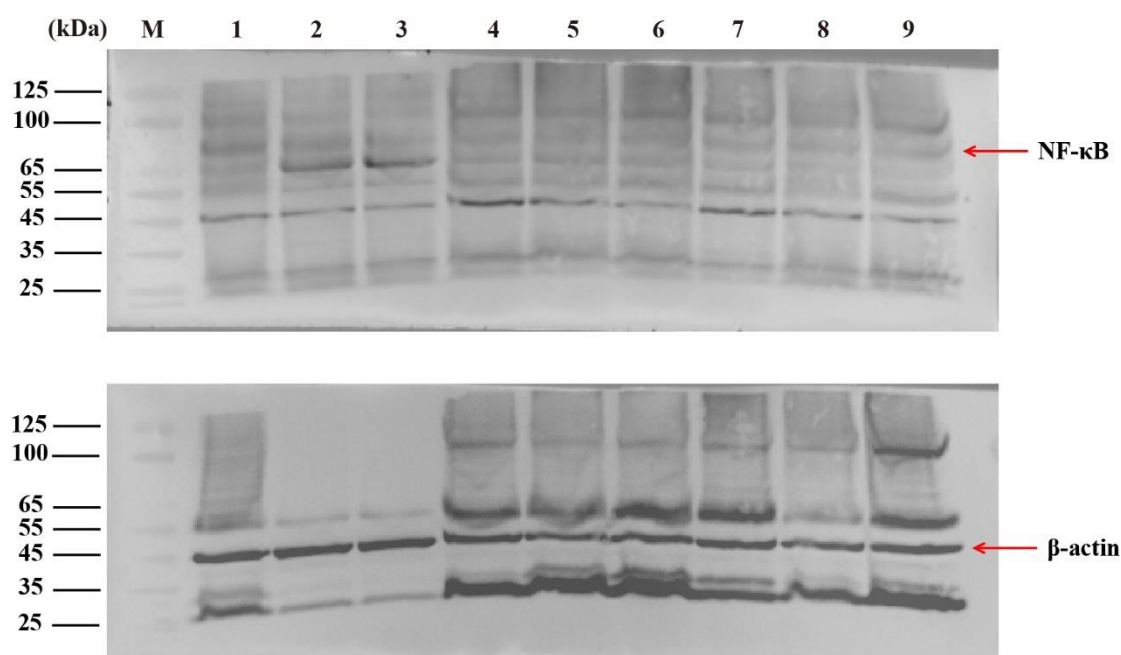

Figure S5. Western blotting raw images of T-bet and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. T-bet bands of lanes 3, 4, and 8 were used in Figure 2C in the manuscript.
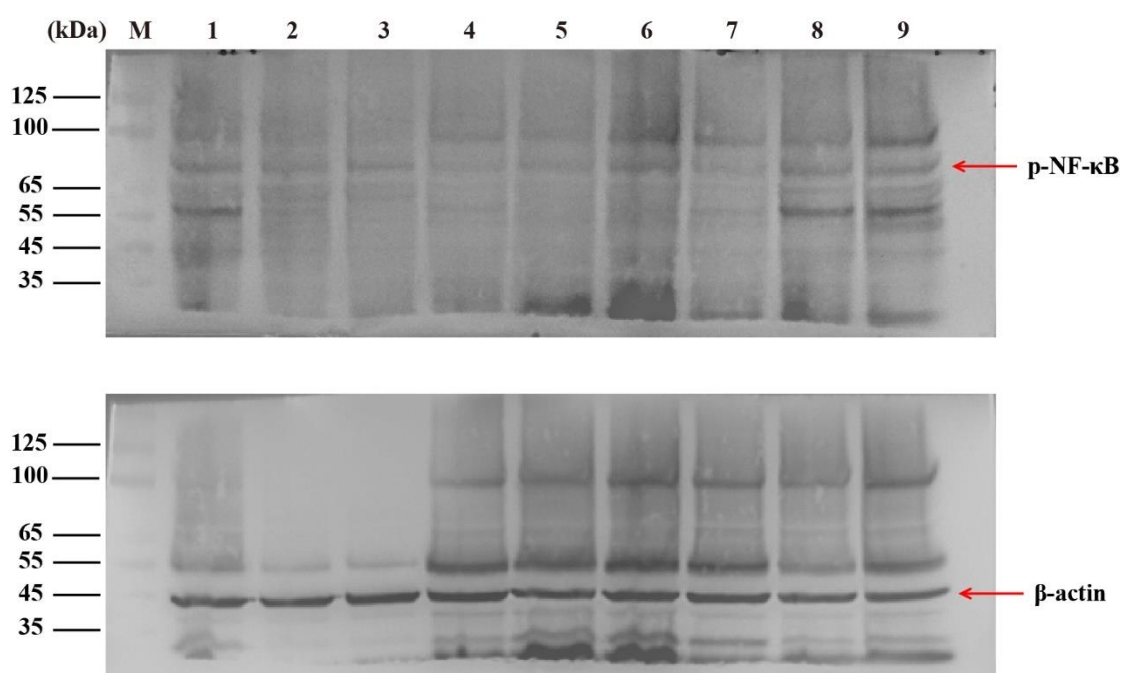
Figure S6. Western blotting raw images of Hes-1 and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. Hes-1 bands of lanes 3, 4, and 7 were used in Figure 2C in the manuscript.

Figure S7. Western blotting raw images of IL-4Rα and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. IL-4Rα bands of lanes 3, 4, and 7 were used in Figure 2C in the manuscript.

Figure S8. Western blotting raw images of NF-κB and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. NF-κB bands of lanes 3, 4, and 7 were used in Figure 2C in the manuscript.

Figure S9. Western blotting raw images of p-NF-κB and β-actin. Three biological samples per group of mice. M, protein markers; 1, 2, and 3, NC group; 4, 5, and 6, MC group; 7, 8, and 9, DAPT group. p-NF-κB bands of lanes 3, 6, and 7 were used in Figure 2C in the manuscript.