

Supplementary Material

1 Supplementary Data

Figure S1 Pam3CSK4 alone or combination with anti-IgE downregulated the expression of FcεRIα in mo-IDECs *in vitro* by flow cytometry. **(A)** Specific gating strategies to identify FcεRIα expression on the surface of live mo-IDEC (CD14⁺CD1a⁺) cells after stimulation with different stimulus for 24 h as measured by flow cytometry (n = 5-6). **(B)** Expression of FcεRIα in mo-IDECs. Data were presented as mean ± SEM. Statistical significance were analyzed by the one-way ANOVA. ^{ns} $p > 0.05$, * $p < 0.05$ and ** $p < 0.01$.

Figure S2 Overview of transcriptome profiling of mo-IDECs in response to Pam3CSK4 combination with anti-IgE *in vitro* by RNA-seq. **(A and B)** Volcano plots of DEGs in mo-IDECs, comparing the Pam3CSK4 combination with anti-IgE treatment and Pam3CSK4 and anti-IgE alone groups, respectively. Horizontal lines in volcano plots were cutoff for $-\log_{10} 0.05$. **(C)** Number of DEGs up- or down-regulated at each treatment group. **(D and F)** Dots diagram of the top 30 KEGG enrichment pathways of upregulated DEGs. **(E and G)** Dots diagram of the top 30 KEGG enrichment pathways of downregulated DEGs. The size of the dots represented the number of the pathway related genes (count). The p -values of each KEGG term were shown by color. The gene ratio described the ratio of the count to the number of all DEGs.

Figure S3 Overview of metabolite profiling of mo-IDECs in response to Pam3CSK4 combination with anti-IgE *in vitro* by LC-MS/MS. **(A)** Number of up- or down-regulated metabolites at each treatment group. **(B and C)** Heat maps represented the differential metabolites among different treatment groups (n = 5). **(D and E)** KEGG pathway enrichment of dysregulated metabolites. BPG, 2,3-diphosphoglycerate. NADPH, nicotinamide adenine dinucleotide phosphate. UMP, uridine 5'-monophosphate.

Figure S4 KEGG pathway enrichment of dysregulated metabolites in mo-IDECs after different stimulation treatments *in vitro* by LC-MS/MS. **(A-E)** KEGG classification according to the pathway types of dysregulated metabolites.

2 Supplementary Figures

Figure S1

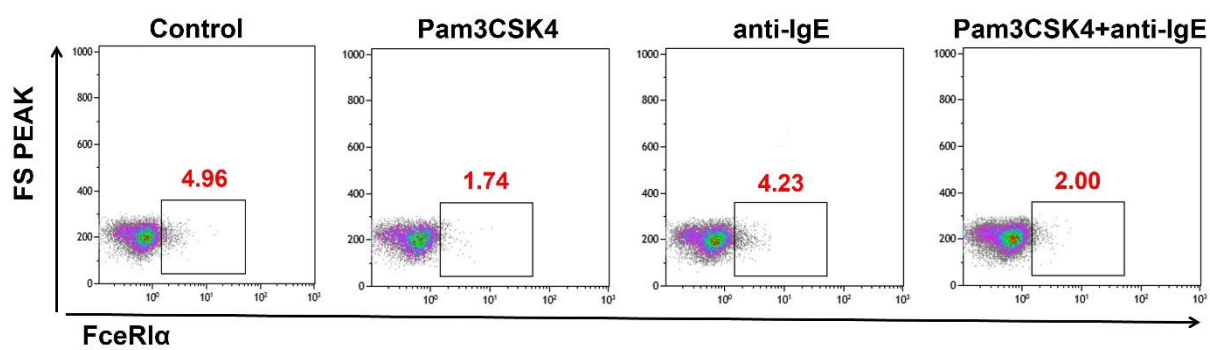
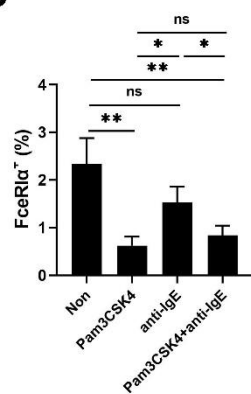
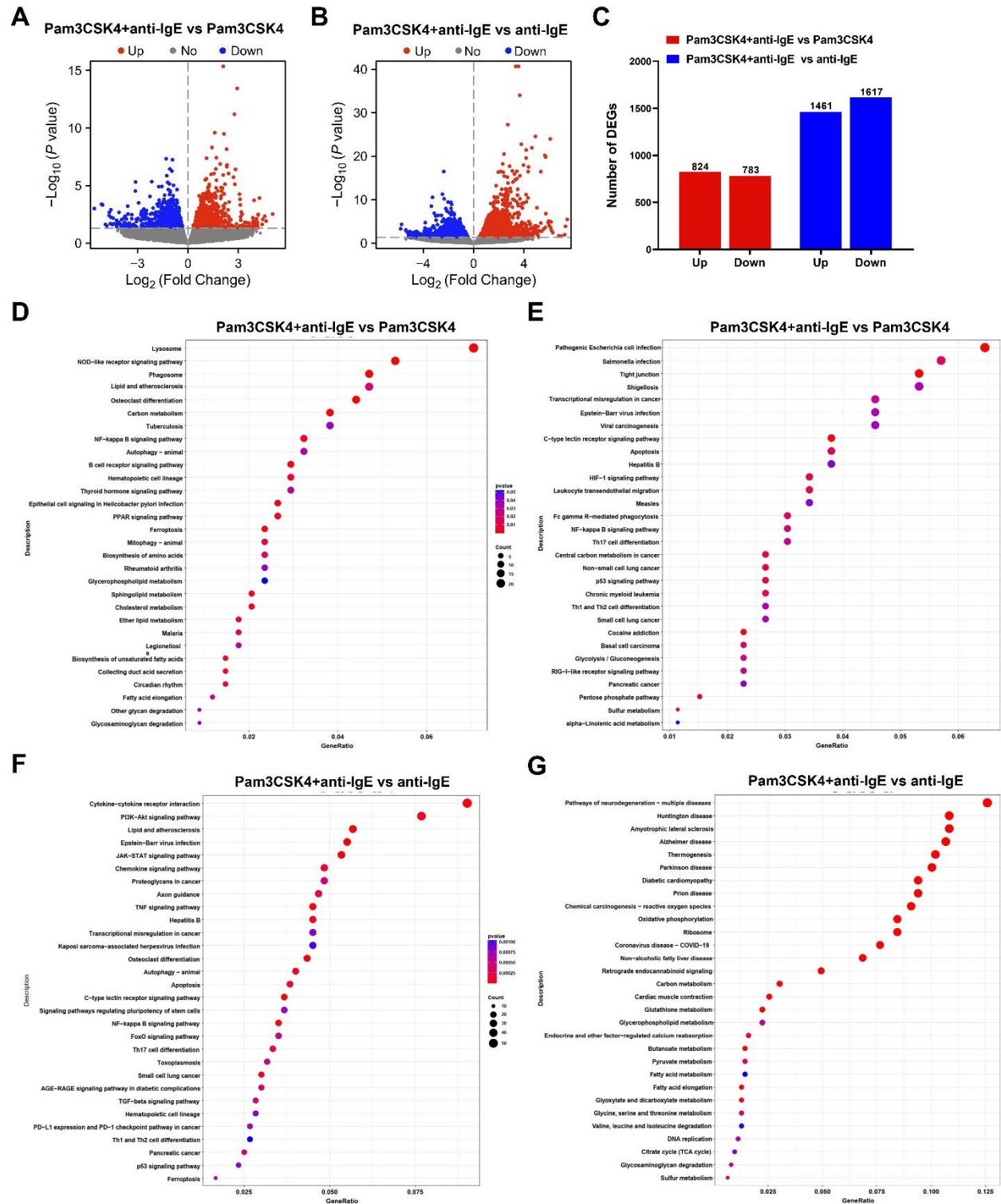
AGated from live CD14⁺CD1a⁺ cells**B**

Figure S2



A

Comparison	Up	Down
Pam3CSK4+anti-IgE vs Pam3CSK4	2	14
Pam3CSK4+anti-IgE vs anti-IgE	8	1

B

C

D

E

A

