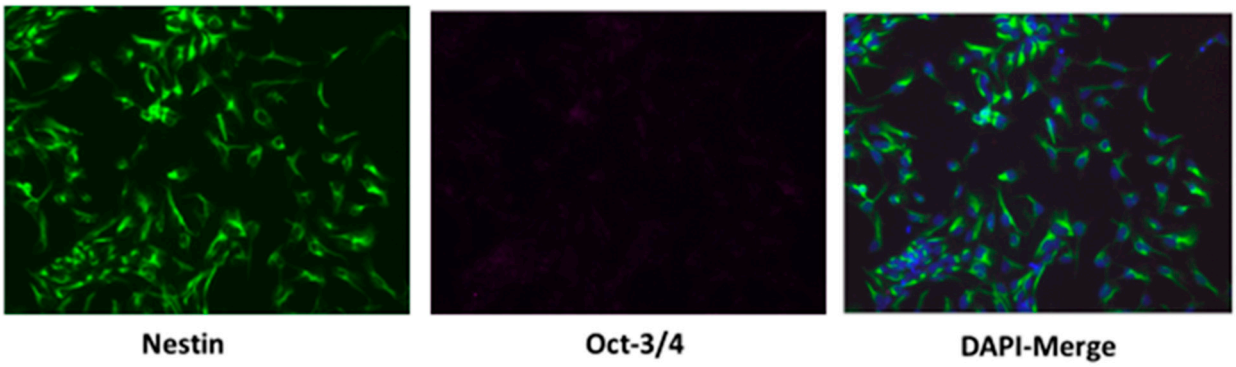
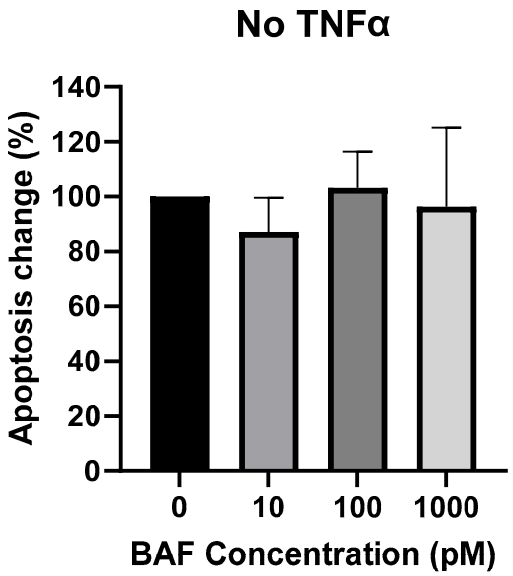
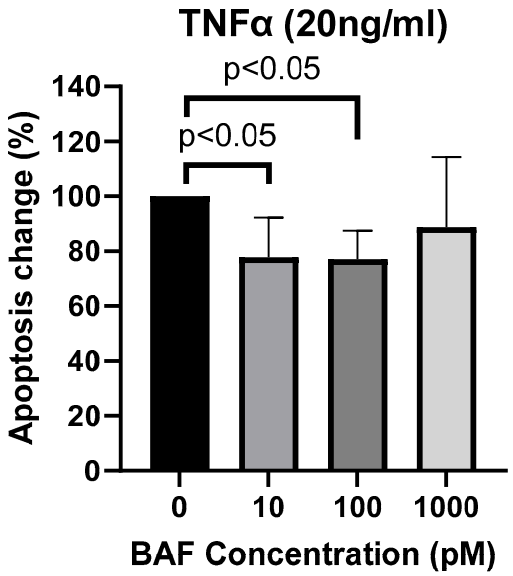


Supplementary Figure S1. **Generation of human neuronal hiPSC-NSCs/NPCs cell line**. Nestin was used as marker for NPCs (green). Lack of Oct-3/4 (red) staining indicated that no remnant iPSCs were present in the culture (almost 100% NSC/NPC). DAPI (blue) stained for nucleus.

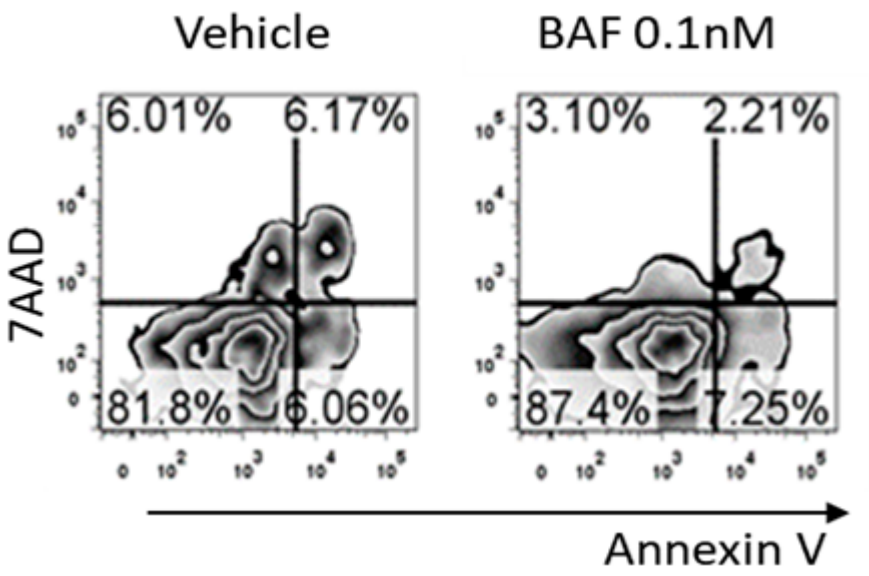
A

B


No TNFα
Apoptosis change (%)
140
120
100
80
60
40
20
0
0
10
100
1000
BAF Concentration (pM)

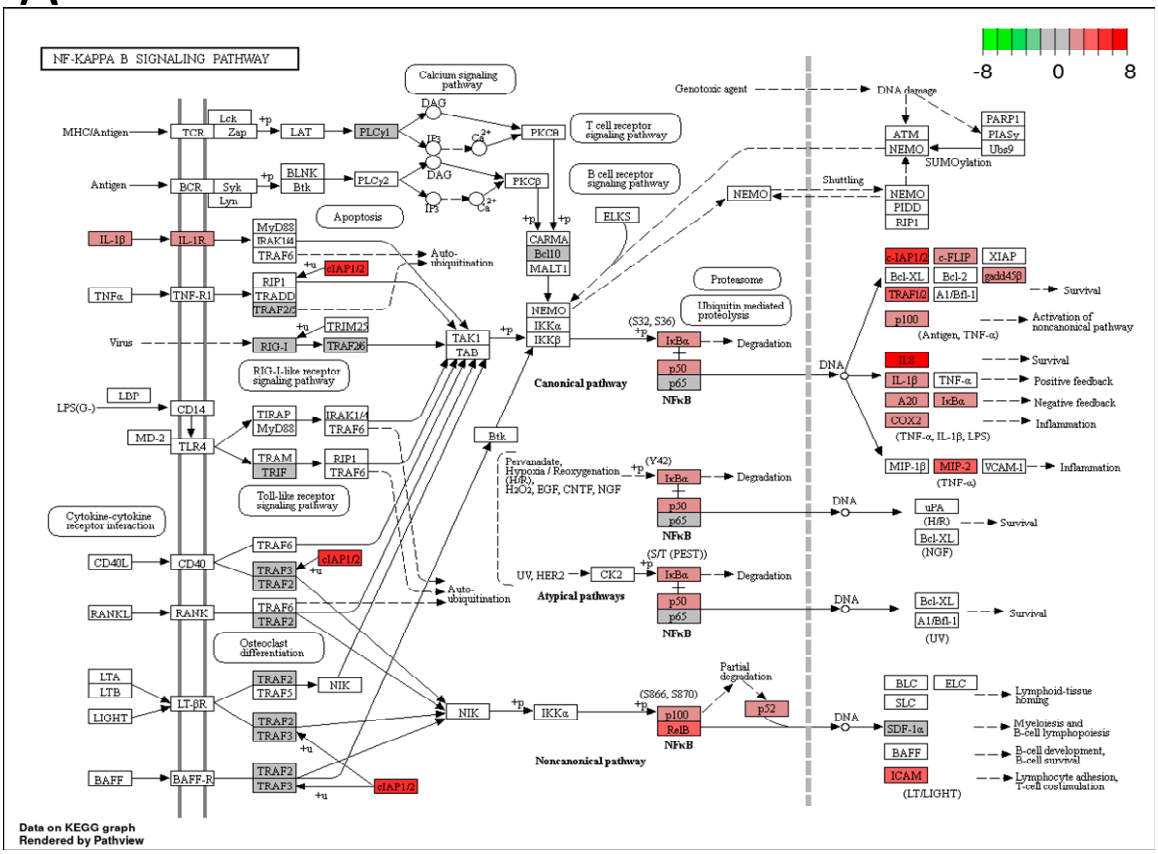

TNFα (20ng/ml)
p<0.05
p<0.05
Apoptosis change (%)
140
120
100
80
60
40
20
0
0
10
100
1000
BAF Concentration (pM)

C



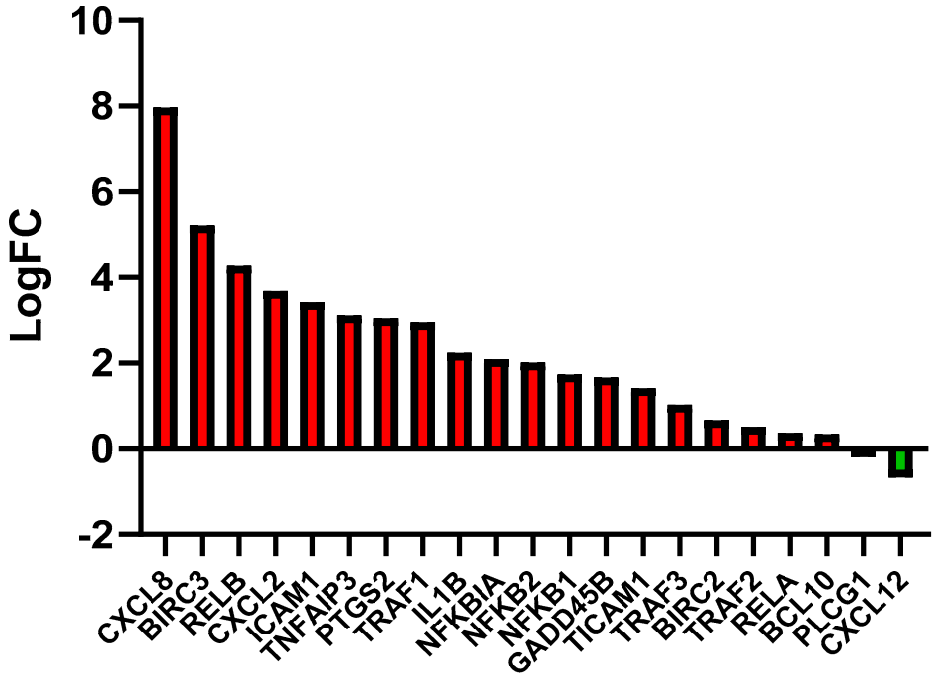
Supplementary Figure S2. Siponimod/BAF312 reduced apoptosis of human neuronal hiPSCs-NSCs/NPCs cells (Annexin V+7AAD-%) based on flowcytometry. Human neuronal hiPSCs-NSCs/NPCs cells treated with Siponimod/BAF312 (abbreviated as BAF) at concentrations of 0, 10, 100, 1000 pM under with **(A)** or without **(B)** TNFα (20ng/ml) treatment for 48h. These experiments were done in duplicate. The average of the duplicate was calculated as fraction of average of the vehicle control (DMSO) in that experiment. The average from four experiments of these fractions were presented as column with SD. Relative cell death or survival was calculated compared to relevant vehicle controls (DMSO). A one-way ANOVA test was used to compare changes in apoptosis between concentrations of Siponimod/BAF312 (BAF). P values <0.05 were considered significant. **(C).** Representative flow plots from three independent experiments.

A



B

Differentially expressed genes
NF-Kappa B signaling pathway (KEGG:04064)



Supplementary Figure S3. TNFα treatment affects genes involved in NFKB signaling pathways in human neuronal hiPSCs-NSCs/NPCs cells. (**A**) The NFKB pathway (KEGG: 04064) diagram is overlaid with the expression changes of each gene. Downregulated genes are shown in green, while upregulated genes are in red. (**B**) The top 20 differentially expressed genes in NFKB signaling pathway (KEGG: 04064) are ranked based on their absolute value of log fold change. Upregulated genes are shown in red, and downregulated genes are shown in green. n = 5-6 sets.