

Supplementary data S6

The identification of enriched transcriptomic signatures

For the identification of enriched transcriptomic signatures, analysis was conducted by using Enrichr website (<https://maayanlab.cloud/Enrichr/>).

Target genes had a significant association with the gene set linked to atopic dermatitis

The enrichment analysis of RNAseq automatic Gene Expression Omnibus (GEO) signatures revealed that active compounds of *S. polyrhiza* (730 target genes) were associated with mouse down gene set including Atopic Dermatitis Nestin-Cre IKK2 (GSE109936).

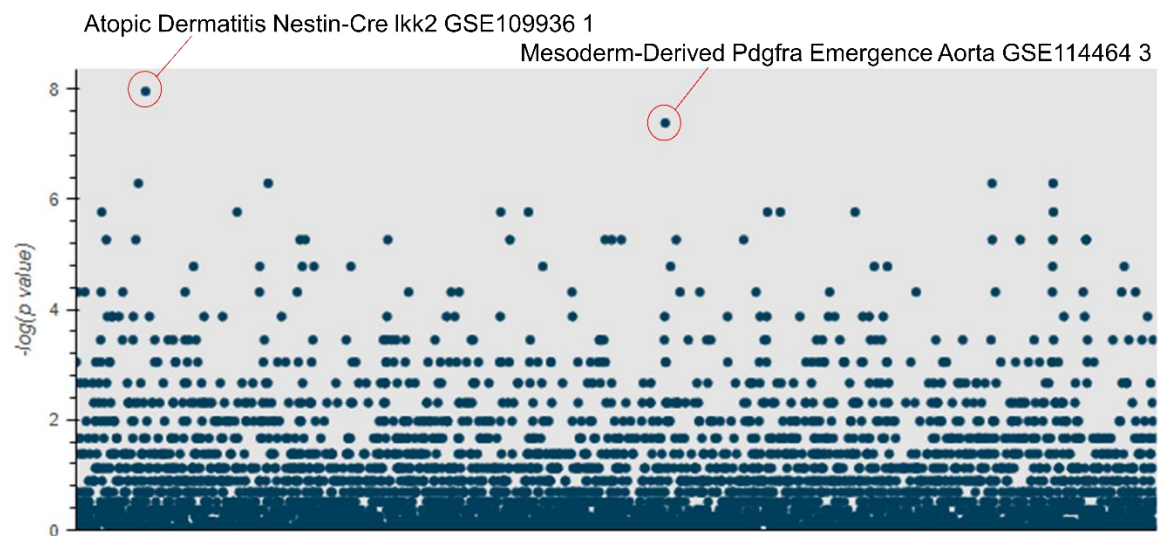


Figure S2. Manhattan plot of terms from the RNA-seq_Automatic_GEO_Signatures_Mouse_Down gene set. Each point represents a single term along the x-axis. The y-values represent the $-\log_{10}$ (p-value) corresponding to the enrichment of the input gene set for the term gene set. Hovering over the point will display the gene set term and the enrichment analysis p -value.