

Supplementary file 2

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Integrative discovery of *Licorice*-derived phytochemicals as potential anti-inflammatory adjuvants targeting immune signatures of *Klebsiella pneumoniae* infection identified by single-cell profiling

Ali Shivaee¹, Samira Asadi Gharibdusti², Farkhondeh Pooresmaeil³, Najmeh Ardeshiri⁴, Bahareh Hajikhani^{5*}, Behnam Hasannejad-Asl^{6*}

¹Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

²Faculty of Basic Sciences, Department of Biology, Tehran East Branch, Islamic Azad University, Tehran, Iran

³Cancer Immunology and Immunotherapy Research Center, Ardabil University of Medical Sciences, Ardabil, Iran

⁴Department of Microbiology, Faculty of Biological Sciences, Alzahra University, Tehran, Iran

⁵Department of Microbiology, School of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran

⁶Arthropod-Borne Diseases Research Center, Ardabil University of Medical Sciences, Ardabil, Iran

*Corresponding authors: Bahareh Hajikhani, Emails: hajikhani@sbm.ac.ir, b.hajikhani@gmail.com; Behnam Hasannejad-Asl, Emails: behnam.hasannejad-asl@arums.ac.ir, behnam.hasannejad@gmail.com

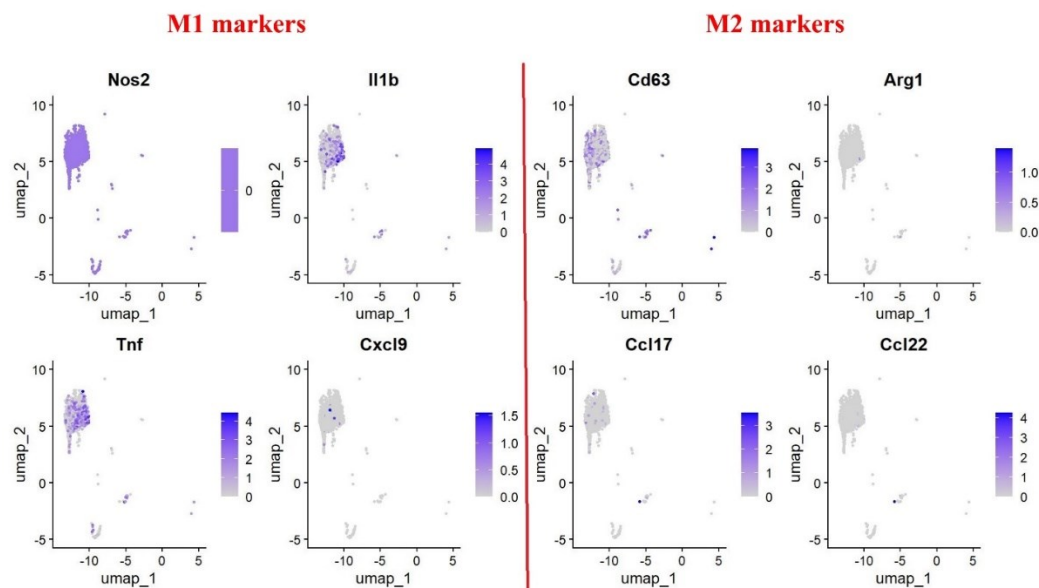


Figure S1. Feature plots showing expression of canonical macrophage polarization markers in the macrophage cluster. M1-associated genes (Nos2, Il1b, Tnf, Cxcl9, and Cd38) were more broadly expressed than M2-associated genes (Cd63, Arg1, Ccl17, and Ccl22), which were limited to few cells or

showed weak expression. Overall, the expression pattern is consistent with a predominantly inflammatory, M1-like macrophage signature and suggests heterogeneity within the macrophage compartment.

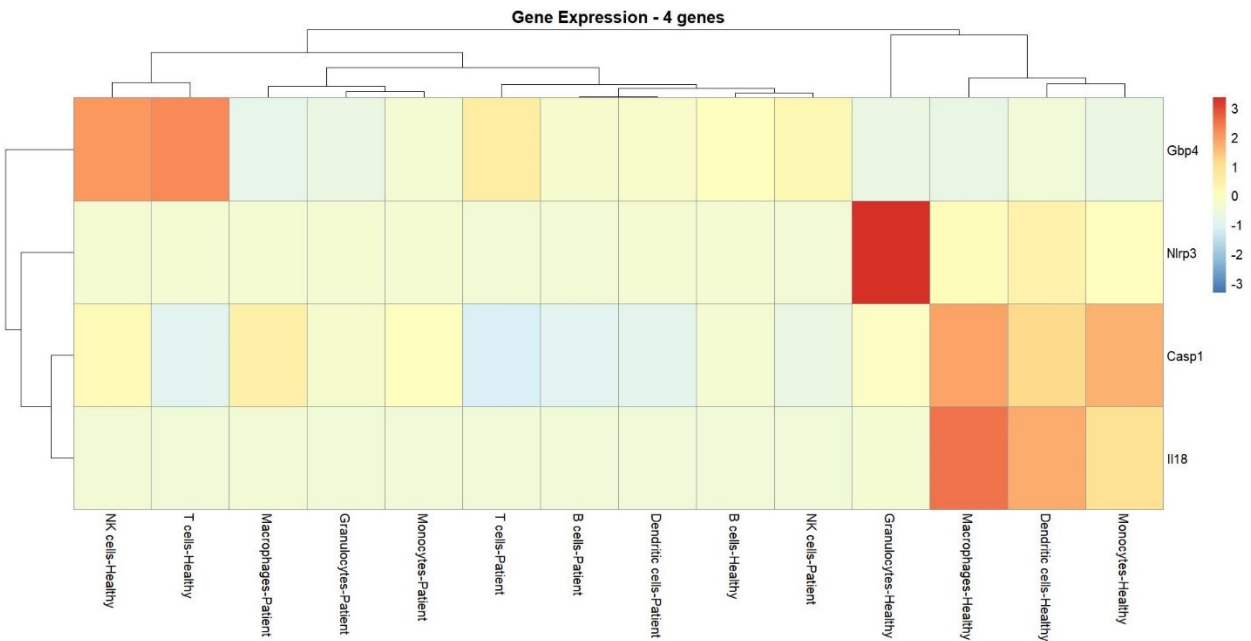


Figure S2. Independent-cohort heatmap of selected inflammasome- and interferon-related genes in GSM8170748 and matched mock-infected samples. The plot shows a myeloid-biased inflammatory signature, with increased NLRP3, CASP1, and IL18 in macrophages and monocytes and a strong NLRP3 signal in granulocytes. Expression values were log2-transformed, z-score normalized by gene, and hierarchically clustered. **GBP5** was not reliably quantified in this dataset, so the figure supports pathway-level validation rather than direct GBP5 upregulation

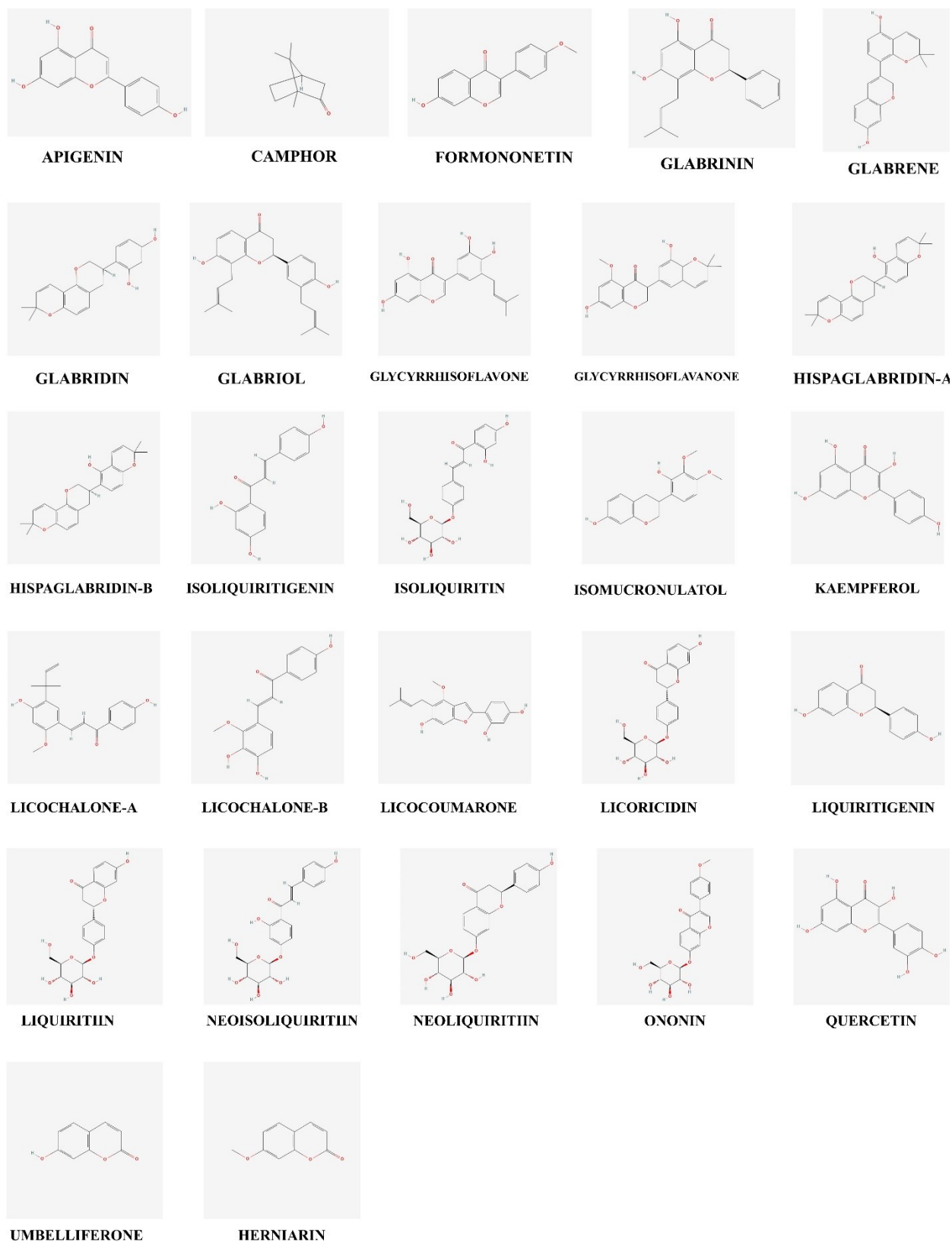


Figure S3. 2-Dimensional structure of drug-like phytochemicals.