Figure S2C. Gene ontology terms of candidate targets of Chaihuqingzao (CHQZ) against COVID-19. The top 20 GO functional categories with P-adjust<0.05 are presented.

a. Biological Process

- response to lipo polysaccharide
- response to molecule of bacterial origin
- response to oxidative stress
- positive regulation of cytokine production
- regulation of apoptotic signaling pathway
- cellular response to biotic stimulus
- cellular response to external stimulus
- T cell activation
- cellular response to lipo polysaccharide
- cellular response to molecule of bacterial origin
- cellular response to abiotic stimulus
- cellular response to environmental stimulus
- regulation of cell–cell adhesion
- neuron death
- response to mechanical stimulus
- extrinsic apoptotic signaling pathway
- response to reactive oxygen species
- regulation of leukocyte cell–cell adhesion
- negative regulation of apoptotic signaling pathway

b. Cellular Component

- membrane skeleton
- membrane microdomain
- membrane region
- focal adhesion
- cell–substrate adhesion junction
- cell–substrate junction
- vesicle lumen
- cytoplasmic vesicle lumen
- nuclear envelope
- transcription factor complex
- cajal body
- plasma membrane raft
- mitochondrial outer membrane
- organelle outer membrane
- outer membrane
- secretory granule lumen
- neuron projection cytoplasm
- phosphatidylinositol 3-kinase complex
- dendrite cytoplasm
- endoplasmic reticulum chaperone complex

b. Molecular Function

- cytokine receptor binding
- phosphatase binding
- protein phosphatase binding
- cytokine activity
- receptor ligand activity
- protein serine/threonine kinase activity
- kinase regulator activity
- ubiquitin–like protein ligase binding
- protease binding
- homeostasis binding
- tetrapyrrole binding
- tumor necrosis factor receptor superfamily binding
- chemokine receptor binding
- phosphoprotein binding
- activating transcription factor binding
- BH domain binding
- death domain binding
- MAP kinase activity
- tumor necrosis factor receptor binding
- phosphotyrosine residue binding