

Supplementary Table 4. KEGG pathway enrichment analysis of DEGs between two clusters.

| Term | Count | FDR |
|------------------------------------------------------------------------|--------------|------------|
| hsa04512:ECM-receptor interaction | 51 | 1.33E-20 |
| hsa04510:Focal adhesion | 73 | 1.70E-15 |
| hsa04151:PI3K-Akt signaling pathway | 95 | 4.90E-11 |
| hsa04514:Cell adhesion molecules | 54 | 3.41E-10 |
| hsa05146:Amoebiasis | 41 | 5.81E-10 |
| hsa04974:Protein digestion and absorption | 41 | 6.96E-10 |
| hsa05144:Malaria | 27 | 8.93E-10 |
| hsa04610:Complement and coagulation cascades | 36 | 1.42E-09 |
| hsa05200:Pathways in cancer | 120 | 3.12E-09 |
| hsa05414:Dilated cardiomyopathy | 36 | 5.88E-08 |
| hsa04060:Cytokine-cytokine receptor interaction | 74 | 1.79E-07 |
| hsa05410:Hypertrophic cardiomyopathy | 33 | 4.69E-07 |
| hsa05412:Arrhythmogenic right ventricular cardiomyopathy | 30 | 4.69E-07 |
| hsa04020:Calcium signaling pathway | 60 | 5.21E-06 |
| hsa04270:Vascular smooth muscle contraction | 40 | 5.87E-06 |
| hsa04640:Hematopoietic cell lineage | 32 | 1.58E-05 |
| hsa05205:Proteoglycans in cancer | 52 | 1.91E-05 |
| hsa04022:cGMP-PKG signaling pathway | 44 | 4.79E-05 |
| hsa04933:AGE-RAGE signaling pathway in diabetic complications | 31 | 5.36E-05 |
| hsa04360:Axon guidance | 46 | 8.23E-05 |
| hsa04611:Platelet activation | 35 | 1.02E-04 |
| hsa05165:Human papillomavirus infection | 71 | 1.02E-04 |
| hsa04080:Neuroactive ligand-receptor interaction | 75 | 1.91E-04 |
| hsa04261:Adrenergic signaling in cardiomyocytes | 39 | 2.00E-04 |
| hsa04061:Viral protein interaction with cytokine and cytokine receptor | 29 | 3.55E-04 |
| hsa05418:Fluid shear stress and atherosclerosis | 36 | 4.51E-04 |
| hsa04015:Rap1 signaling pathway | 47 | 0.00126 |
| hsa04921:Oxytocin signaling pathway | 37 | 0.0017 |
| hsa04924:Renin secretion | 21 | 0.002423 |
| hsa04010:MAPK signaling pathway | 59 | 0.003256 |
| hsa04810:Regulation of actin cytoskeleton | 46 | 0.005231 |
| hsa05217:Basal cell carcinoma | 19 | 0.005347 |
| hsa04062:Chemokine signaling pathway | 41 | 0.008065 |
| hsa05202:Transcriptional misregulation in cancer | 41 | 0.008697 |
| hsa04340:Hedgehog signaling pathway | 17 | 0.009668 |
| hsa04926:Relaxin signaling pathway | 30 | 0.010632 |
| hsa04916:Melanogenesis | 25 | 0.011776 |
| hsa04371:Apelin signaling pathway | 31 | 0.01651 |
| hsa04024:cAMP signaling pathway | 44 | 0.018462 |
| hsa04540:Gap junction | 22 | 0.019733 |
| hsa04350:TGF-beta signaling pathway | 23 | 0.020045 |
| hsa05150:Staphylococcus aureus infection | 23 | 0.025764 |
| hsa01521:EGFR tyrosine kinase inhibitor resistance | 20 | 0.026021 |
| hsa04713:Circadian entrainment | 23 | 0.028093 |
| hsa04145:Phagosome | 32 | 0.029498 |

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|----------------------------------------------|----|----------|
| hsa05222:Small cell lung cancer | 22 | 0.029929 |
| hsa04925:Aldosterone synthesis and secretion | 23 | 0.029929 |
| hsa03320:PPAR signaling pathway | 19 | 0.029929 |
