**Supplementary Table 1. Means, SDs, and one-way ANOVA of cell length, cell area, nuclear area, cytoplasmic area, and nuclear-cytoplasmic ratio of cells treated with different concentrations of dexamethasone.**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Variable | Control | 0.25 M | 0.5 M | ANOVA | |
|  | M ± SD | | | F value | *P\_adj* value |
| Cell lengths (µm) | 84.32 ± 12.68 | 118.1 ± 22.34 | 129.8 ± 21.79 | 54.996 | <0.001 |
| Cell areas (µm²) | 2048 ± 703.9 | 4754 ± 1780 | 4994 ± 1790 | 37.518 | <0.001 |
| Nuclear areas (µm²) | 671.5 ± 155.8 | 831.2 ± 195.6 | 921.2 ± 175.0 | 10.308 | <0.001 |
| Cytoplasmic areas (µm²) | 1278 ± 166.2 | 3874 ± 1458 | 4390 ± 1704 | 62.012 | <0.001 |
| Nuclear-cytoplasmic ratios | 0.4248 ± 0.1596 | 0.2387 ± 0.1059 | 0.2209 ± 0.06600 | 13.756 | <0.001 |

*Notes*: 0.25M and 0.5M indicate treatment with 0.25 and 0.5 µM dexamethasone, respectively.

**Supplementary Table 2. Post hoc comparisons**

|  |  |  |
| --- | --- | --- |
| Variable | Treatment groups | *P \_adj* value |
| Cell length | 0 vs. 0.25 | <0.001 |
| 0 vs. 0.5 | <0.001 |
| 0.25 vs. 0.5 | 0.161 |
| Cell areas | 0 vs. 0.25 | <0.001 |
| 0 vs. 0.5 | <0.001 |
| 0.25 vs. 0.5 | 0.965 |
| Nuclear areas | 0 vs. 0.25 | 0.016 |
| 0 vs. 0.5 | <0.001 |
| 0.25 vs. 0.5 | 0.248 |
| Cytoplasmic areas | 0 vs. 0.25 | <0.001 |
| 0 vs. 0.5 | <0.001 |
| 0.25 vs. 0.5 | 0.672 |
| Nuclear-cytoplasmic ratio | 0 vs. 0.25 | <0.001 |
| 0 vs. 0.5 | <0.001 |
| 0.25 vs. 0.5 | 0.895 |

*Notes*: 0, 0.25, and 0.5 indicate treatment with 0, 0.25, and 0.5 µM dexamethasone, respectively.

**Supplementary Table 3. Key genes within the top 20 pathways related to the morphological and biological effects of dexamethasone on HLECs identified through KEGG and GO analyses.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | | | | | | | |
| TNFRSF11B | CXCL2 | THBS2 | PLXND1 | FOS | CDH4 | CXCL6 | CAMK2A |
| IL1B | CCL2 | PDGFA | PBX1 | FBXO32 | SDC2 | CXCL3 | ADRA1B |
| LIF | TNFAIP3 | COL4A6 | NKX3-1 | IGFBP2 | HLA-G | CXCL5 | CAMK2D |
| IL7 | CXCL8 | COL4A3 | GREB1L | ZFP36 | HLA-F | MAPK13 | ITPR2 |
| IL11 | LCN2 | MYB | HHIP | AREG | NCAM2 | IL1B | PTK2B |
| CXCL12 | CCL20 | DDIT4 | NPNT | KLF9 | FOXA1 | CXCL1 | TNNC1 |
| TNFSF4 | CSF2 | PPP2R2B | DCHS1 | SSTR2 | COL11A1 | IL6 | PDGFA |
| GDF6 | FOSL1 | COL6A3 | GBX2 | HTR1B | ATP1A2 | CCL20 | P2RX6 |
| CXCL6 | IL1B | ANGPT1 | TBX3 | LOX | COL25A1 | TNFRSF19 | ERBB4 |
| IL18 | CXCL6 | TGFA | SOX9 | ATP1A2 | COL4A6 | CSF2 | NTRK3 |
| INHBA | CXCL3 | IL6 | MSX2 | DUSP1 | COL4A3 | CXCL3 | TGFA |
| CXCL5 | CXCL5 | LPAR1 | AREG | CA2 | SLC7A8 | TNFRSF9 | ADORA2A |
| SDC3 | MAPK13 | IGF2 | FOXC2 | FOSL1 | COL27A1 | CXCL1 | HRH1 |
| PTPRF | FOS | LAMA4 | CXCL2 | ALPL | COL12A1 | CD70 | PLCD1 |
| ICAM1 | CXCL1 | COL6A6 | CCL2 | TXNIP | COL6A3 | CCL2 | BDKRB2 |
| ITGB2 | IL6 | IL7 | CXCL8 | DDIT4 | COL6A6 | IL32 | PLCB1 |
| F11R | CXCL2 | AREG | CXCL12 | NTRK3 | COL8A1 | CXCL8 | PTGFR |
| JAM2 | CCL2 | ITGA2 | CCL20 | AKR1C3 | COL14A1 | IL15RA | ADRB1 |
| OCLN | TNFAIP3 | IRS1 | CXCL6 | PPARGC1B | COL4A4 | BMP4 | ADRB2 |
| LRRC4 | ICAM1 | ITGA10 | ACKR1 | FOXO1 | DPP4 | IL6 | BDKRB1 |
| ALCAM | LIF | ITGB4 | CXCL5 | PTGER2 | EFNA1 | CXCL2 | PDGFD |
| HLA-B | IRF1 | TNC | CXCL1 | FOS | COMP | TNFSF10 | CAMK4 |
| CADM3 | CSF2 | PDGFD | CXCL3 | FBXO32 | TLR2 | INHBB | FLT1 |
| ICOSLG | BCL3 | COL4A4 | CXCL2 | IGFBP2 | ERBB4 | CCL20 | VDR |
| NRCAM | FOS | FLT1 | CCL2 | ZFP36 | LAMC2 | IL1A | TNC |
| TNIP3 | AREG | DDIT4 | ANKRD1 | FOSL1 | ZFP36 | SERPINE1 | ID1 |
| ANKRD1 | KLF9 | NTRK3 | FLT1 | ALPL | PDGFD | IL6 | MTSS2 |
| CXCL8 | SFRP1 | PPARGC1B | FOXO1 | DUSP1 | ERBB4 | SSTR2 | NTRK3 |
| LCN2 | WNT10A | CXCL3 | PTN | NLRP3 | CILP | TXNIP | CXCL8 |
| CSF2 | GATA6 | ZFP36 | TWIST1 | CXCL5 | FEZ1 | PLSCR4 | CCL2 |
| TNFSF4 | PDE3A | TLR2 | GAS1 | CXCL1 | BAIAP2 | CXCL6 |  |

**Supplementary Table 4.** **The information of differentially expressed genes associated with autophagy.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene name | Fold change  (0.25µM DEX/0µM DEX) | TPM  （0µM DEX） | TPM  （0.25µM DEX） | *P \_adj* value |
| RPS6KA2 | 13.94334742 | 4.28 | 46.3733 | <0.001 |
| DDIT4 | 3.214346461 | 84.51 | 249.6133 | <0.001 |
| IRS1 | 2.007629075 | 10.6467 | 19.6933 | <0.001 |

*Notes*: 0M DEX and 0.25M DEX indicate the control group and the group treated with 0.25 µM dexamethasone, respectively.

Supplementary Fig.1

**Supplementary Fig.1. Gating strategy and** **flow cytometry analysis process.** Flow cytometry was performed to analyze the size and granularity of cells in the sample. The first row shows forward scatter (FSC) and side scatter (SSC) dot plots, with gating applied to select living cells for further analysis. The percentages of living cells are indicated within each gate (62.6% and 58.4%, respectively). Histograms corresponding to the FSC-H and SSC-H parameters for the gated populations are presented in the second row, displaying cell size (FSC-H) and internal complexity or granularity (SSC-H). The final row compares the histograms for each group, with blue and red overlays representing control group and 0.25 µM dexamethasone group respectively.