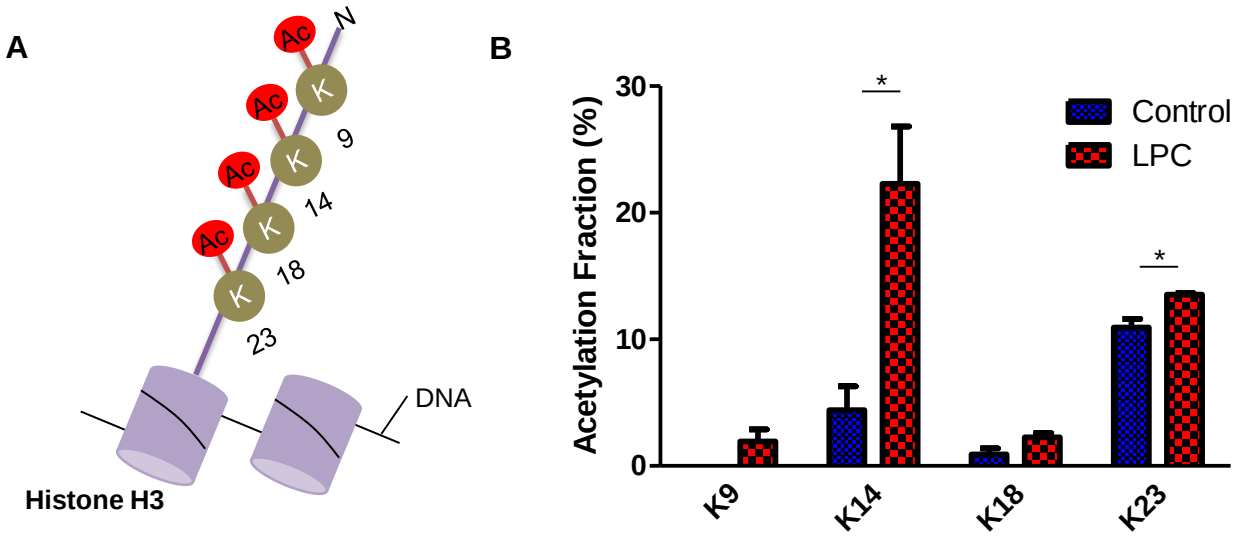
Supplemental Material




**Supplemental Figure I. Lysophosphatidylcholine (LPC) significantly induces site-specific H3K14ac in human aortic endothelial cells. A.** Schematic representation of the four histone acetylation sites on histone H3. **B**. After treatment of human aortic endothelial cells (HAECs) with LPC (10μM) for 2 hours, histones were purified. After propionylation and trypsin digestion, the acetylation fractions on individual lysine residues on histone H3 were measured by HPLC-MS method. Statistical analysis of the acetylation fractions on lysine residues of H3 between control and LPC treatment group were shown.

# Supplemental Table I. Genes significantly induced by LPC in HAECs.

| Gene Symbol | Fold regulation | *p*-value | Gene Symbol | Fold regulation | *p*-value |
|---|---|---|---|---|---|
| KIZ | 3.47 | 0.036 | NSDHL | 1.67 | 0.003 |
| IGFBP5 | 3.23 | 0.000 | SULT1A1 | 1.63 | 0.018 |
| LYPD5 | 2.99 | 0.031 | IGF2 | 1.61 | 0.024 |
| SELE | 2.87 | 0.002 | PLA2G4C | 1.61 | 0.005 |
| S100A4 | 2.73 | 0.000 | EBP | 1.59 | 0.009 |
| IL32 | 2.70 | 0.000 | RELB | 1.59 | 0.021 |
| DENND2A | 2.61 | 0.042 | CXCL1 | 1.59 | 0.014 |
| CAPN3 | 2.58 | 0.048 | MMAB | 1.59 | 0.015 |
| ZNF778 | 2.45 | 0.004 | AOX1 | 1.58 | 0.018 |
| LAT | 2.44 | 0.027 | HMGCS1 | 1.58 | 0.007 |
| TRAF1 | 2.30 | 0.012 | ZNF185 | 1.57 | 0.005 |
| GCH1 | 2.18 | 0.004 | GSDMC | 1.56 | 0.028 |
| BIRC3 | 2.17 | 0.022 | IL1RL1 | 1.55 | 0.006 |
| CDRT4 | 2.15 | 0.043 | GBP1 | 1.55 | 0.015 |
| CCDC24 | 2.14 | 0.026 | RPL21 | 1.53 | 0.011 |
| DCAF12L1 | 2.13 | 0.034 | QPCTL | 1.53 | 0.026 |
| PRPF38B | 2.06 | 0.000 | LIPG | 1.52 | 0.015 |
| C8orf4 | 1.99 | 0.010 | TMEM154 | 1.52 | 0.015 |
| MVK | 1.94 | 0.000 | AKR1C3 | 1.51 | 0.011 |
| LDLR | 1.87 | 0.000 | ROGDI | 1.49 | 0.048 |
| FADS2 | 1.85 | 0.000 | MSMO1 | 1.49 | 0.012 |
| IL1B | 1.85 | 0.037 | TRIM16 | 1.49 | 0.015 |
| MVD | 1.83 | 0.000 | LSS | 1.48 | 0.015 |
| DHCR7 | 1.82 | 0.000 | SLC2A6 | 1.47 | 0.022 |
| ST6GALNAC1 | 1.81 | 0.023 | TM7SF2 | 1.46 | 0.042 |
| HIST1H4K | 1.81 | 0.006 | INSIG1 | 1.46 | 0.018 |
| SCD | 1.79 | 0.000 | GALNT6 | 1.45 | 0.022 |
| TNFSF15 | 1.79 | 0.006 | **ICAM1** | **1.45** | **0.026** |
| SFMBT1 | 1.78 | 0.028 | CALD1 | 1.44 | 0.023 |
| CCL2 | 1.78 | 0.000 | CCDC69 | 1.44 | 0.028 |
| CREB5 | 1.77 | 0.023 | CXCL8 | 1.43 | 0.034 |
| TGFB3 | 1.75 | 0.034 | ADAMTS1 | 1.43 | 0.046 |
| RSPH3 | 1.73 | 0.033 | SQLE | 1.42 | 0.027 |
| TMEM158 | 1.71 | 0.006 | CYP51A1 | 1.42 | 0.027 |
| HMGXB4 | 1.70 | 0.045 | FDFT1 | 1.38 | 0.044 |
| TAF7L | 1.68 | 0.042 | RDH11 | 1.38 | 0.044 |

# Supplemental Table II. Genes significantly suppressed by IL-35 in HAECs.

| Gene Symbol | Fold regulation | *p*-value | Gene Symbol | Fold regulation | *p*-value |
|---|---|---|---|---|---|
| BOLA2/BOLA2B | minus inf | 0.000 | TDRD10 | -1.58 | 0.044 |
| TMEM189-UBE2V1 | -4851.45 | 0.012 | COMMD6 | -1.569 | 0.003 |
| ZNF273 | -4.533 | 0.047 | QSER1 | -1.561 | 0.002 |
| FAM45A | -3.067 | 0.003 | BOLA1 | -1.502 | 0.049 |
| NEK3 | -3.044 | 0.001 | CD58 | -1.493 | 0.034 |
| IL33 | -3.016 | 0.012 | ZNF182 | -1.493 | 0.033 |
| GOLGA8A/GOLGA8B | -2.827 | 0.013 | RRAGC | -1.491 | 0.016 |
| NLGN4Y | -2.706 | 0.041 | USP14 | -1.49 | 0.010 |
| FSIP1 | -2.413 | 0.048 | NIPBL | -1.49 | 0.006 |
| ZBED3 | -2.386 | 0.031 | PTPN12 | -1.484 | 0.006 |
| CAPN3 | -2.335 | 0.042 | NUS1 | -1.454 | 0.039 |
| RMI1 | -2.279 | 0.002 | PSME4 | -1.452 | 0.007 |
| KARS | -2.163 | 0.003 | MBTPS2 | -1.448 | 0.040 |
| CYP26B1 | -2.056 | 0.001 | CXCL1 | -1.446 | 0.025 |
| C15orf52 | -1.991 | 0.000 | ZMYM1 | -1.446 | 0.044 |
| ZNF620 | -1.942 | 0.017 | CNOT6 | -1.441 | 0.017 |
| GLTSCR1 | -1.924 | 0.045 | RELB | -1.44 | 0.033 |
| CDRT4 | -1.886 | 0.042 | SEC63 | -1.423 | 0.029 |
| POLR2A | -1.882 | 0.000 | C18orf54 | -1.419 | 0.047 |
| IGFBP5 | -1.878 | 0.000 | UBE2B | -1.412 | 0.035 |
| MCEE | -1.866 | 0.008 | SLC46A3 | -1.404 | 0.025 |
| SMG7 | -1.83 | 0.000 | ZFC3H1 | -1.391 | 0.043 |
| PLCB4 | -1.777 | 0.024 | CCNG2 | -1.389 | 0.035 |
| CST4 | -1.776 | 0.018 | VPS13B | -1.379 | 0.044 |
| SAMD10 | -1.739 | 0.021 | SREK1IP1 | -1.379 | 0.031 |
| BICD1 | -1.727 | 0.023 | HNRNPA3 | -1.377 | 0.034 |
| CXCL8 | -1.712 | 0.000 | LYST | -1.376 | 0.049 |
| IL1B | -1.703 | 0.036 | HNRNPD | -1.369 | 0.043 |
| TGFB3 | -1.64 | 0.029 | **ICAM1** | **-1.363** | **0.031** |
| PRDM5 | -1.627 | 0.038 | SON | -1.362 | 0.023 |
| RAD51B | -1.618 | 0.029 | RAPGEF5 | -1.361 | 0.036 |
| TRAF1 | -1.61 | 0.050 | PTP4A1 | -1.359 | 0.034 |
| STC1 | -1.608 | 0.030 | ABI3BP | -1.349 | 0.047 |
| HERC6 | -1.604 | 0.018 | PABPC3 | -1.344 | 0.048 |

# Supplemental Table III. Ingenuity pathway analysis of LPC-induced and IL-35-suppressed genes in HAECs.

| Diseases or Functions Annotation | p-Value | Molecules | # Molecules |
|---|---|---|---|
| arrest in movement of cells | 1.02E-10 | CXCL1,CXCL8,ICAM1,IL1B | 4 |
| cell death of epithelial cells | 8.92E-10 | CXCL8,ICAM1,IGFBP5,IL1B,RELB,TGFB3,TRAF1 | 7 |
| cell rolling of granulocytes | 2.10E-09 | CXCL1,CXCL8,ICAM1,IL1B | 4 |
| TH1 immune response | 1.38E-08 | CXCL8,ICAM1,IL1B,RELB | 4 |
| immune response of phagocytes | 1.69E-08 | CXCL1,CXCL8,ICAM1,IL1B,RELB | 5 |
| response of myeloid cells | 2.02E-08 | CXCL1,CXCL8,ICAM1,IL1B,RELB | 5 |
| immune response of neutrophils | 2.80E-08 | CXCL1,CXCL8,ICAM1,RELB | 4 |
| adhesion of neutrophils | 3.10E-08 | CXCL1,CXCL8,ICAM1,IL1B | 4 |
| growth of tumor | 3.18E-08 | CXCL1,CXCL8,ICAM1,IGFBP5,IL1B,RELB,TGFB3 | 7 |
| arrest in cell rolling of leukocytes | 3.26E-08 | CXCL8,ICAM1,IL1B | 3 |
| migration of dermal cells | 3.93E-08 | CXCL1,CXCL8,ICAM1,TGFB3 | 4 |
| differentiation of cells | 4.59E-08 | CAPN3,CXCL1,CXCL8,ICAM1,IGFBP5,IL1B,RELB,TGFB3,TRAF1 | 9 |
| TH1 immune response of T lymphocytes | 4.76E-08 | CXCL8,ICAM1,IL1B | 3 |
| binding of cells | 5.21E-08 | CXCL1,CXCL8,ICAM1,IGFBP5,IL1B,RELB | 6 |
| extravasation of neutrophils | 5.65E-08 | CXCL1,ICAM1,IL1B | 3 |
| allergic inflammation | 8.97E-08 | CXCL1,CXCL8,IL1B | 3 |
| migration of neutrophils | 1.04E-07 | CXCL1,CXCL8,ICAM1,IL1B | 4 |
| binding of professional phagocytic cells | 1.37E-07 | CXCL1,CXCL8,ICAM1,RELB | 4 |
| apoptosis of epithelial cells | 1.47E-07 | CXCL8,IGFBP5,IL1B,RELB,TGFB3 | 5 |
| activation of epithelial cells | 1.51E-07 | CXCL8,ICAM1,IL1B | 3 |