Supporting Information

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SI Materials and Methods

ELISA. Control siRNA- and GATA binding protein 2 (*GATA-2*) siRNA-transfected cells were treated with 10 ng/mL recombinant human TNF-α (Miltenyi Biotec) or an equal volume of vehicle (1% BSA in water) for 6 h before collection 24 h post-transfection. Supernatants were collected and analyzed for IL-8 by ELISA (Quantikine kit; R&D Systems). Gene expression was analyzed in each sample to validate the GATA-2 knockdown.

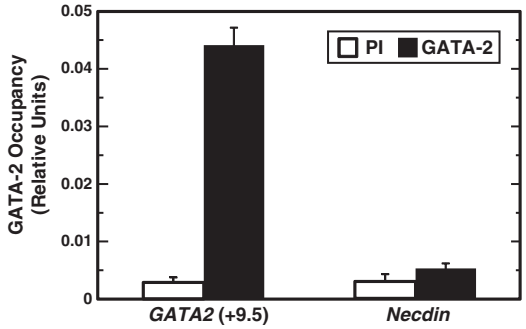

Fig. S1. Quantitative ChIP validation of samples used for ChIP sequencing (ChIP-seq). Quantitative ChIP analysis of GATA-2 occupancy at the *GATA2* +9.5-kb intronic enhancer. The *Necdin* promoter was analyzed as a negative control. Data shown are mean ± SE; $n = 3$. PI, preimmune control.

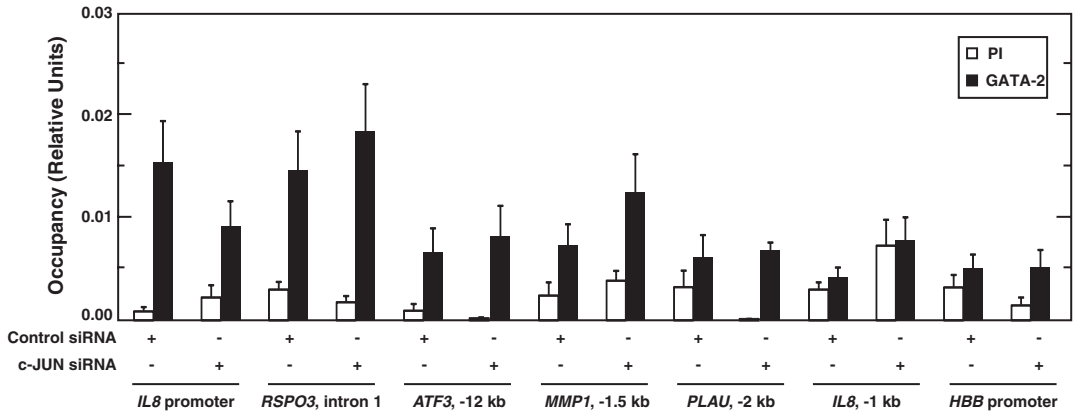

Fig. S2. The jun proto-oncogene (c-JUN) knockdown does not affect GATA-2 chromatin occupancy. Quantitative ChIP at GATA-2/AP-1–regulated genes [*IL-8*, *RSPO3*, activating transcription factor 3 (*ATF3*), *MMP1*, and *PLAU*] and negative controls [human β-globin (*HBB*) promoter and a site 1 kb upstream of the *IL-8* promoter]. Data shown are mean ± SE; $n = 5$. PI, preimmune.

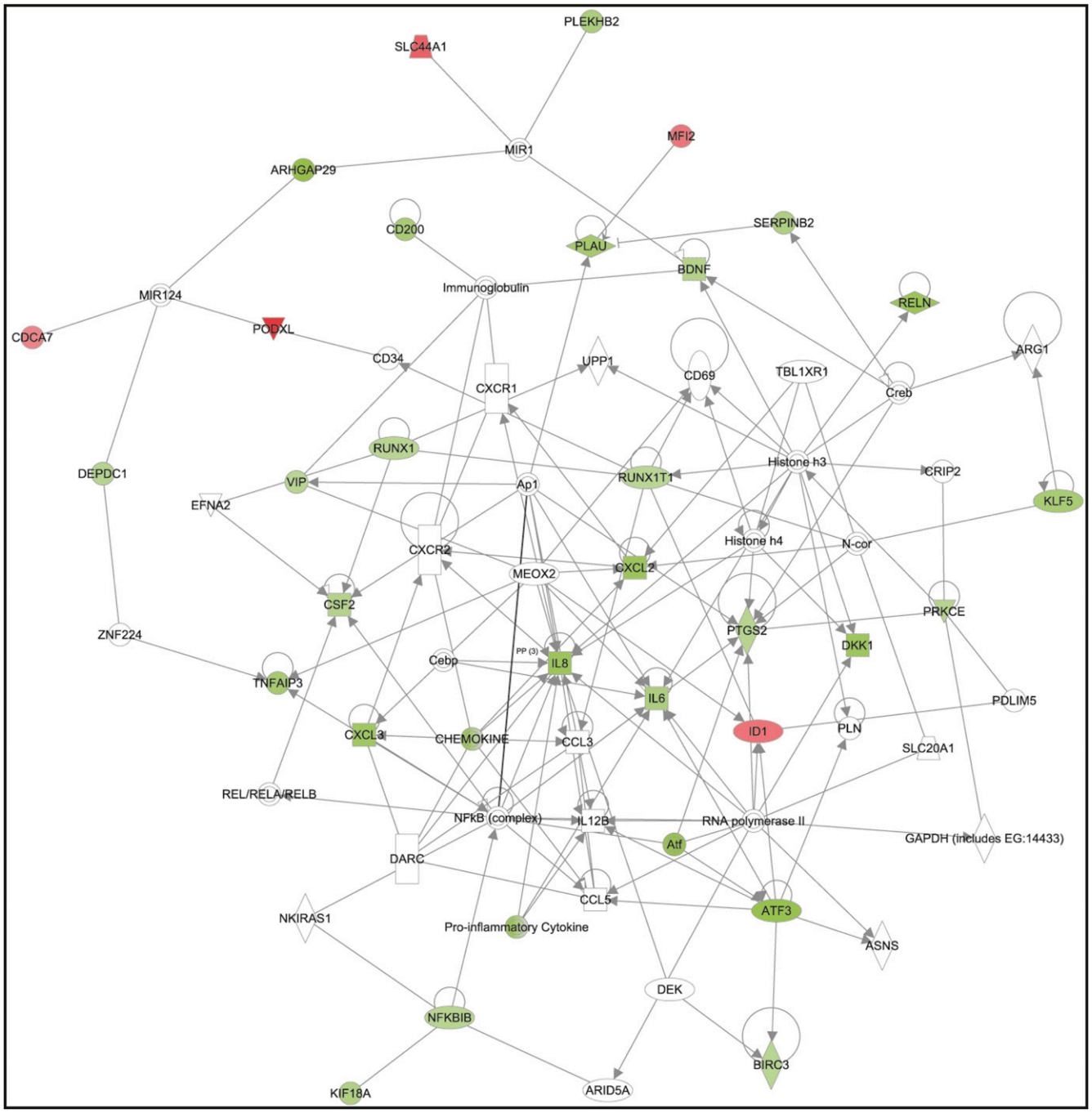

Fig. S3. GATA-2 proinflammatory gene network. We analyzed 116 genes occupied by GATA-2 and dysregulated upon knocking down GATA-2 in HUVEC using Ingenuity Pathways. Direct interactions are depicted. A line connecting two components denotes binding. A line with an arrow indicates that one component (gene or protein) acts on the other. A line with a perpendicular bar at the end indicates that one component inhibits the other. Up-regulated molecules are shown in red; down-regulated molecules are shown in green. Distinct shapes of molecules reflect their different functional activities. Square, cytokine; circle, other; triangle, kinase; rectangle, G protein coupled receptor; oval, transcription regulator; diamond, enzyme.

Dataset S1. Genomic locations of GATA-2 ChIP-seq peaks

Dataset S1

The 15,529 GATA-2–occupied peaks were classified relative to the nearest transcription start site: 5d, regions 10–100 kb upstream of a reference sequence (RefSeq) gene; 5p2, regions 2–10 kb upstream of a RefSeq gene; 5p1, regions <2 kb upstream of a RefSeq gene; gene, any exon or intron of a RefSeq gene; 3p1, regions <2 kb downstream of the last exon of a RefSeq gene; 3p2, regions 2–10 kb downstream of the last exon of a RefSeq gene; 3d, regions between 10–100 kb downstream of the last exon of a RefSeq gene; gd, gene desert (includes regions >100 kb from a RefSeq gene).

Dataset S2. GATA-2 occupancy of genes encoding ETS/ETS-variant transcription factors

Dataset S2

The ETS and ETS-variant transcription factors were organized with respect to subfamily. GATA-2 peaks associated with each gene locus are indicated.

Dataset S3. Locations and peak heights of genomic loci occupied by both GATA-2 and c-JUN

Dataset S3

Dataset S4. Locations and peak heights of genomic loci occupied by both GATA-2 and c-FOS

Dataset S4

Dataset S5. PCR primer sequences

Dataset S5