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Supplementary Materials for

EGR1 is a gatekeeper of inflammatory enhancers in human macrophages

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The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/7/3/eaaz8836/DC1)

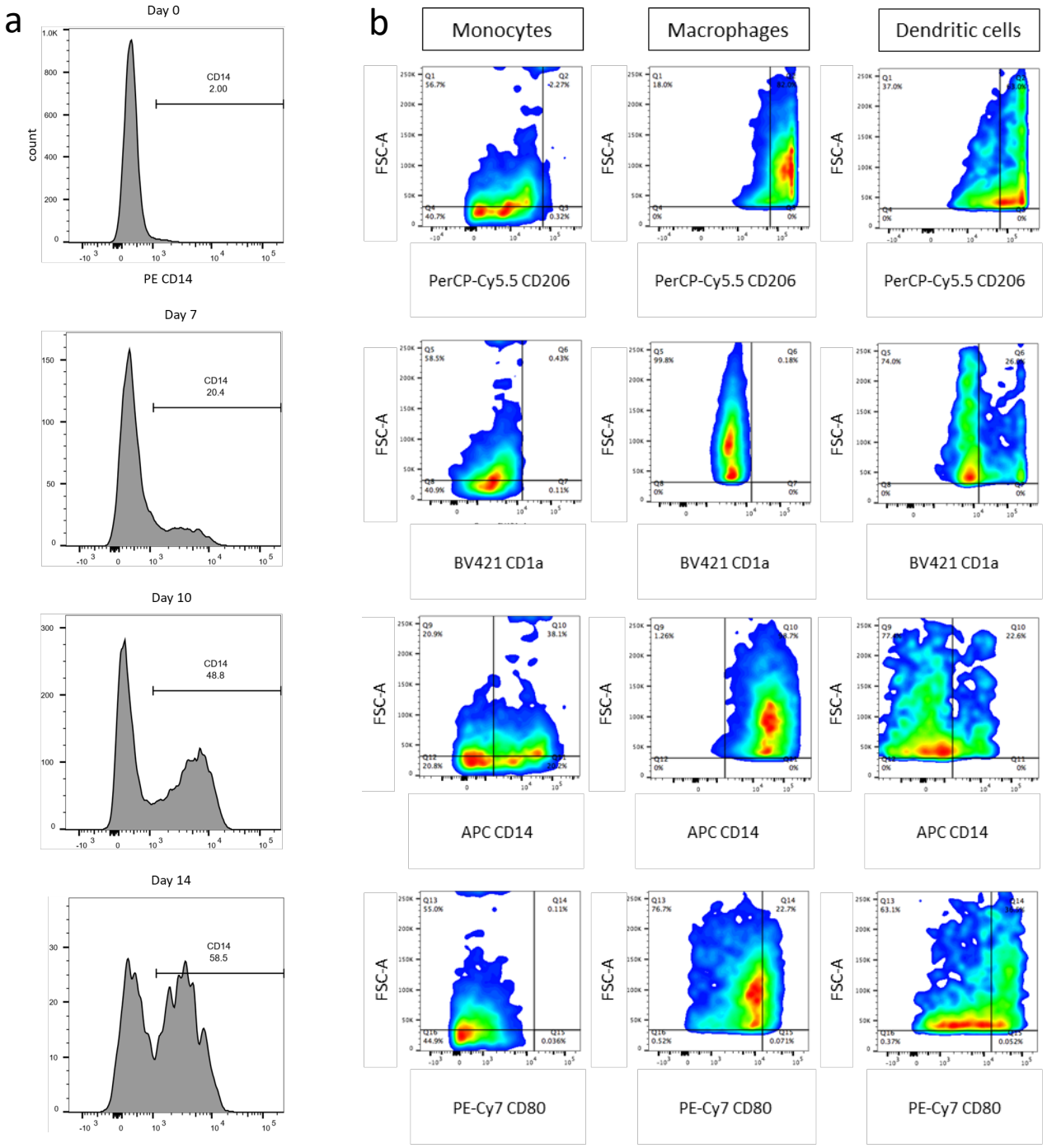


Figure S1. (a) Histogram of flow cytometry results shows increasing proportion of CD14+ monocytes over 14 day course of differentiation from CD34+ HSCs. CD14+ cells make up nearly 1/2 of live cells at two weeks. **(b)** Flow cytometry results from populations of monocytes and day 6 differentiated macrophages and dendritic cells. Cells from each population were stained against antibodies for the markers CD206, CD1a, CD14 and CD80. Results for individual fluorescence channels are shown. Positive/negative gating for each marker was determined using an isotype control for the corresponding immunoglobulin of each antibody to establish a negative threshold ≥99% of events.

Fig 1c monocyte diff.

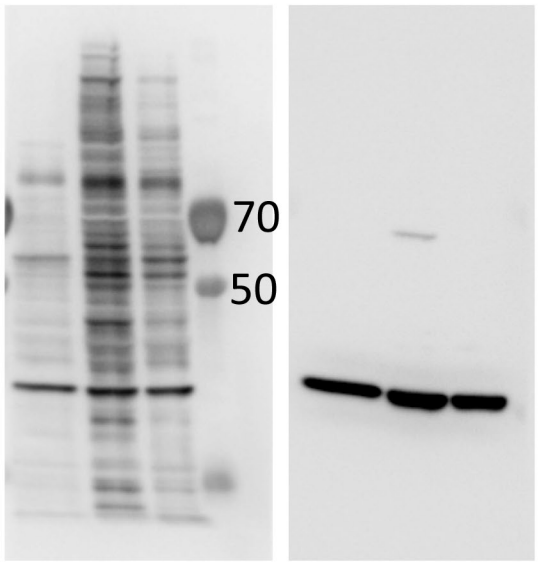


Fig 1c macrophage diff.

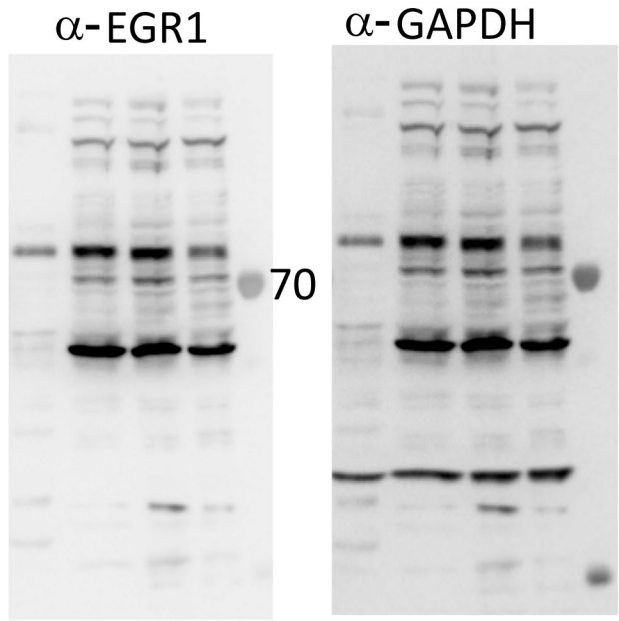


Fig 5b LPS treatment of macrophage diff.

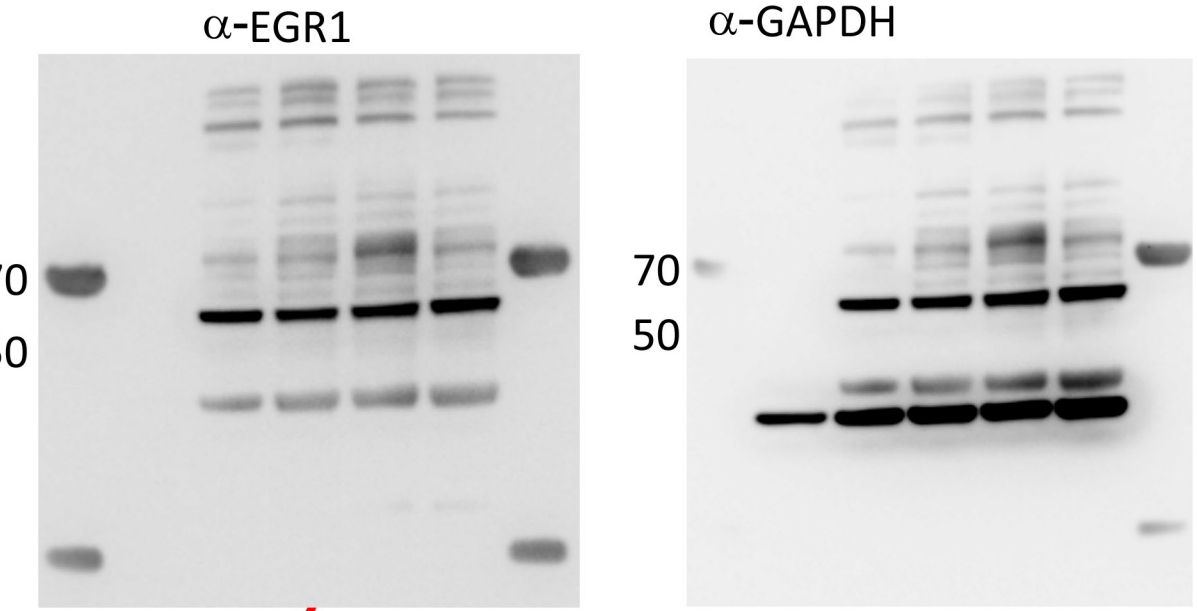
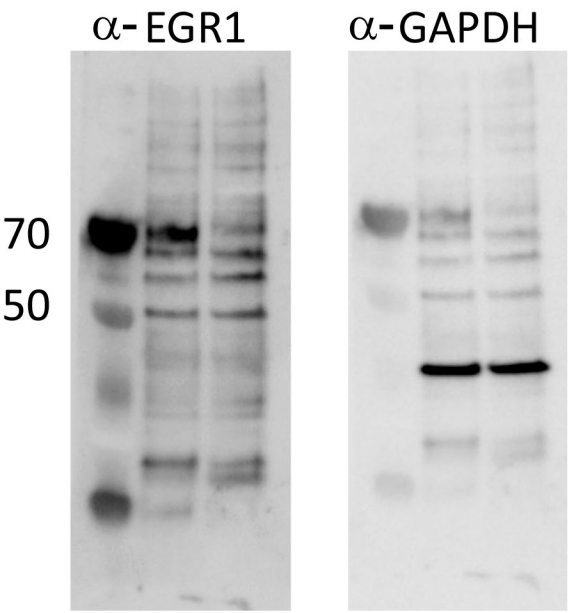


Fig 3a EGR1-KD



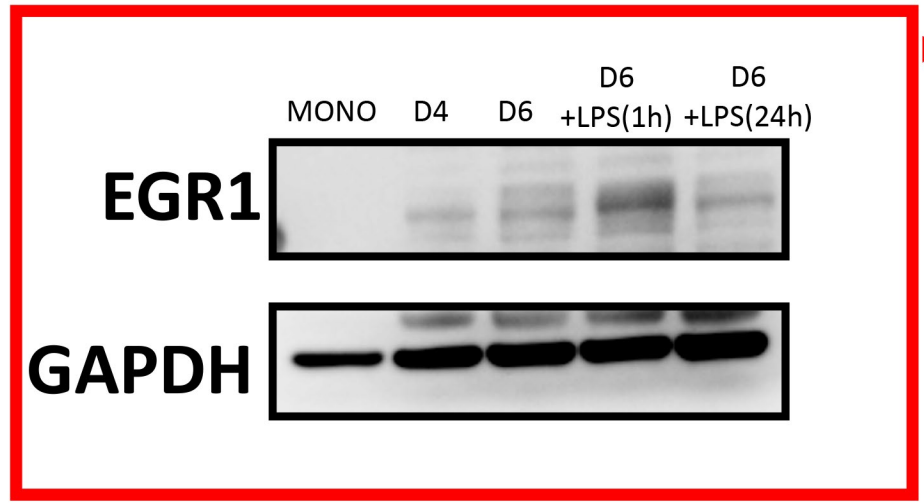
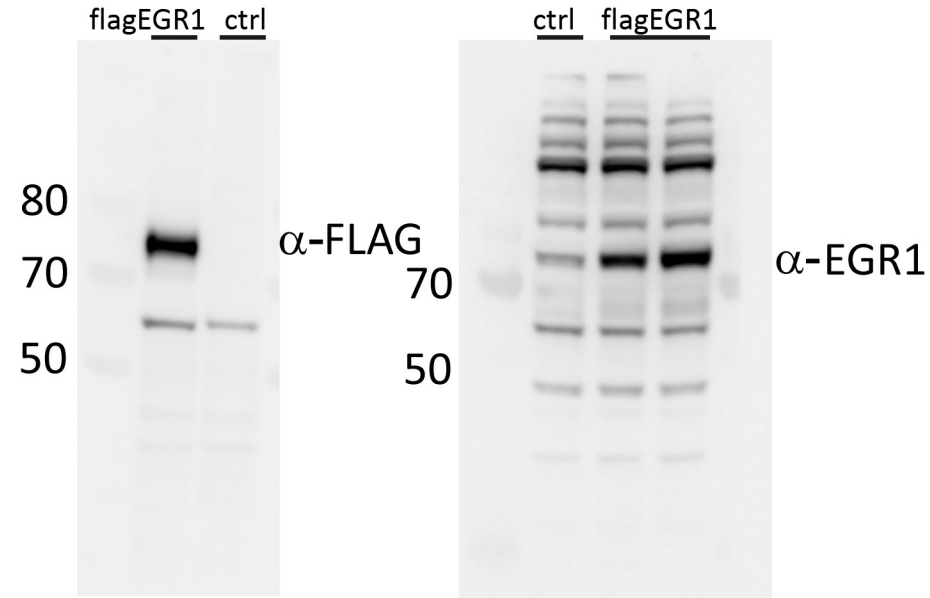


Fig 4b FLAG-EGR1 OVEREXPRESSION



Supplementary Figure S2:
Full membrane western-blots.

Supplementary Figures. Contains Supplementary Fig. S1 and S2

Supplementary File S1. Motif analysis of accessible regions in differentiating macrophages. MEME-ChIP and TOMTOM analysis were performed on newly accessible sites.

Supplementary File S2. Ingenuity Pathway Analysis of EGR1 regulated genes. Differentially regulated genes from shRNA EGR1 cells vs shLUC cells were subjected to the analysis.

Supplementary File S3. Ingenuity Pathway Analysis of EGR1 regulated genes. Differentially regulated genes in macrophages overexpressing EGR1 vs control vector were subjected to the analysis.

Supplementary Table S1. Motifs enriched at different EGR1 binding sites.

Supplementary Table S2. Differential H3K27 acetylation upon EGR1 depletion (EGR1 co-activator sites).

Supplementary Table S3. Differential H3K27 acetylation upon EGR1 depletion (EGR1 co-repressor sites).

Supplementary Table S4. 893 differentially expressed genes by RNA-seq analysis (shEGR1 vs shLUC).

Supplementary Table S5. List of 270 LPS responsive genes in human macrophages.

Supplementary Table S6. List of NGS experiments and replicates performed in this study.

Supplementary Table S7. Oligonucleotides used for qPCR analysis.