

Elongator is required for pattern recognition receptor and type I interferon signaling in macrophages.

Jamie Murphy¹, Marcin Baran¹, Corinna Grünke², Darya Haas², Gillian Barber¹, Andreas Pichlmair^{2, 3, 4} and Andrew G Bowie^{1*}

¹School of Biochemistry and Immunology, Trinity Biomedical Sciences Institute, Trinity College Dublin, Dublin 2, Ireland.

²Institute of Virology, School of Medicine, Technical University of Munich, Munich, Germany.

³Institute of Virology, Helmholtz Center Munich, Munich, Germany

⁴German Centre for Infection Research (DZIF), Partner site Munich, Germany

* Correspondence: agbowie@tcd.ie

Supporting information includes Table S1 and Figures S1-S3.

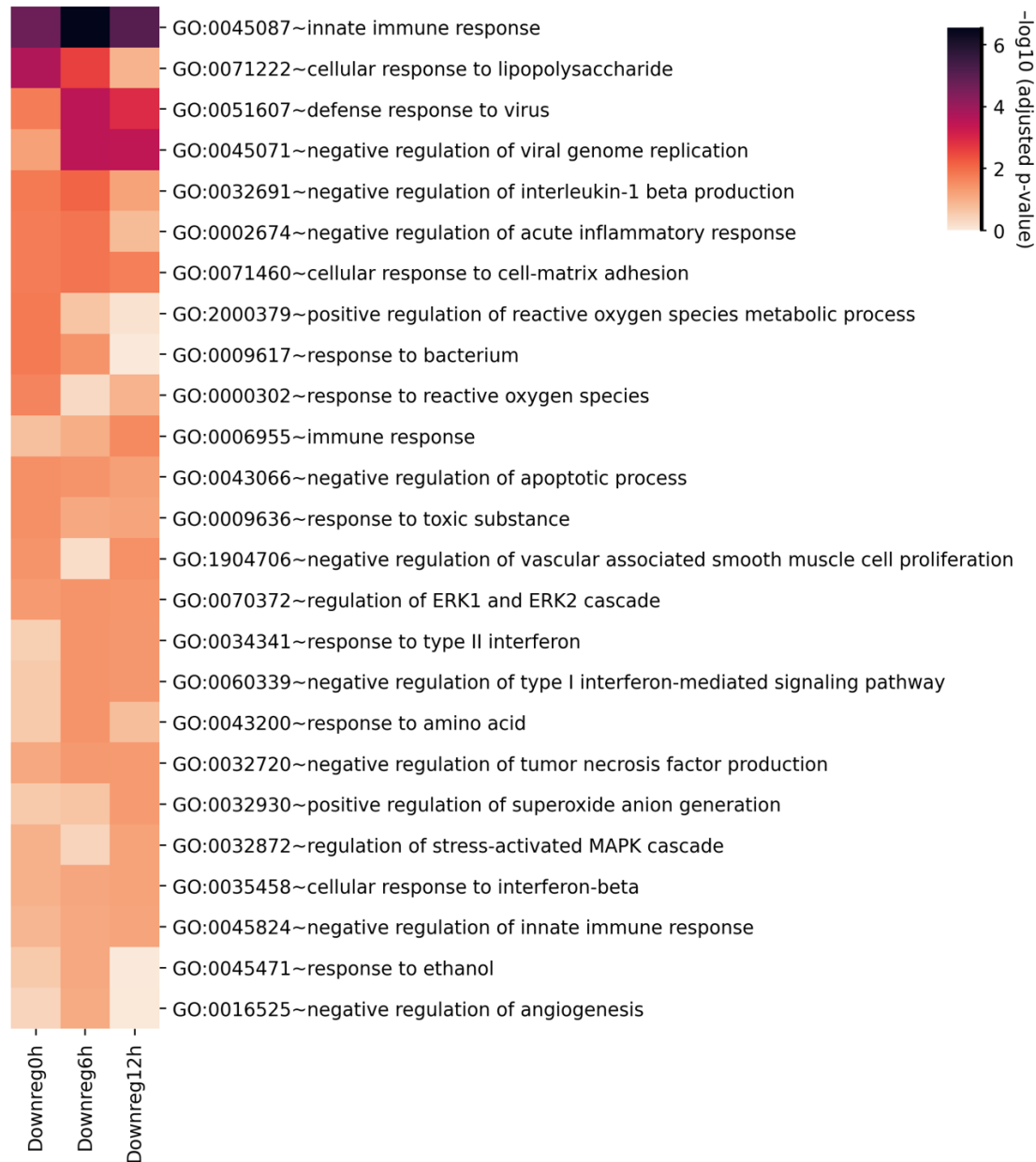


Figure S1. Gene Ontology enrichment analysis for biological processes in *Elp3*^{-/-} compared to WT cells

Gene Ontology (GO) enrichment analysis of biological processes was performed on significantly upregulated or downregulated proteins identified in each comparison: *Elp3*^{-/-} vs. WT at 0 h (mock), 6 h LPS stimulation, and 12 h LPS stimulation. Significant GO terms are visualized as a heatmap. No terms met the significance threshold in the upregulated protein sets; therefore, only results from the downregulated sets are shown.

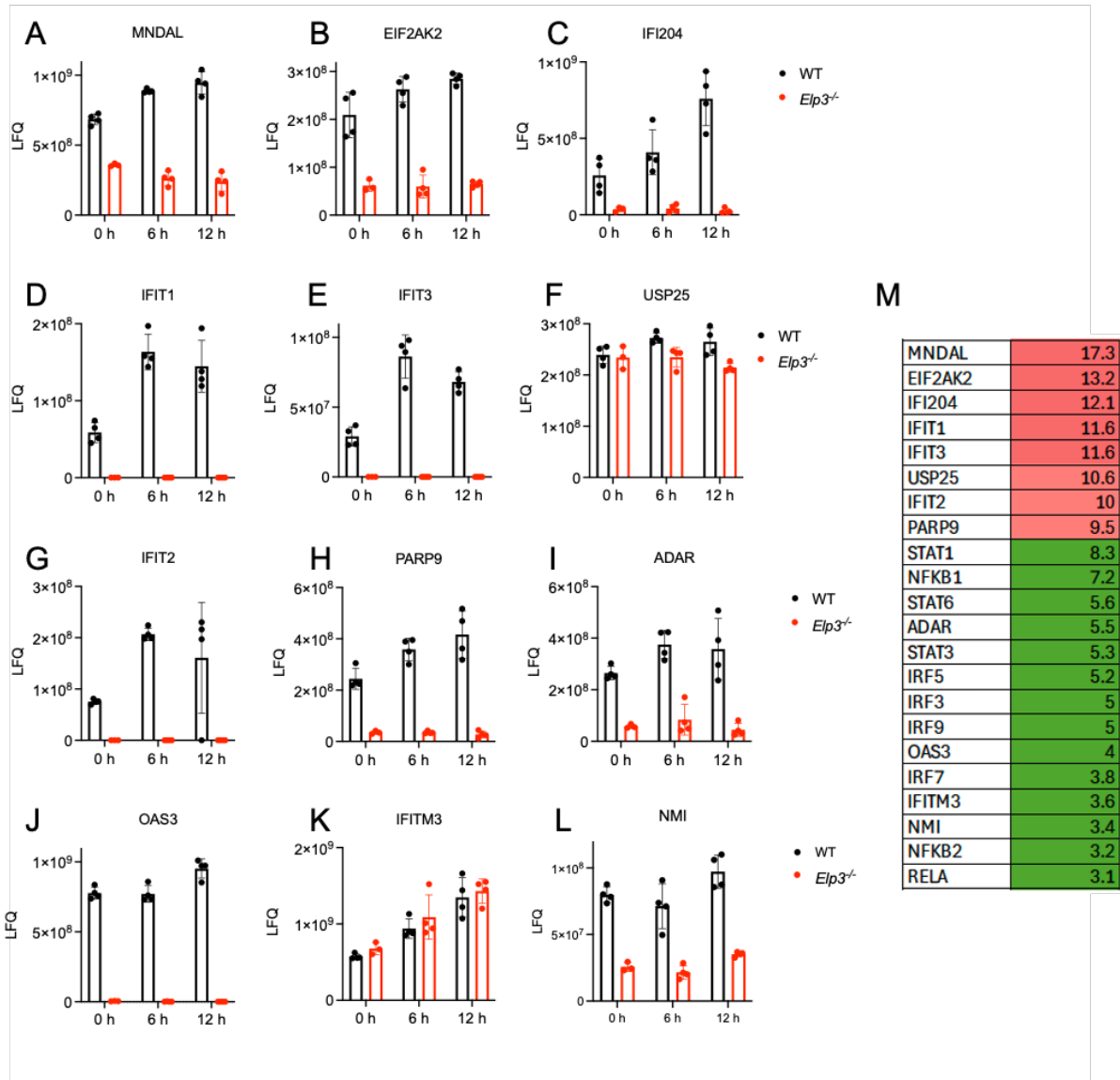


Figure S2. Elongator dependency of ISGs.

(A-L) Label free quantification intensity values detected by mass spectrometry in WT and *Elp3*^{-/-} cells stimulated for 0, 6 or 12 h with LPS for peptides from ISG-encoded proteins MNDAL (A), EIF2AK2 (B), IFI204 (C), IFIT1 (D), IFIT3 (E), USP25 (F), IFIT2 (G), PARP9 (H), ADAR (I), OAS3 (J), IFITM3 (K) and NMI (L). Data are mean ± SD for quadruplicate (or triplicate for WT 0 h sample) measurements. (M) Predicted percentage of ELP-dependent codons (EDCs) for ISGs shown here and transcription factors in Figure 4.

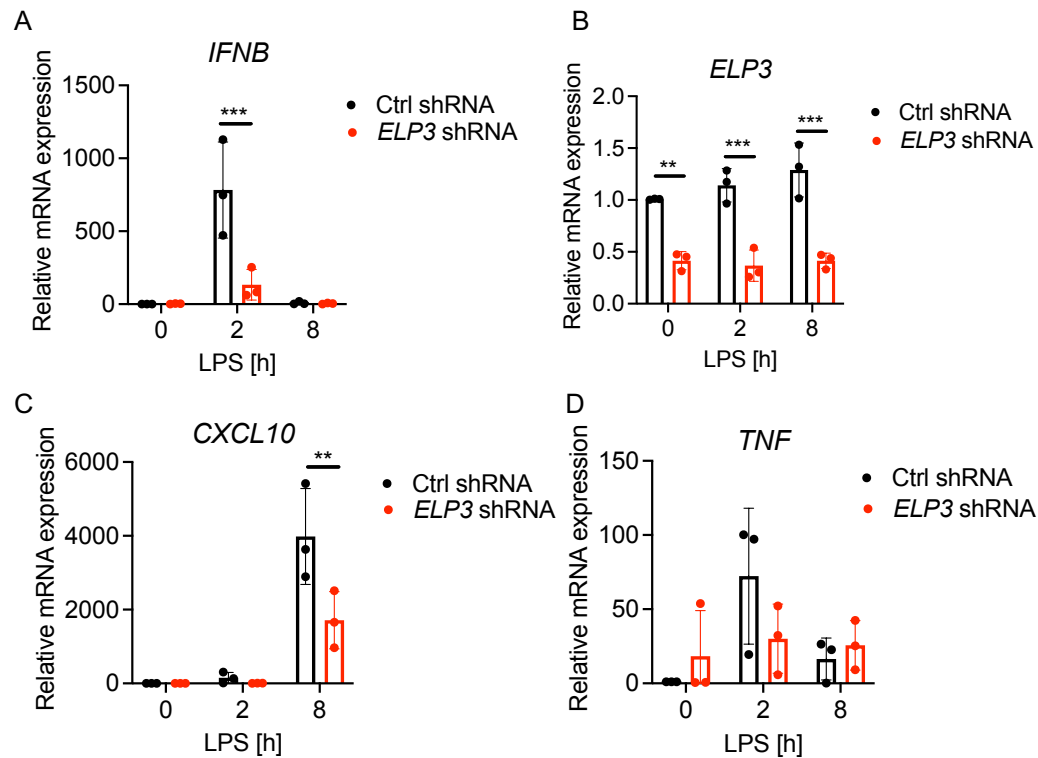


Figure S3 - ELP3 is required for LPS-stimulated IRF3-dependent genes in human THP-1 cells

(A-D) THP1 cells expressing shRNA (control or *ELP3* targeting) were stimulated with 100 ng/ml of LPS for 2 or 8 h. Following stimulation, gene expression of *ELP3* (A), *IFNB* (B), *CXCL10* (C) and *TNF* (D) was measured by real time PCR. Data are mean \pm SD gene expression relative to the unstimulated control (Ctrl) shRNA sample and presented as average of 3 independent experiments, each performed in triplicate. Data significance was tested with a 2-way ANOVA using Šídák's multiple comparisons test. ** p<0.01 and *** p<0.001.