Supporting Information

ELF4 facilitates innate host defenses against *Plasmodium* by activating transcription of *Pf4* and *Ppbp*

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Fig. S1. Elf4 deficiency results in compensatory hemolytic anemia.

Fig. S2. Heat maps of functional groups for up- and down-regulated transcripts in bone marrow and spleens.

Fig. S3. ELF4 targets the promoter of *Pf4* and *Ppbp*

Fig. S4. ELF4 activates transcription of *PF4* and *PPBP*

Table S1. List of oligonucleotide primers used in this study.

Table S2. Gene list and analysis results of bone marrow RNA-seq data.

Table S3. Gene list and analysis results of spleen RNA-seq data.

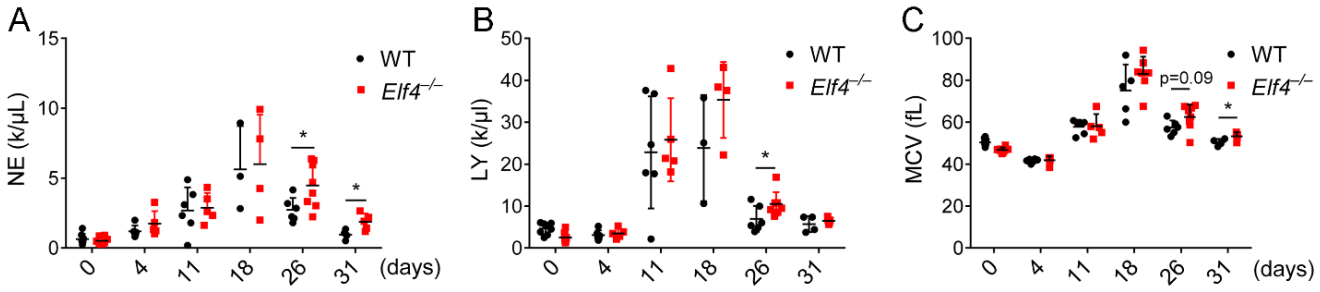

Fig. S1. Elf4 deficiency results in compensatory hemolytic anemia.

(**A**-**C**) Neutrophilicgranulocyte (NE) (**A**), lymphocyte (LY) (**B**), and mean corpuscular volume (MCV) (**C**) were measured and compared between *Elf4*$^{+/+}$ and *Elf4*$^{-/-}$ mice at indicated days post *P. yoelii* 17XNL infection. All data are means ± s.d. from three experiments; *t*-test, *P < 0.05.

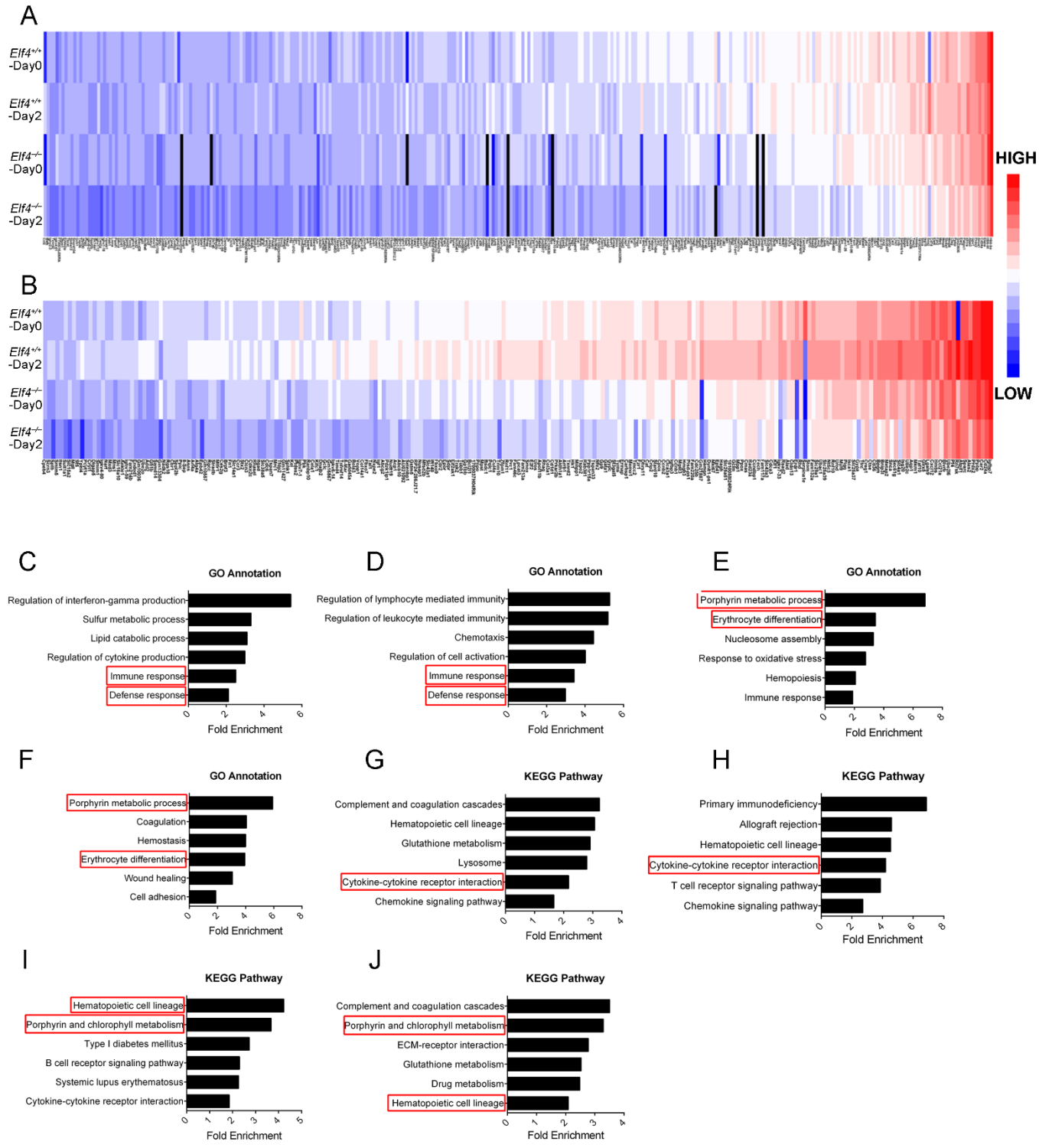

Fig. S2. Heat maps of functional groups for up- and down-regulated transcripts in bone marrow and spleens.

(**A**-**B**) Heat map showing differentially expressed transcripts in bone marrow (**A**) and spleens (**B**) of *Elf4*$^{+/+}$ and *Elf4*$^{-/-}$ mice 2 days after infection with *P. yoelii* 17XNL (1×10^5 infected red blood cells). Uninfected control mice (Day0) were injected with an equivalent amount of uninfected RBC. Columns represent

individual mice, and rows represent differentially expressed genes in *P. yoelii* 17XNL-infected *Elf4*$^{-/-}$ mice compared with *Elf4*$^{+/+}$mice. The color bar indicates relative expression of genes, with red indicating higher expression and blue indicating lower expression. (**C**-**J**) Functional enrichment analysis showing overrepresentation of genes upregulated in mouse bone marrow (**C**, **D**) and spleens (**G**, **H**) after infection with *P. yoelii* 17XNL or downregulated in mouse bone marrow (**E**, **F**) and spleens (**I**, **J**) after infection with *P. yoelii* 17XNL. The notable genes and related biological pathways are highlighted. Technical replication was performed twice independently and data are representative of a single experiment.

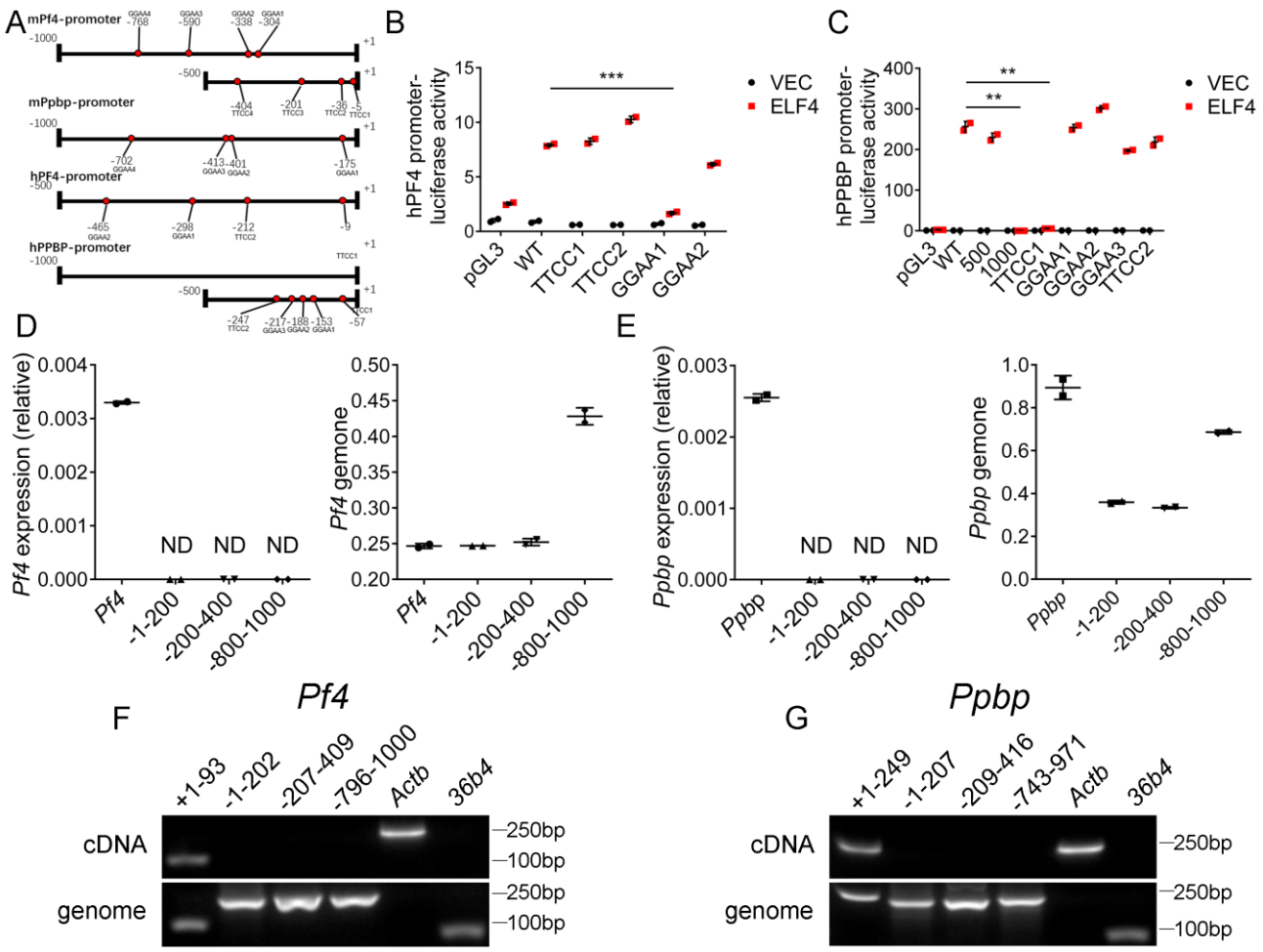

Fig. S3. ELF4 targets the promoter of Pf4 and Ppbp.

(**A**) Illustration of human *PF4* and *PPBP*, mouse *Pf4* and *Ppbp* promoter and their mutants-driven luciferase plasmids constructs. (**B**-**C**) Luciferase activity in HEK293T cells transfected with human *PF4* (**B**) or *PPBP* (**C**) promoter or the different GGAA (or TTCC) -mutated promoters-driven luciferase reporters, together with *Elf4* expression plasmid or empty vectors. (**D**) Relative quantification of +1-93 region and several upstream regions of *Pf4* was assessed by quantitative PCR (qPCR) in mouse megakaryocytes. (**E**) Relative quantification of +1-249 region and several upstream regions of *Ppbp* was assessed by quantitative PCR (qPCR) in mouse megakaryocytes. (**F**) RT-PCR analysis assessing the quantity of +1-93 region and several upstream regions of *Pf4* in total RNA reverse-transcribed cDNA or genome of megakaryocytes. (**G**) RT-PCR analysis assessing the quantity of +1-249 region and several upstream regions of *Ppbp* in total RNA reverse-transcribed cDNA or genome of megakaryocytes. For (**D**) and (**E**), quantity was relative to *Actb* in cDNA and *36b4* in genome. For (**F**) and (**G**), *Actb* primer overlaps the second exon and the first and second intron of *Actb* gene. *36b4* primer was designed within the second intron of mouse *36b4* gene. Thus, *Actb* was a positive control in cDNA but a negative control in genome and *36b4* was a positive control in genome but a negative control in cDNA. All data are means ± s.d. from three independent experiments; *t*-test, **P < 0.01; ***P < 0.001; ND, no detected.

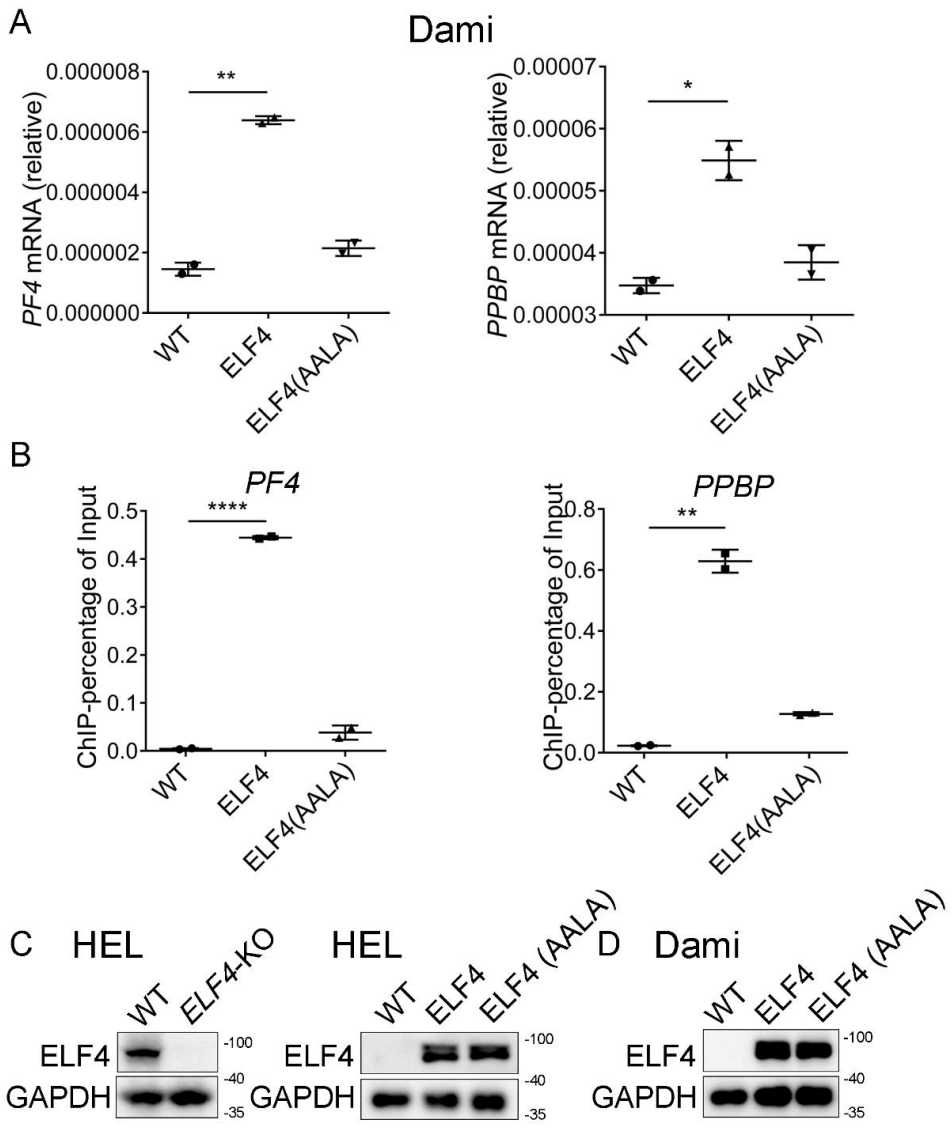

Fig. S4. ELF4 activates transcription of *PF4* and *PPBP*.

(**A**) Expression of *PF4* and *PPBP* in wild-type (WT) Dami cells or Dami cells stably transfected with ELF4 or ELF4 (AALA) was assessed by quantitative PCR (qPCR) analysis. (**B**) Binding ability of ELF4 on *PF4* and *PPBP* promoters was assessed by chromatin immunoprecipitation followed by quantitative PCR (ChIP-qPCR) analysis in WT Dami cells or Dami cells stably transfected with ELF4 or ELF4 (AALA). (**C**-**D**) ELF4 expression in WT and modified HEL cells (**C**) or Dami cells (**D**) was assessed by immunoblot. GAPDH was used as control. Data in (**A**-**B**) are means ± s.d. from three independent experiments; *t*-test, *P < 0.05; **P < 0.01; ****P < 0.0001.

Table S1. List of oligonucleotide primers used in this study.

Gene	Forward (5' to 3')	Reverse (5' to 3')
36b4	TTGTGCAAAGGGCTGAGACT	GTCACTCAACAGCAGCCTGA
Actb	CACTGTCGAGTCGCGTCCA	TGACCCATTCCCACCATCAC
GAPDH	GAAGGTGAAGGTCGGAGTC	GAAGATGGTGATGGGATTTC
Hprt	CATTATGCCGAGGATTTGGA	AATCCAGCAGGTCAGCAAAG
Ifnb1	TCCGAGCAGAGATCTTCAGGAA	TGCAACCACCACTCATTCTGAG
Isg15	GAGCTAGAGCCTGCAGCAAT	AGACCCAGACTGGAAAGGGT
Ifng	AGACAATCAGGCCATCAGCA	TGGACCTGTGGGTTGTTGAC
m*Pf4*	CGCTGCGGTGTTTCGAGG	TCACCTCCAGGCTGGTGA
Pf4(+1-93)	CCTGTATCCTGGGTTTCCGGAC	CTAGGGCTCTTAAGTGCAGGC
h*PF4*	CGAGTTTCCCATCGCACTGA	AGCGCTGGCGAAGGC
m*Ppbp*	TGCCCACTTCATAACCTC	GGGTCCAGGCACGTTTT
Ppbp(+1-249)	AACATAGCAGCAGTGTTCTGG	GGGAAGCAGCCTTCATACTCA
h*PPBP*	TGCAGACTTGTAGGCAGCAA	TGCAAGGCATGAAGTGGTCT
ChIP-*PF4*	CATGCTTCACACACAAAGCCA	TCTCTGCTGTCATCATGCAACT
ChIP-*PPBP*	TTGGGCACAGCTTCAAATGC	TGGCTTCTCATGCCCTGAAG

Table S2. Gene list and analysis results of bone marrow RNA-seq data.

Table S3. Gene list and analysis results of spleen RNA-seq data.