Supplementary Information:

A Non-linear Reverse-engineering Method for Inferring Genetic Regulatory Networks

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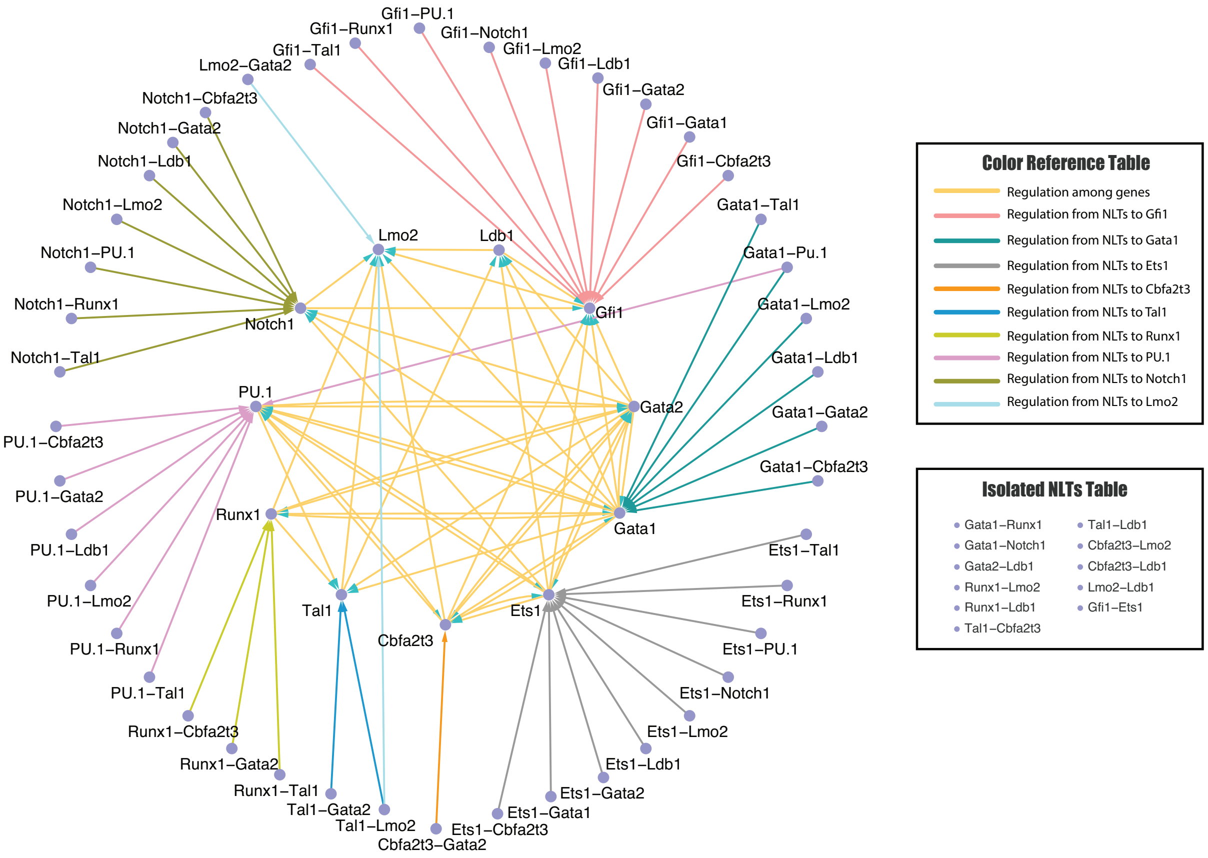
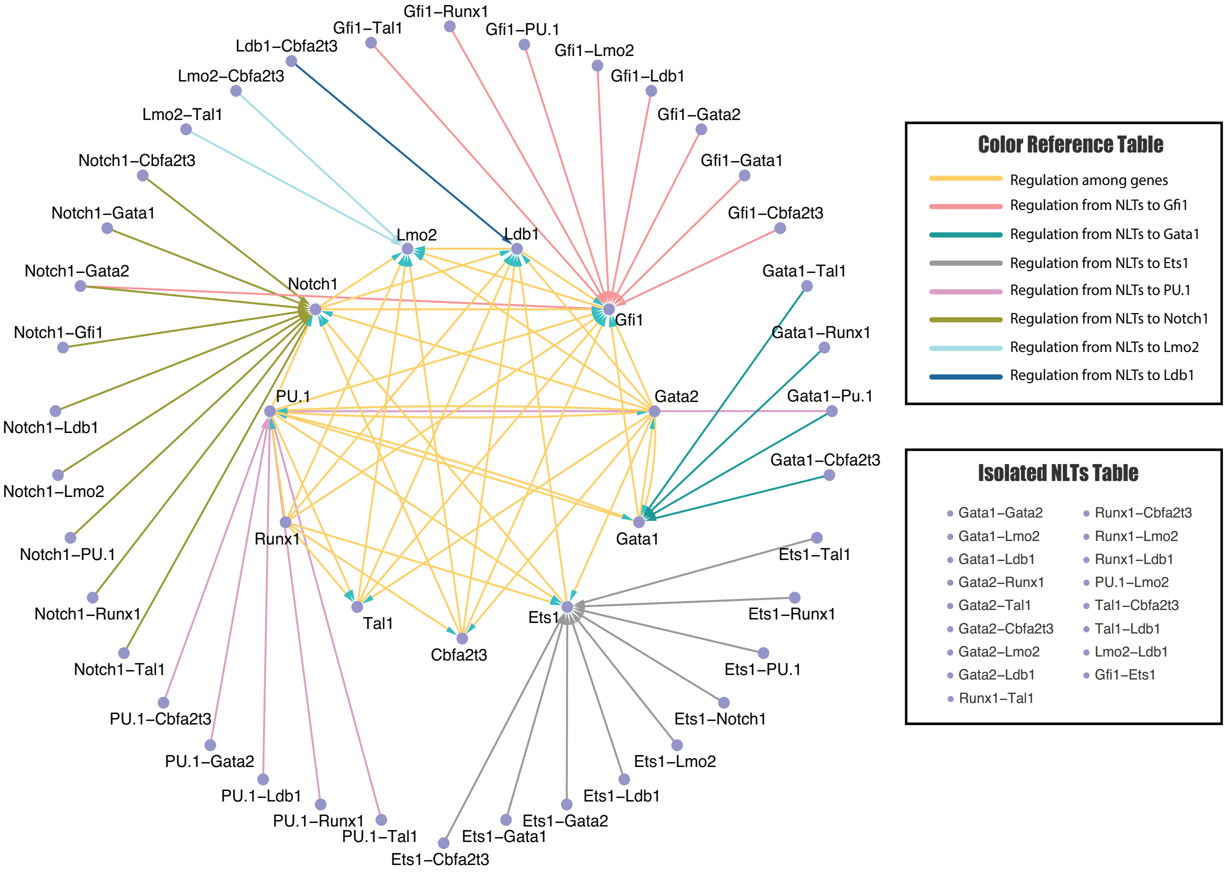
1. Inferred regulatory network for the differentiation of erythrocyte by EFSA



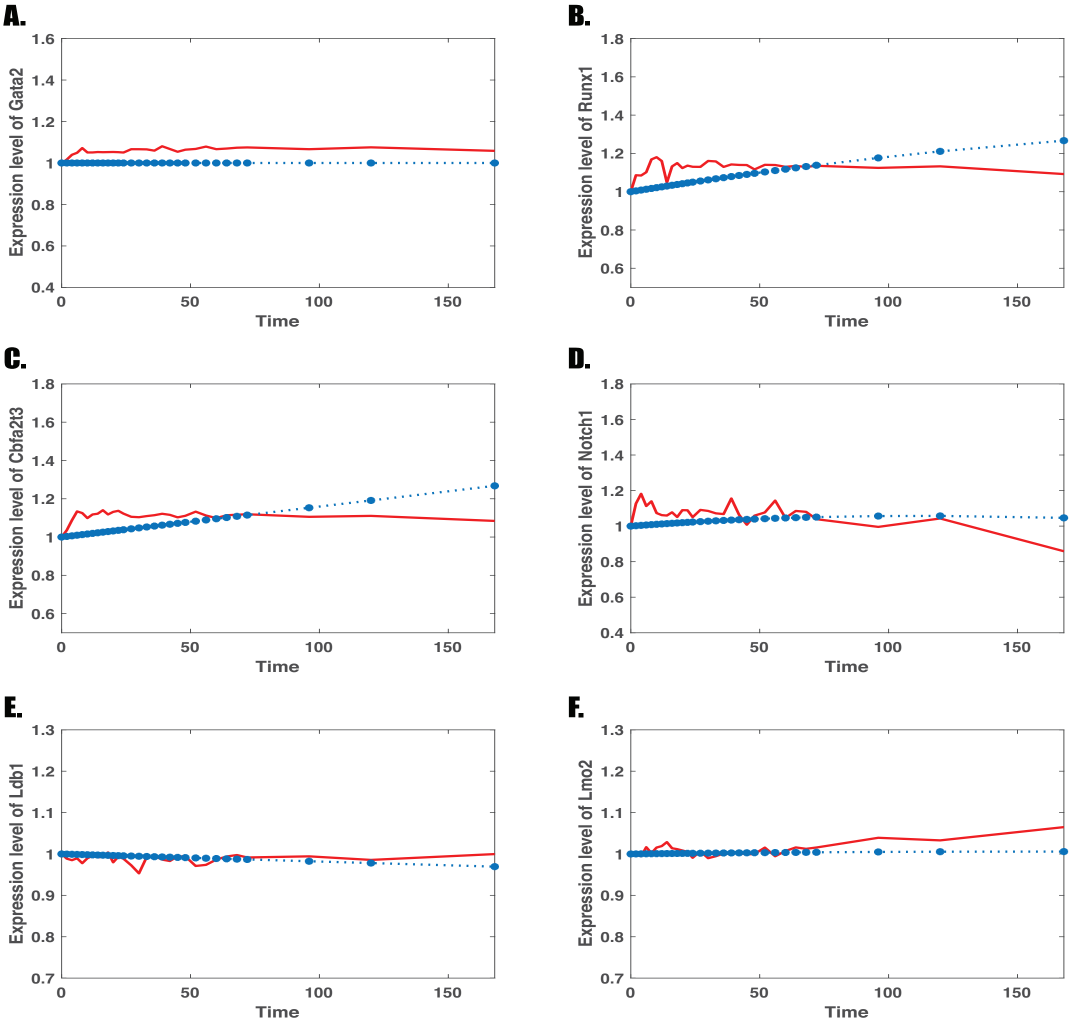
SFigure 1. Inferred network structure before edges deletion. The genetic regulatory network predicted by EFSA with 11 genes and 44 NLTs (11 isolated terms excluded), which is related to the fate determination of erythrocyte pathway: Regulatory network for hematopoietic stem cells differentiate to megakaryocyte-erythroid progenitors. The network is visualized by Cytoscape software.

2. Inferred regulatory network for the differentiation of neutrophil by EFSA



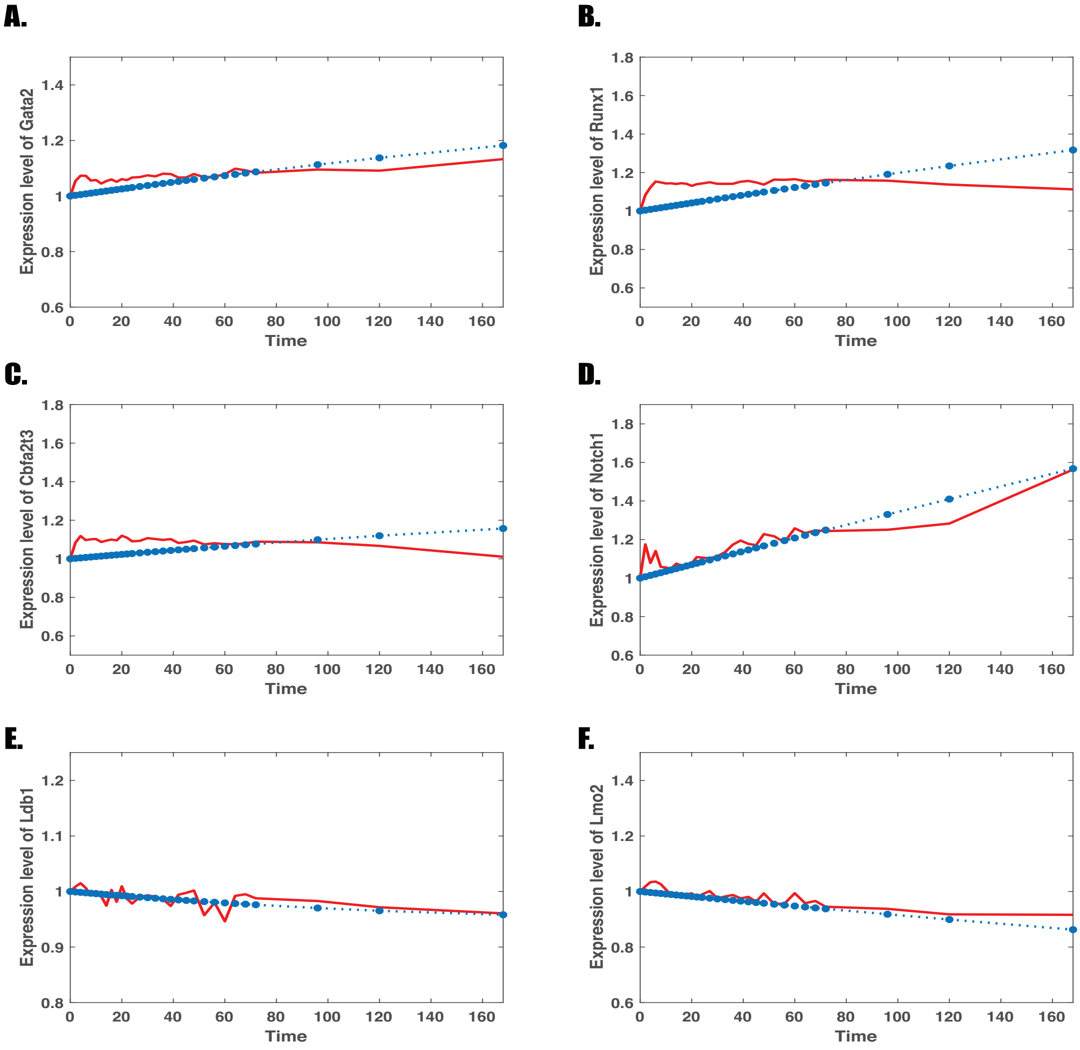
SFigure 2. Inferred network structure before edges deletion. The genetic regulatory networks predicted by EFSA with 11 genes and 38 NLTs (17 isolated terms excluded), which is related to the fate determination of neutrophil pathway: Regulatory network for hematopoietic stem cells differentiate to granulocyte-macrophage progenitors. The network is visualized by Cytoscape software.

3. Simulation results and experimental data of the regulatory network for the erythrocyte differentiation



SFigure 3. Simulation results and experimental data of the regulatory network for the erythrocyte differentiation. (Red solid line: experimental microarray data; Blue star dash line: simulation of the regulatory network).

4. Simulation results and experimental data of the regulatory network for the neutrophil differentiation



SFigure 4. Simulation results and experimental data of the regulatory network for the neutrophil differentiation. (Red solid line: experimental microarray data; Blue star dash line: simulation of the regulatory network).

5. Selection of 30 candidate genes for differentiation of hematopoietic stem cells

STable 1: Information of the 30 candidate genes for differentiation of hematopoietic stem cells. The 30 genes in "This study" are the combination of the genes in two published studies.

Reference Paper	Gene number	Gene name
Moignard et al., 2013, Figure 1	18	Gata1, Gata2, PU.1, Gfi1, Gfi1b, Hhex, Ldb1 Lmo2, Lyl1, Meis1, Mitf, Nfe2, Runx1, Tal1, Etv6, Erg, Cbfa2t3
Moignard et al., 2015, Figure 3	26	Mesi1, Mitf, Etv2, Fli1, Tal1, Gata1, Hoxb4, Lyl1, Notch1, Sox7, PU.1, Ets1, Erg, Nfe2, Cbfa2t3, Lmo2, Myb, Hoxb2, Sox17, Gfi1, Gfi1b, Hhex, Tbx3, Tbx20, FoxH1, Ikaros
This study	30	Gata1, Gata2, PU.1, Gfi1, Gfi1b, Hhex, Ldb1 Lmo2, Lyl1, Meis1, Mitf, Nfe2, Runx1,Tal1, Etv6, Erg, Cbfa2t3, Etv2, Fli1, Hoxb4, Notch1, Sox7, Ets1, Hoxb2, Sox17, Tbx3, Tbx20, FoxH1, Ikaros, Myb

References

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6. Literature review for the selection of 11 important genes

Stable 2. Literature information for the selected 11 genes in this study.

These genes are selected from STable 1 based on their relationship with the three genes Gata1, Gata2 and PU.1. The details of information is also described in the Methods section of the paper. Here is the the summary table.

Gene Name	Reference
Gata1	Friedman, 2007; Liew et al., 2006; Ling et al., 2004
Gata2	Friedman, 2007; Liew et al., 2006; Ling et al., 2004
PU.1	Friedman, 2007; Liew et al., 2006; Ling et al., 2004
Runx1	North et al., 2004
Cbfa2t3	Goardon et al., 2006
Ets1	Lulli et al., 2006
Notch1	Kumano et al., 2001; Stier et al., 2002
Tal1	Goardon et al., 2006; Shivdasani et al., 1995; Zhang et al., 2005; Porcher et al., 1996; Real et al., 2012
Ldb1	Soler et al., 2010; Li et al., 2011
Gfi1	North et al., 2004; van der Meer et al., 2010; Lancrin et al., 2012
Lmo2	Inouea et al., 2013; Visvader et al., 1997

References

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