

# In Silico Gene Regulatory Network of the Maurer's Cleft Pathway in *Plasmodium falciparum*



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**ABSTRACT:** The Maurer's clefts (MCs) are very important for the survival of *Plasmodium falciparum* within an infected cell as they are induced by the parasite itself in the erythrocyte for protein trafficking. The MCs form an interesting part of the parasite's biology as they shed more light on how the parasite remodels the erythrocyte leading to host pathogenesis and death. Here, we predicted and analyzed the genetic regulatory network of genes identified to belong to the MCs using regularized graphical Gaussian model. Our network shows four major activators, their corresponding target genes, and predicted binding sites. One of these master activators is the serine repeat antigen 5 (SERA5), predominantly expressed among the SERA multigene family of *P. falciparum*, which is one of the blood-stage malaria vaccine candidates. Our results provide more details about functional interactions and the regulation of the genes in the MCs' pathway of *P. falciparum*.

**KEYWORDS:** Maurer's cleft, gene regulatory network, *Plasmodium falciparum*, graphical Gaussian model

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## Introduction

The existence of multiple-stained structures known to be Maurer's clefts (MCs) in the cytosol of erythrocytes derived from patients with *Plasmodium falciparum* malaria using light microscopy was first detected by George Maurer.<sup>1-3</sup> For over a century, the functions of the MCs remained obscure.<sup>4</sup> In the last decade, scientists have been interested in the mediatory role the MCs play in protein transportation from the cytoplasm of *P. falciparum* to the surface of the erythrocyte of the host, which they consider an unconventional and intriguing biological procedure.<sup>5,6</sup>

Upon evasion, *P. falciparum* totally recasts the infected human red blood cells to access nutrients and to elude the immune system.<sup>7</sup> The erythrocytes have no secretory systems that the parasite can subvert. As such, it evolves trafficking pathways for the export of macromolecules.<sup>8</sup> More than 10% of all the parasite's proteins (>400 proteins) are smuggled to the cytosol of its host.<sup>7,9</sup> The transported proteins induce extreme structural adjustment to the red blood cell, such as increasing the toughness of the cell of its host and the development of lumps. This in turn makes the affected cells adhere to the endothelium, hence leading to the development of malaria.<sup>8,10,11</sup> Reports also show that MCs are created at various portions in the life cycle of the parasite, and this affirms their relevance to parasite development and survival.<sup>4</sup>

Computationally, only about one-third of the transcription factors (TFs) expected of the genome of the size of *P. falciparum* are known, while the knowledge of the corresponding binding sites is lacking. A few works have experimentally validated motifs in the parasite, but their binding proteins are unknown. Others have identified some transcription-associated proteins, but very little is known about their binding sites.<sup>12-15</sup> This study is an attempt to identify novel transcriptional regulators (master activators/inhibitors) of the MC pathway in *P. falciparum* by predicting its gene regulatory network (GRN) from gene expression data.

**Gene regulatory networks.** Gene networks depict transcriptional regulation, ie, how genes respond to signals.<sup>16</sup> GRNs simply show how and when genes in a cell interact with each other. GRNs expressly depict the causality of developmental processes.<sup>17</sup> Several methods exist for the modeling and simulation of GRNs from high throughput experimental data, such as expression profiles, genomic sequences, and TF-binding site assays. These include, but are not limited to, Boolean models,<sup>18,19</sup> Petri net models,<sup>20,21</sup> neural network models,<sup>22,23</sup> ordinary differential equation models,<sup>24,25</sup> Bayesian network (BN) models,<sup>24</sup> relevance/association networks,<sup>26</sup> and graphical Gaussian models (GGMs).<sup>27-29</sup>



A commonly used computational method in modeling GRNs is to compute the Pearson correlation coefficients ( $r$ ) between all possible combinations of the genes of interest. Any of such combinations having Pearson correlation coefficients above a predefined threshold is considered to be significant, ie, exhibit useful relationships, influence, or dependence.<sup>27</sup> Such networks are referred to as relevance/association networks. It is important to note that they may lead to vague results, particularly if it is a dense system of connections.<sup>30</sup>

BNs are classified as probabilistic graphical models.<sup>31</sup> BNs are also a type of directed acyclic graphs that are other types of graphical model structures. BNs and its extensions have been used extensively to predict regulatory networks.<sup>32–38</sup> However, there are drawbacks with using BNs for modeling GRNs. Some drawbacks include the difficulty in dealing with time series data, ie, higher number of genes compared to sample size, and inability to capture feedback regulation/loops that are normal in real-life gene networks and are nondeterministic polynomial-time hard learning problems.<sup>39–41</sup> The implementation of dynamic BNs also has some drawbacks, including excessive computing time, result precision largely dependent on quantity of genes, and requirement of more prior information of the transcription regulation.<sup>5,41–43</sup>

GGM is a preferred alternative. It uses partial correlation (pcor) to ensure a rich appraisal of a direct relationship between any combinations of genes.<sup>44,45</sup> Unlike Pearson correlation, pcor of two genes calculates the amount of correlation left after eliminating the influence of other genes. Previous works have established that GGMs are very effective in inferring conditional dependency and modeling interactions among genes.<sup>27,45–49</sup> Earlier, predicting network interactions using GGM had been limited to data sets with fewer genes due to the fact that gene expression experiments had few samples ( $n$ ), which are usually very less compared to the amount of genes ( $P$ ).<sup>45,46</sup> This scenario is referred to as small sampling problem, ie,  $P \gg n$  cannot be accommodated by standard GGM.<sup>49,50</sup> One possibility of resolving this problem is by using the regularized GGM approach proposed by Schäfer and Strimmer.<sup>48</sup> This approach is referred to as the shrinkage approach that is suited to cases where the number of genes is slightly larger than the number of samples.<sup>51,52</sup> In order to introduce directionality into the network, as GGMs are essentially undirected networks displaying only direct linear relationships, Opgen-Rhein and Strimmer<sup>53</sup> introduced an extension of the shrinkage approach to graphical Gaussian modeling, which they referred to as causation networks. We have used this regularized directed GGM, as implemented in the GeneNet R package, to build a gene network for MC pathway of *P. falciparum* based on gene expression profiles.

## Materials and Methods

**Microarray data.** Gene expression data with accession number GSE24416 were downloaded from the Gene Expression Omnibus (GEO) database ([www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/),

accessed 11/02/2015). The experiment was done by Foth et al.<sup>54</sup> The 24 time point samples were harvested from a tightly synchronous 6.5-L biofermenter culture of *P. falciparum* (Dd2) at two-hour intervals during one entire (48 hours) intraerythrocytic developmental cycle and compared against a 3D7 RNA reference pool.

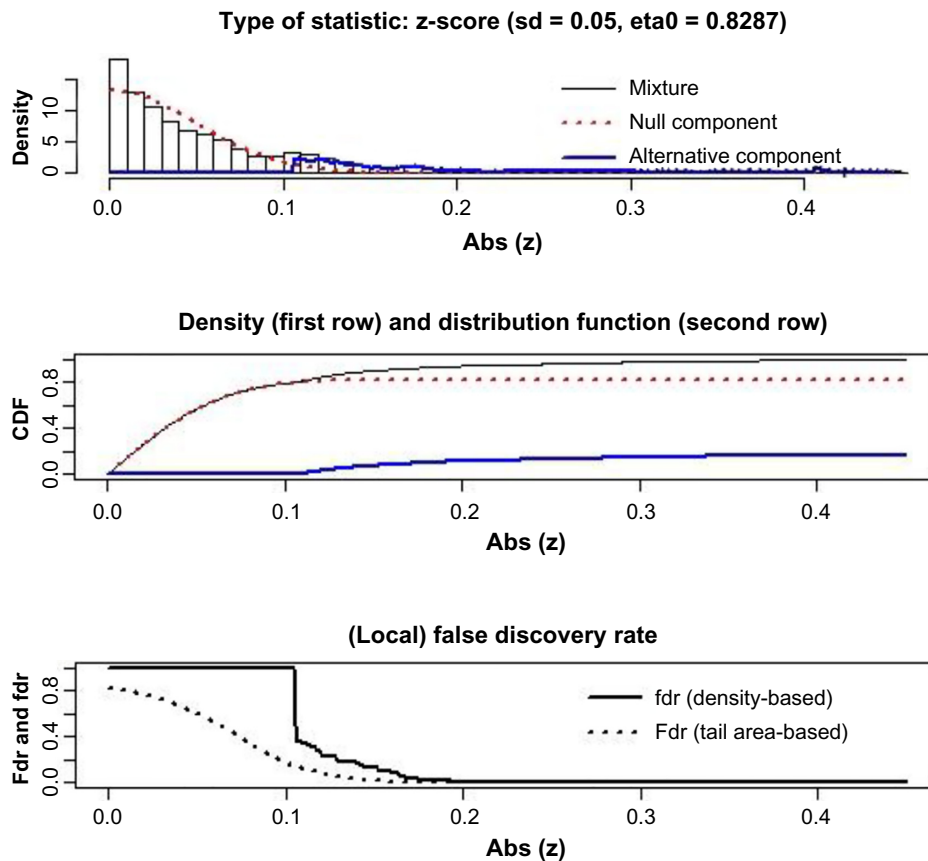
**MC pathway proteins of *P. falciparum*.** Genes that belong to the MCs' pathway were downloaded from PlasmoDB version 13.0 (<http://plasmodb.org>, accessed 11/02/2015). Nine pathways concerned with the MCs, based on the classification from Hagai Ginsburg's Malaria Parasite Metabolic Pathways database (at <http://mpmp.huji.ac.il/>), were used for this study. They include "Biogenesis of Maurer's clefts" – 3 genes, "Characteristics of *Plasmodium falciparum* export proteins that remodel infected erythrocytes" – 41 genes, "Established and putative Maurer's clefts proteins" – 134 genes, "Exported parasite proteins associated with Maurer's clefts" – 11 genes, "Genes coding for protein traffic related proteins" – 61 genes, "Maurer's clefts" – 7 genes, "Properties of proteins exported to erythrocyte" – 39 genes, "Subcellular location of exported proteins" – 43 genes, and "Subcellular localization of proteins involved in invasion" – 81 genes. Expression values were found for 319 of them from the gene expression data set used. The list of genes used for this study with their gene IDs is provided in Supplementary File S01.

**Network construction.** All analyses were done in R version 3.1.1 ([www.R-project.org](http://www.R-project.org)), Bioconductor version 2.14,<sup>55</sup> and RStudio version 0.98.978.<sup>56</sup> The following R packages were used for the network modeling: GEOquery version 2.30.1 to load the gene expression data from GEO database directly into R<sup>57</sup>; GeneNet version 1.2.12 to model the GRN<sup>58</sup>; Graphviz version 2.38,<sup>59</sup> dnet version 1.0.7,<sup>60</sup> venerable version 3.0,<sup>61</sup> and igraph version 0.7.1<sup>62</sup> for network visualization; and BCRANK version 1.26.0.<sup>63</sup> The detailed computational pipeline used for the analyses is presented in Supplementary File S02. The R source code for the analyses is provided in Supplementary File S03.

## Results

The dynamic shrinkage approach as implemented in the GeneNet<sup>58</sup> R package was used to estimate the pcor matrix of all possible edges. The resulting pcor network had 50,721 edges connecting 319 nodes with pcor values ranging from  $-0.20$  to  $+0.213$ . The density function, distribution function, and local false discovery rate (FDR) values are shown in Figure 1.

Our approach favored the edges with lower pcor values. This is because pcors having the lowest absolute values mean they have the largest amount of effects after other genes have been removed. We extracted edges whose  $|pcor|$  is  $\geq 0.04$ . This resulted in 1160 edges out of 50,721 edges. The Pearson correlation coefficient ( $r$ ) was estimated for these edges and used to further prune the network by eliminating edges with  $-0.60 \leq r \leq 0.60$  as any  $r$  close to 0 indicates independence.



**Figure 1.** Plot of the density function, distribution function, and local FDR values. The null distribution is depicted by the dashed line; it follows a normal distribution with 0 mean and a standard deviation of 0.05. The solid line signifies the alternative distribution. The empirical distribution (indicated by the histogram) is composed of the null distribution and the alternative distribution.

This left us with 178 edges. We then selected the top 100 edges (sorted according to the absolute strength of the correlation from the strongest to the weakest), representing  $\sim 0.2\%$  of all possible edges as significant edges. The resulting GRN of the MCs' pathway is shown in Figure 2. The complete significant edge list with their pcor coefficients, Pearson correlation coefficients,  $P$ -values,  $q$ -values, and FDR values is presented in Supplementary File S04.

From this network, we estimated the out-degree of the participating nodes to identify hubs. The hubs are major players in the network (master activation/master inhibitors). Our hypothesis here is that these genes are possibly playing a key role in the regulation of the pathway, ie, the protein trafficking activities of the parasite, and should be further investigated. From our analysis, four genes had the highest number of direct connections in the network: PFL0780w, PFB0340c, MAL7P1.92, and PF08\_0002. We extracted the subnetworks of the genes. Our hypothesis is that these genes are the possible target genes of the respective hub genes. The subnetworks are shown in Figure 3A–D.

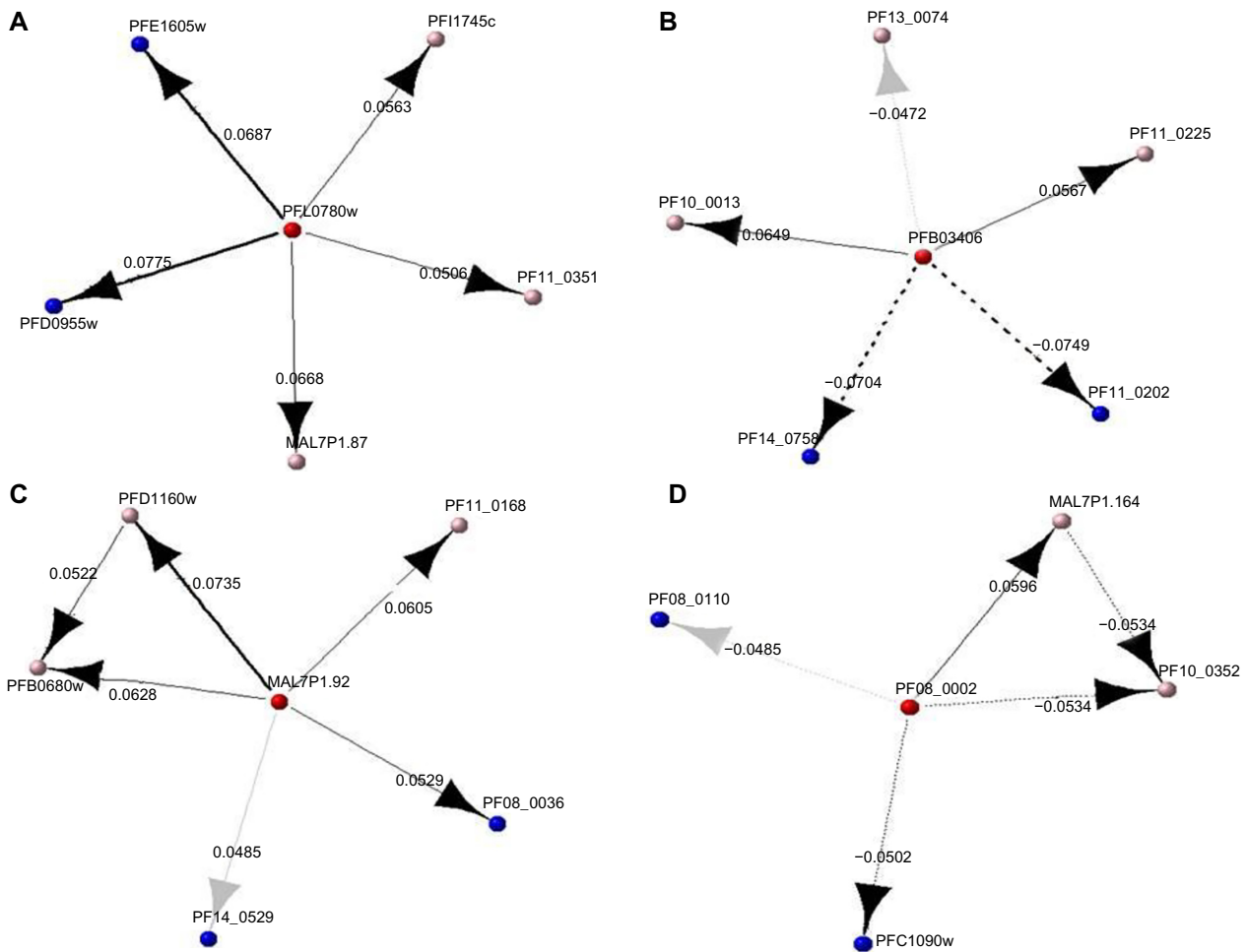
**Predicting binding sites.** We extracted 1000 bp upstream of transcription start site for the target genes identified for each master activator from PlasmoDB in FASTA format. The sequences in each group were ranked (arranged

according to the strength of correlation with their master activator. We then used the methods implemented in the R package BCRANK to find the overrepresented motifs in the upstream sequences. BCRANK is useful for predicting binding site consensus for ranked DNA sequences. See the package manual for more details on the BCRANK algorithm.<sup>52</sup> A number of predictions resulted from the running of this algorithm, and the first motif was selected as the candidate motif as it is the most statistically significant motif. Details on the resulting motifs for each set are provided in Supplementary File S05.

## Discussion

Our results show four major players that we hypothesized to play important roles in the regulation of activities in the MCs. The first is PFL0780w; from our network, we predicted the following target genes: PFD0955w, PFE1605w, MAL7P1.87, PFI1745c, and PF11\_0351. The first two have the motif ACATGTAA overrepresented in their upstream sequence that we predicted to be the binding site of the TF. PFL0780w was reported by the ontology-based pattern identification database to be involved in translational regulator activity and tRNA metabolic process, which is in line with our predictions. From life cycle expression data (combined





**Figure 3.** Subnet for the master activators/repressors with their target genes. The red nodes are the predicted TFs, while the blue nodes are the predicted target genes that share an overrepresented motif in their promoter region (predicted binding site) and the pink nodes are predicted target genes that do not share the motif but have a direct interaction from the predicted regulatory network in Figure 2: (A) subnetwork for PFL0780w, (B) subnetwork for PFB0340c, (C) subnetwork for MAL7P1.92, and (D) subnetwork for PF08\_0002.

**Table 1.** Full details of the predicted TFs and their target genes.

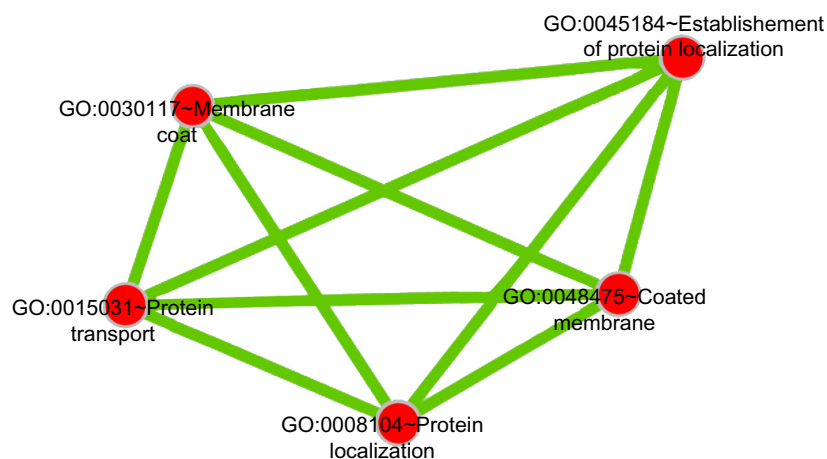
TRANSCRIPTION FACTOR	TARGET GENES	GENE NAME	PRODUCT DESCRIPTION	ANNOTATED GO FUNCTION TERM	ANNOTATED GO PROCESS TERM
<b>PFL0780w</b>			Glycerol-3-phosphate dehydrogenase, putative	NAD binding, glycerol-3-phosphate dehydrogenase [NAD+] activity, protein homodimerization activity	Carbohydrate metabolic process, glycerol-3-phosphate catabolic process, glycerol-3-phosphate metabolic process, oxidation-reduction process
	PFD0955w	<i>Pf34</i>	Apical merozoite protein (Pf34)		
	PFE1605w	<i>LyMP</i>	Lysine-rich membrane-associated PHISTb protein (LyMP)	Protein binding	
	MAL7P1.87		Conserved Plasmodium protein, unknown function	ATP binding, actin binding, calmodulin binding, motor activity	
	PFI1745c		Early transcribed membrane protein		
	PF11_0351	<i>HSP70-3</i>	Heat shock protein 70 (HSP70-3)	ATP binding, unfolded protein binding	Protein folding, response to heat, response to unfolded protein
<b>PFB0340c</b>		<i>SERA5</i>	Serine repeat antigen 5 (SERA5)	Cysteine-type peptidase activity	Immunoglobulin production, proteolysis, regulation of immune response

(Continued)



Table 1. (Continued)

TRANSCRIPTION FACTOR	TARGET GENES	GENE NAME	PRODUCT DESCRIPTION	ANNOTATED GO FUNCTION TERM	ANNOTATED GO PROCESS TERM
	PF11_0202		AP-4 complex subunit mu, putative	Protein binding	Intracellular protein transport, vesicle-mediated transport
	PF14_0758	<i>PTP3</i>	EMP1-trafficking protein (PTP3)		
	PF10_0013		Plasmodium exported protein (hyp12), unknown function (PfJ13)		
	PF11_0225	<i>GCN20</i>	Protein GCN20 (GCN20)	ATP binding, ATPase activity, coupled to transmembrane movement of substances	Regulation of translation, transport
	PF13_0074	<i>SURF13.1</i>	Surface-associated interspersed protein 13.1 (SURFIN 13.1), pseudo-gene (SURF13.1)		
<b>MAL7P1.92</b>		<i>CRMP2</i>	Cysteine repeat modular protein 2 (CRMP2)	Protein binding	Intracellular receptor mediated signaling pathway, intracellular transport
	PFD1160w	<i>SURF4.2</i>	Surface-associated interspersed protein 4.2 (SURFIN 4.2) (SURF4.2)		
	PFB0680w	<i>RON6</i>	Rhoptry neck protein 6 (RON6)		Entry into host
	PF11_0168	<i>RON4</i>	Rhoptry neck protein 4 (RON4)		
	PF08_0036	<i>SEC23</i>	Protein transport protein SEC23 (SEC23)	Zinc ion binding	ER to Golgi vesicle-mediated transport, intracellular protein transport
	PF14_0529		AP-1 complex subunit gamma, putative	Binding, protein transporter activity	Intracellular protein transport, vesicle-mediated transport
<b>PF08_0002</b>		<i>SURF8.2</i>	Surface-associated interspersed protein 8.2 (SURFIN 8.2) (SURF8.2)	Binding, protein transporter activity	
	MAL7P1.164		AP-4 complex subunit beta, putative	Binding, protein transporter activity	Intracellular protein transport, vesicle-mediated transport
	PF10_0352	<i>MSP11</i>	Merozoite surface protein (MSP11)		
	PFC1090w	<i>EPF4</i>	Exported protein family 4 (EPF4)		
	PF08_0110	<i>RAB18</i>	Ras-related protein Rab-18 (RAB18)	GTP binding, GTPase activity	GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, regulation of vesicle-mediated transport, small GTPase mediated signal transduction



**Figure 4.** Enrichment analysis map of all predicted TFs and their target genes for the MCs' pathway at a significant level of  $P = 0.001$  and  $q = 0.05$ . The enrichment map gives a graphical representation of the GO terms that were found to be significantly overrepresented in the context of the GO hierarchy.



membrane coat, protein localization, coated membrane, and establishment of protein localization.

## Conclusion

We have successfully predicted the GRN of a very important pathway in the deadly malaria parasite *P. falciparum*. A number of predictions have been made from our analyses that should be further validated experimentally. Our results have also confirmed findings from previous studies and yielded new information, which shed more light and help improve our understanding of the genetic regulation activities of *P. falciparum* in our quest to fully overcome the malaria endemic. The knowledge of the predicted TFs, their target genes, and their predicted binding sites will indeed increase our understanding of the mechanism that underlay the tight transcriptional control of *P. falciparum* and also help in the rational design of promoters to ease the study of essential genes of the parasite.

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## Author Contributions

All authors contributed to this work. Original idea and conception: II, JO, BB, EA. Implementation of research methods: II. Writing and revision of the manuscript: II, JO. All authors reviewed and approved the final manuscript.

## Supplementary Material

**Supplementary File S01.** Gene\_list.txt.

**Supplementary File S02.** Computational pipeline.pdf.

**Supplementary File S03.** MC-GRN\_sourcecode.R.

**Supplementary File S04.** Filtered\_network.xlsx.

**Supplementary File S05.** Motifs.txt.

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