The impact of Iso-mukaadial acetate on *Plasmodium falciparum* transcriptional gene regulation

Supplementary data

Figure Section:

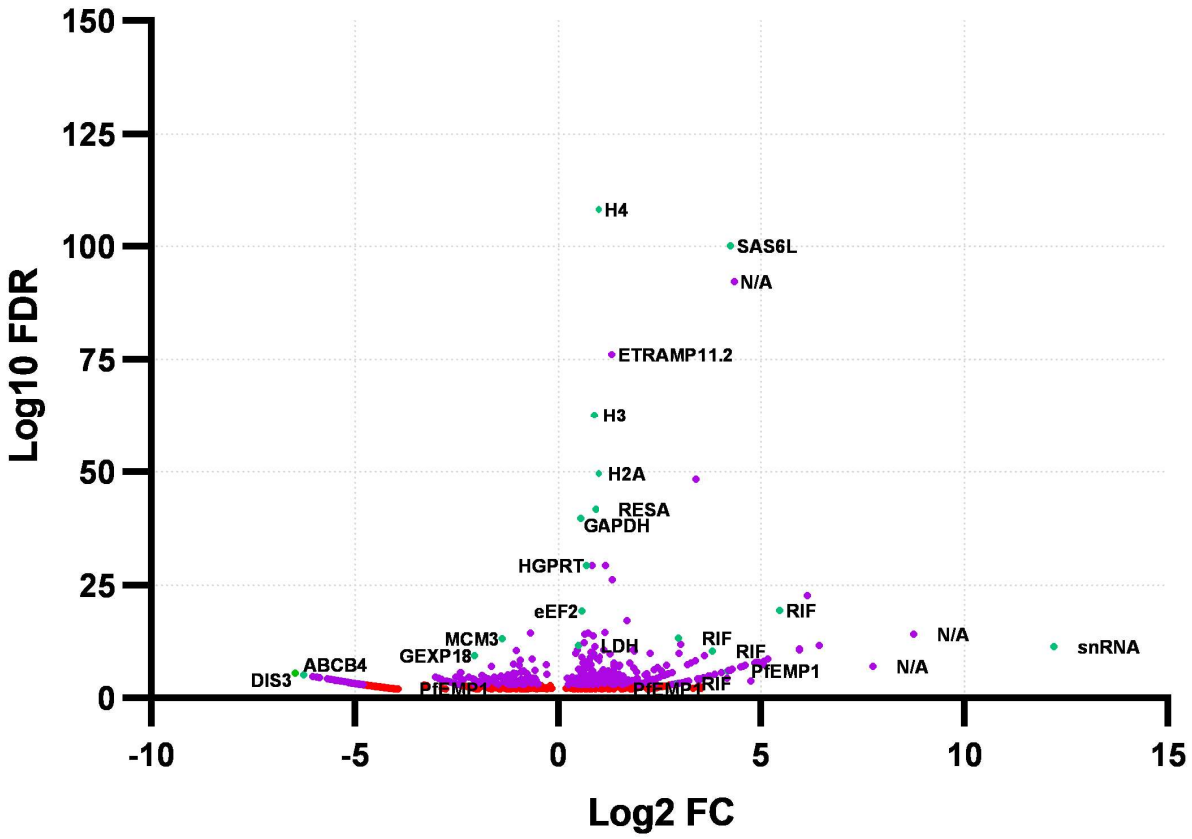

Figure S1 An enhanced volcano plot of CQ-induced P. falciparum genes during the intraerythrocytic stage. Log_2FC represents the differentially expressed genes plotted against $-Log_{10}$ FDR denoting significant genes. A false discovery rate (FDR) of 0.001 was selected to determine the most statistically significant genes. More significant Plasmodium genes were upregulated compared to those downregulated.

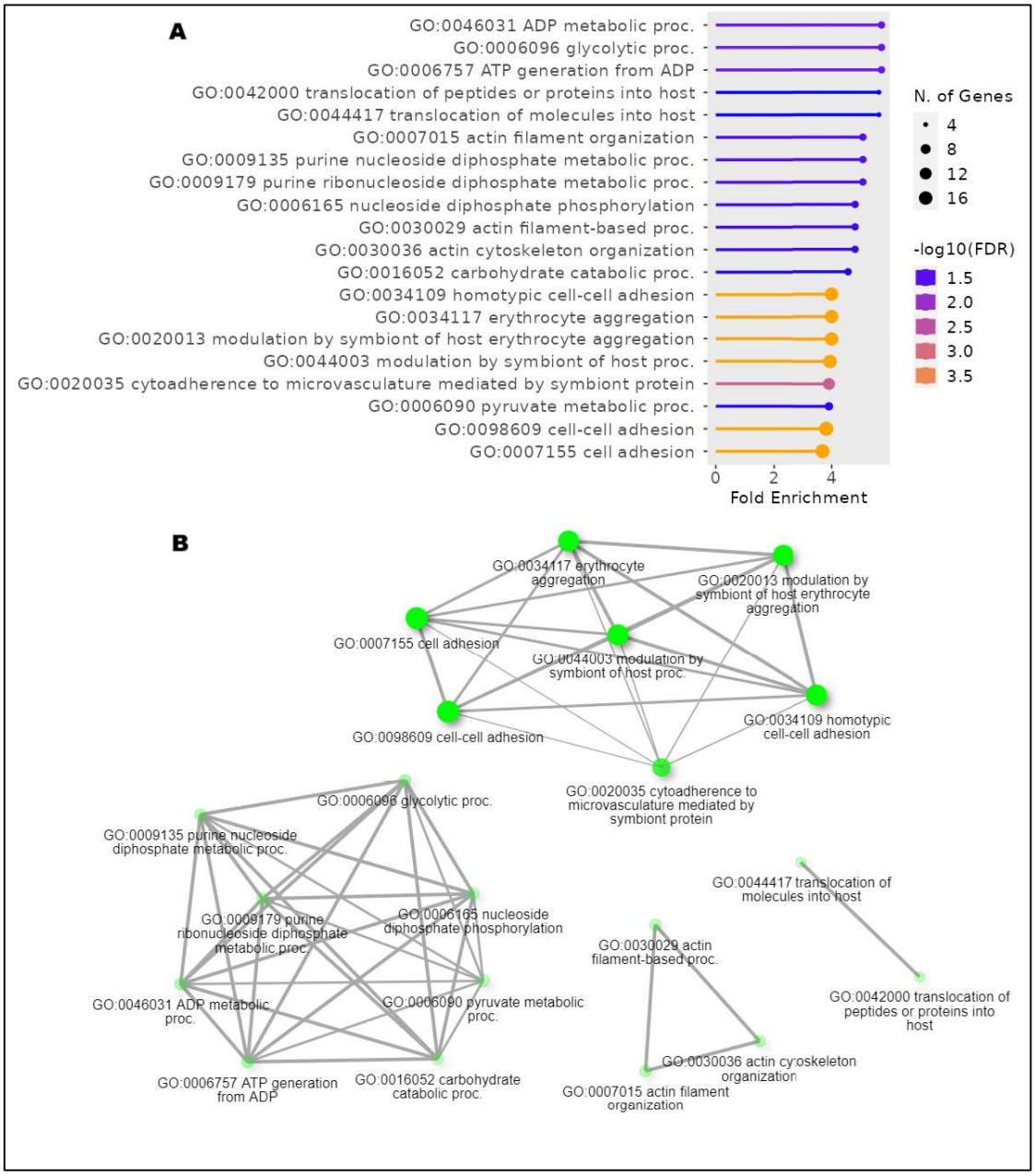

Figure S2 Gene ontology biological processes of upregulated *Plasmodium* genes associated with CQ treatment. (**A**) The lollipop chart illustrates the ADP metabolic and glycolic processes as the most enriched process and the erythrocyte aggregation and cell-adhesion process as the most significantly involved biological process based on a higher -Log_{10}FDR > 3.5. (**B**) An interconnected network diagram illustrating the connections between the purine metabolism and glycolytic processes. The size of the green nodes indicates more significant enriched gene sets, while thicker edges represent a higher number of overlapping genes.

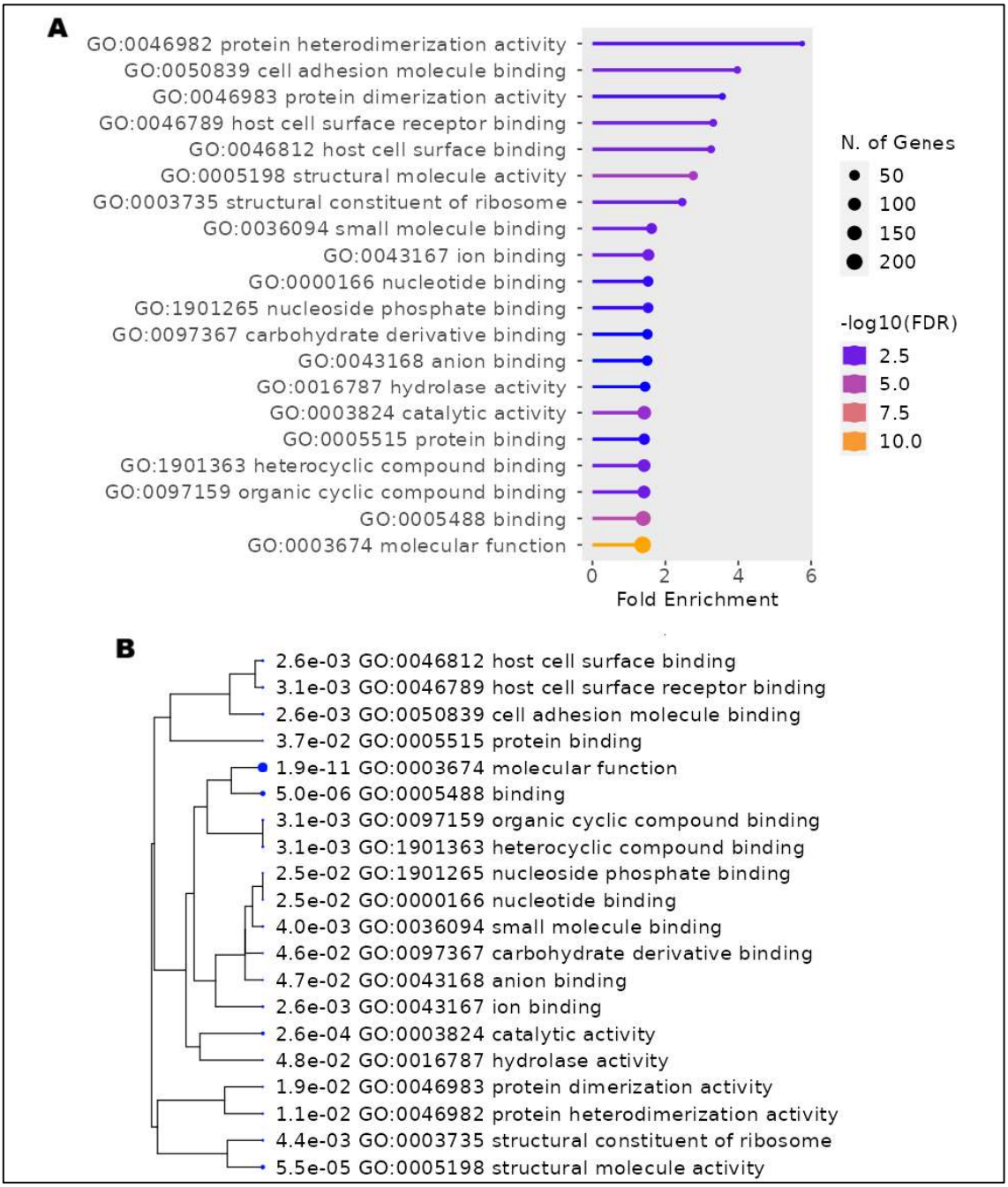

Figure S3 Gene ontology for molecular functions of CQ-induced upregulated genes. (**A**) The lollipop chart illustrates the *Plasmodium* protein dimerisation activities as the most enriched. (**B**) A hierarchical clustering tree summarising the correlation among the significant molecular functional activities, with pathways sharing genes clustered together. Bigger blue dots indicate more significant FDR values.

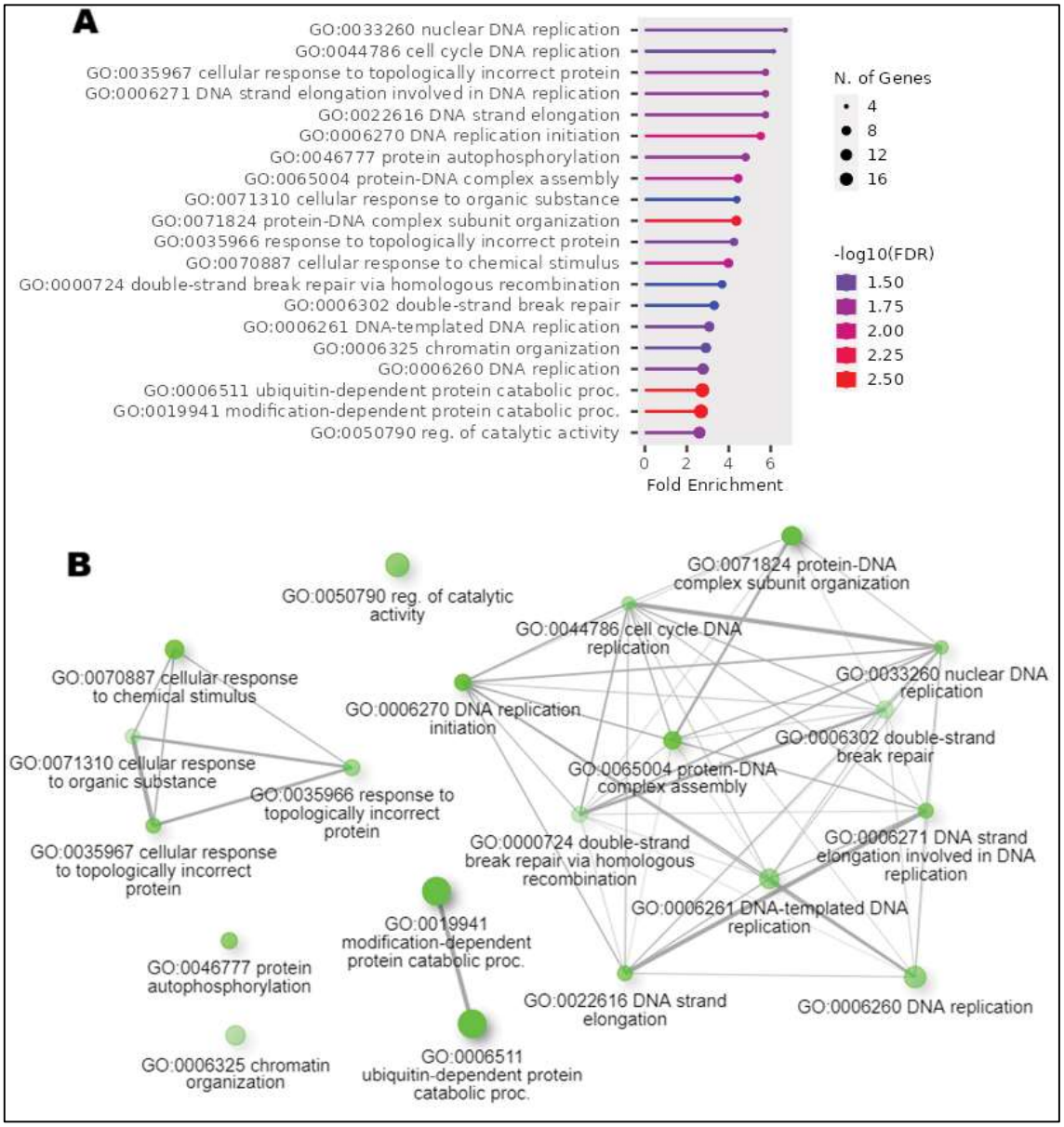

Figure S4 Gene ontology biological processes of downregulated *Plasmodium* genes associated with CQ treatment. (**A**) The lollipop chart illustrates the DNA replication process as the most enriched process and the dependent–protein catabolic process as the most significantly involved biological process based on a higher -Log_{10}FDR value. (**B**) An interconnected network diagram illustrating the connections between the DNA replication and the protein-DNA complexes. The size of the green nodes indicates more significant enriched gene sets, while thicker edges represent a higher number of overlapping genes.

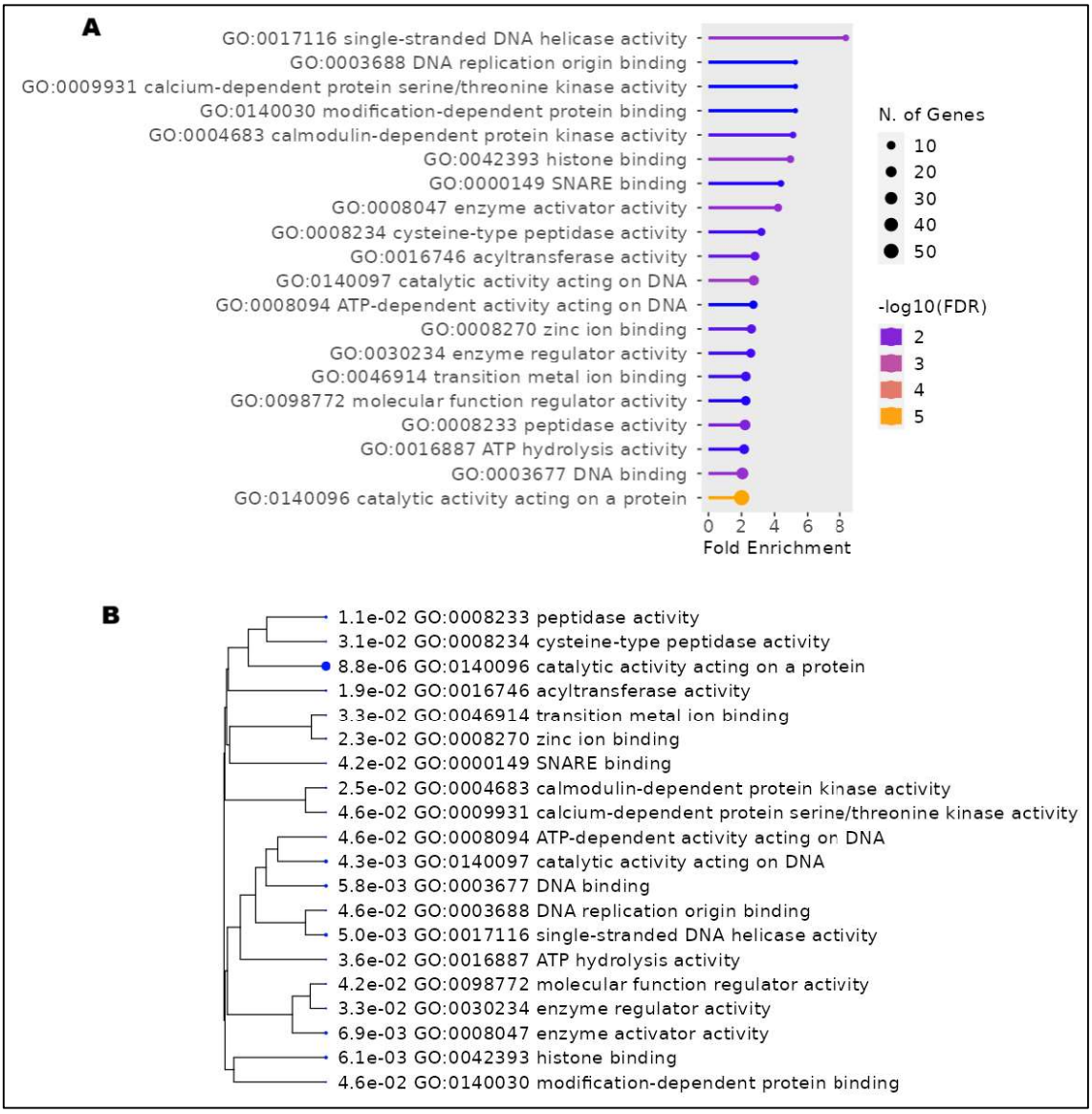

Figure S5 Gene ontology for molecular functions of CQ-induced downregulated genes. (**A**) The lollipop chart illustrates the DNA helicase activity as the most enriched and the catalytic activity acting on *Plasmodium* proteins as the most significant molecular function with a higher -Log_{10}FDR > 5. (**B**) A hierarchical clustering tree summarising the correlation among the significant molecular functional activities, with pathways sharing genes clustered together. Bigger blue dots indicate more significant FDR values.

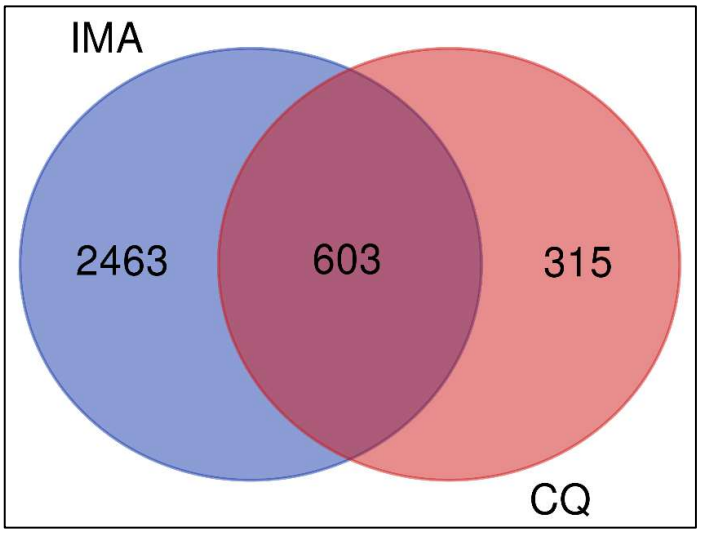

Figure S6 A Venn diagram showing the amounts of unique and shared regulated genes of P. falciparum expressed between CQ and IMA parasitised - erythrocyte with FDR value of 0.001 as shown on the Volcano plots; figure 1 and 2 above.

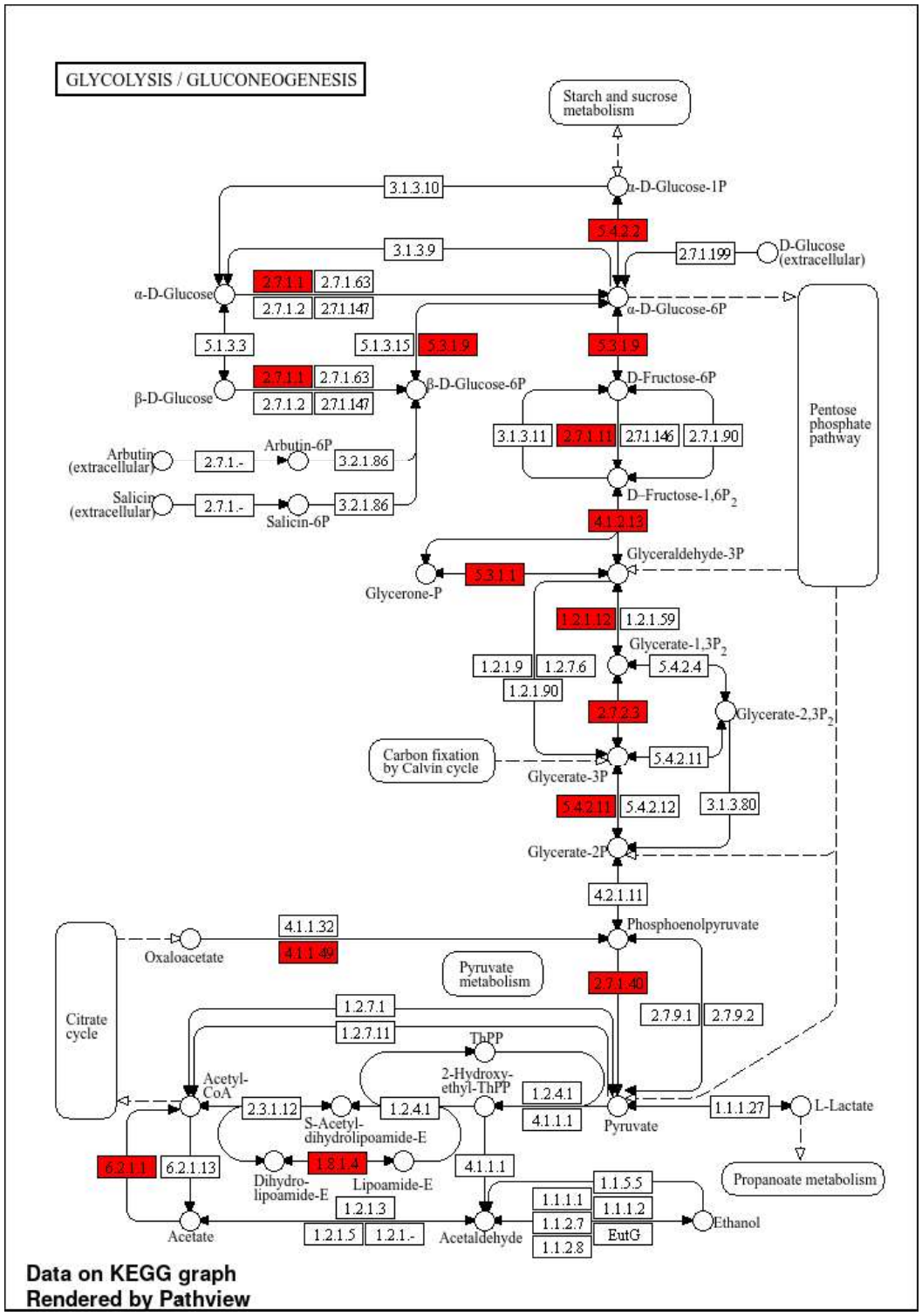

Figure S7 Glycolysis/gluconeogenesis KEGG pathway map (*Pf*a00010) [1–3] of *Plasmodium* intraerythrocytic parasites treated with IMA. The downregulated enzymes are represented with EC numbers highlighted in red generated by Pathview on the basis of the *P. falciparum* KEGG pathway.

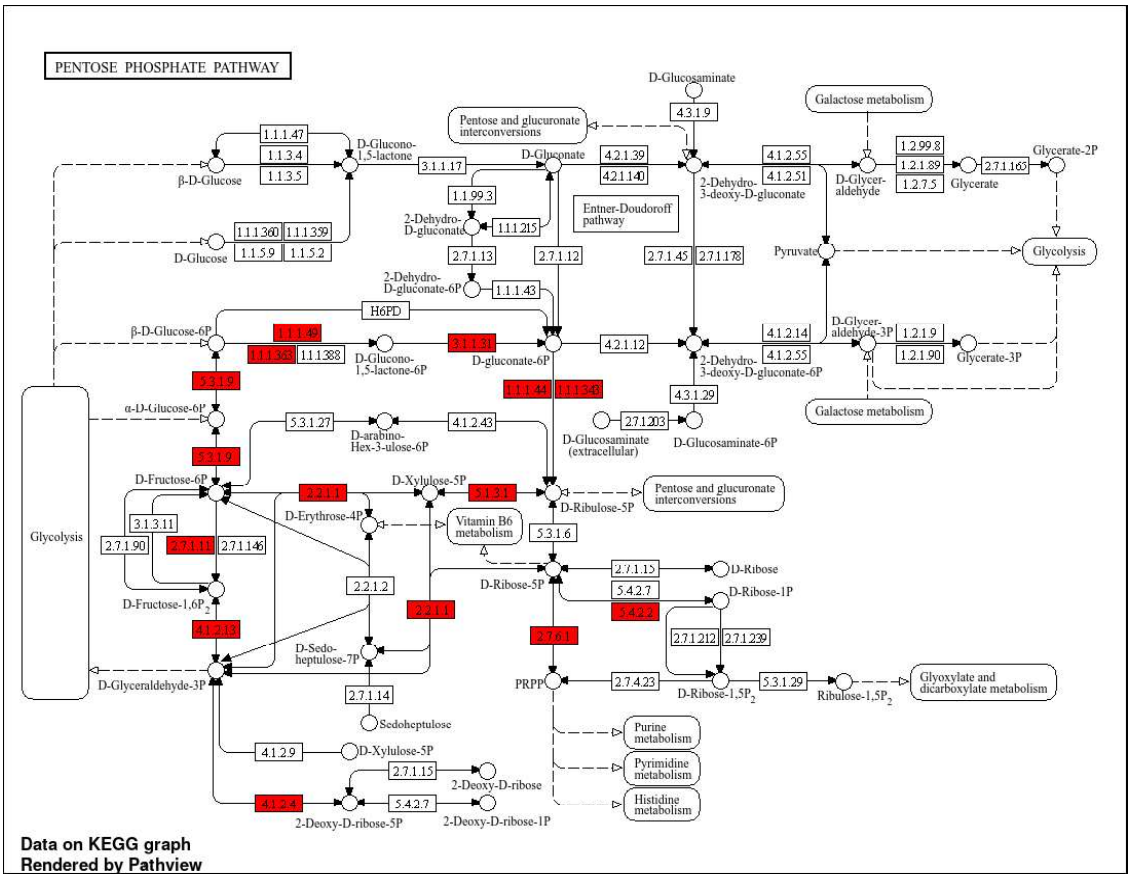

Figure S8 Pentose phosphate KEGG pathway map (*Pf*a00030) [1,3] of intraerythrocytic *Plasmodium* treated with IMA. The downregulated enzymes are represented with EC numbers highlighted in red, generated via Pathview on the basis of the *P. falciparum* KEGG pathway.