

Figure S1. Additional metabolic pathways associated with pharmacological activity of MTX in K562 cells. The metabolic network built in Cytoscape was divided into clusters using the community cluster tool within Cytoscape. The resulting clusters represent intermediates of lipid metabolism enriched in (A) triglycerides and fatty acids, (B) phospholipids and lysophospholipids, (C) cholesterol esters, and (D) intermediates of the TCA cycle. Red denotes metabolites found to significantly increase with MTX treatment and blue denotes metabolites found to significantly decrease with MTX treatment. Node size is directly proportional to measured fold-change. Blue lines between nodes represent KEGG reaction pairs, while gray lines represent pairing based on chemical similarity.

