

# Glycolysis Network

John Santiago

2023-12-06

## Contents

- 
- 
- 
- 
- 
- 
- 
- 
- 
- 
- 
- 
-

Select by id

## GR.F vs WT.F

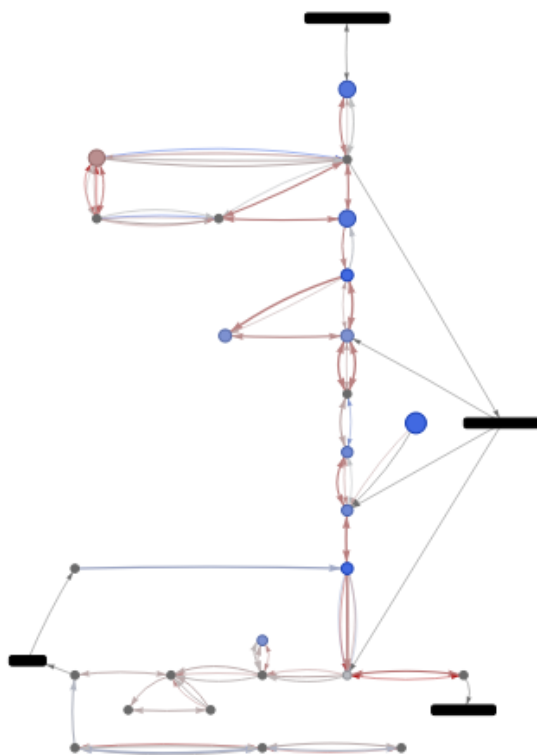


Figure 1: G85R relative to WT. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## GR.M vs WT.M

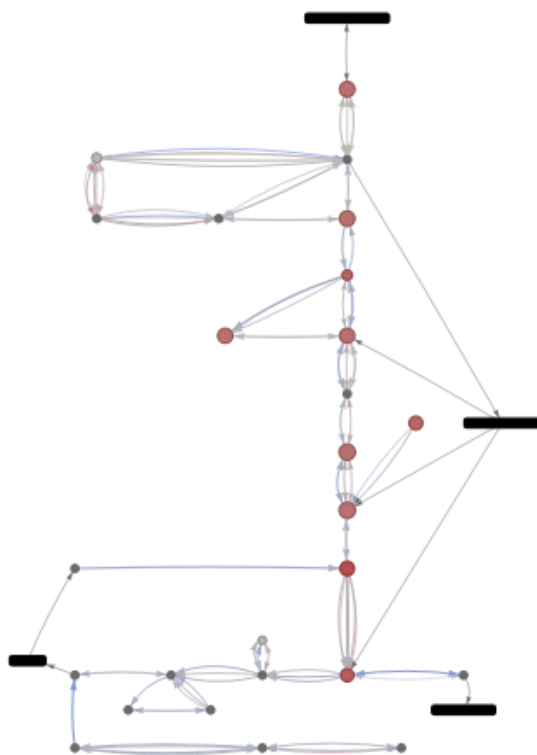


Figure 2: G85R relative to WT. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

### TktDfGR.F vs TktDfWT.F

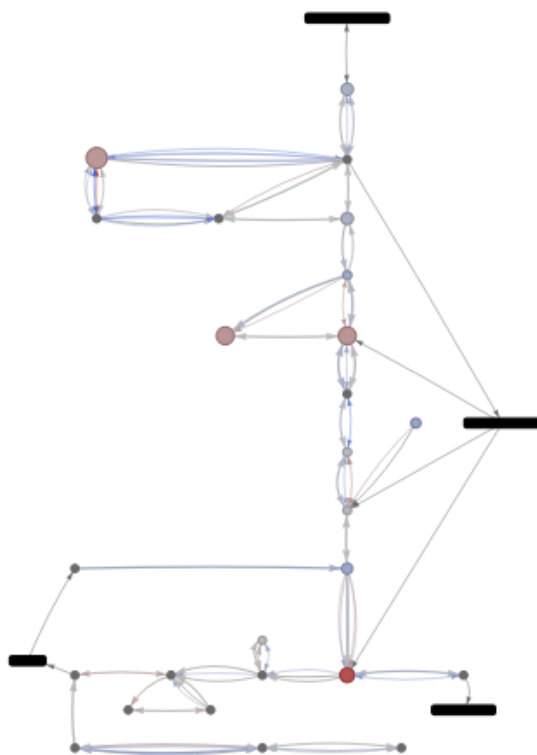


Figure 3: G85R TKT-Df relative to WT TKT-Df. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktDfGR.M vs TktDfWT.M

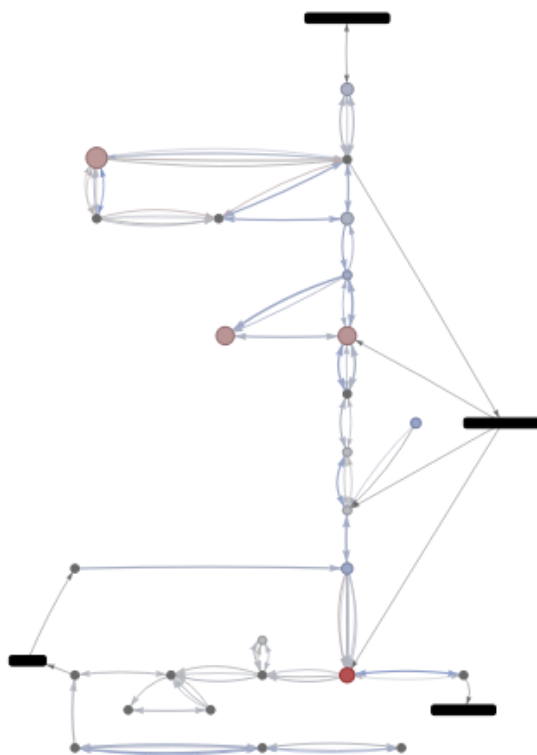


Figure 4: G85R TKT-Df relative to WT TKT-Df. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEGR.F vs TktOEWT.F

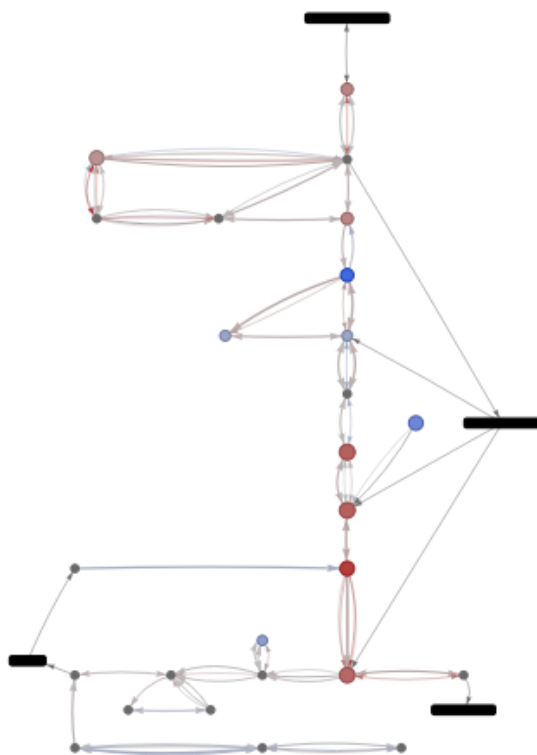


Figure 5: G85R TKT-OE relative to WT TKT-OE. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEGR.M vs TktOEWT.M

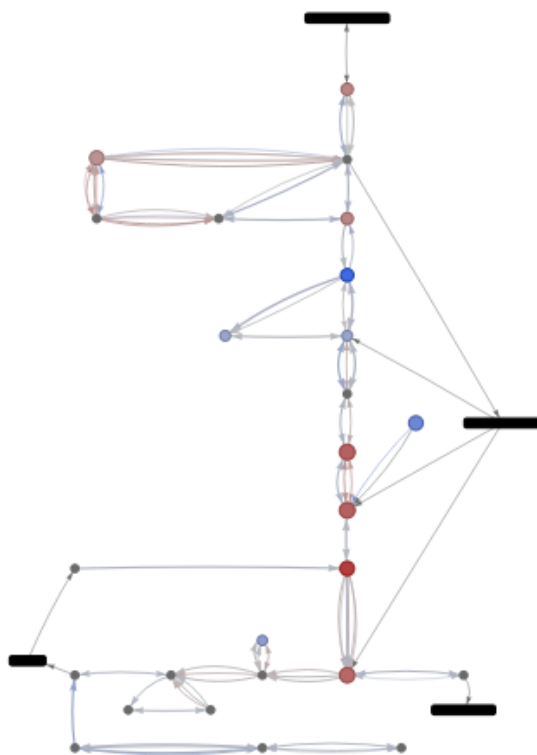


Figure 6: G85R TKT-OE relative to WT TKT-OE. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktDfGR.F vs GR.F

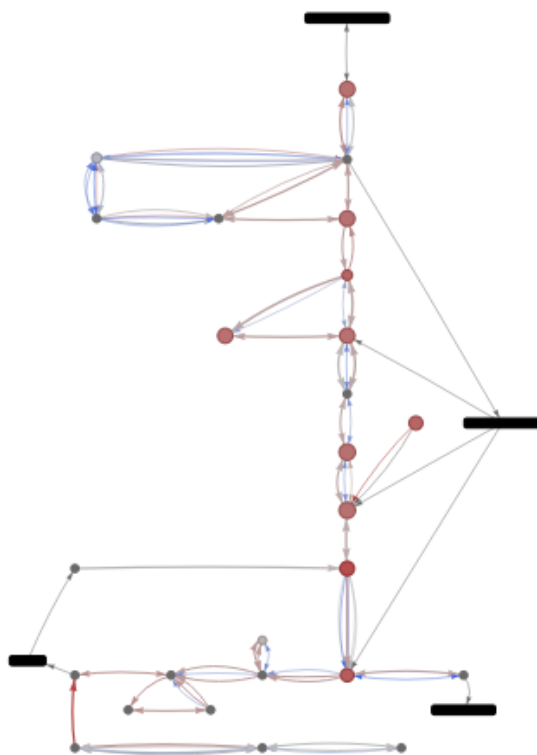


Figure 7: G85R control relative to G85R TKT-Df. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)



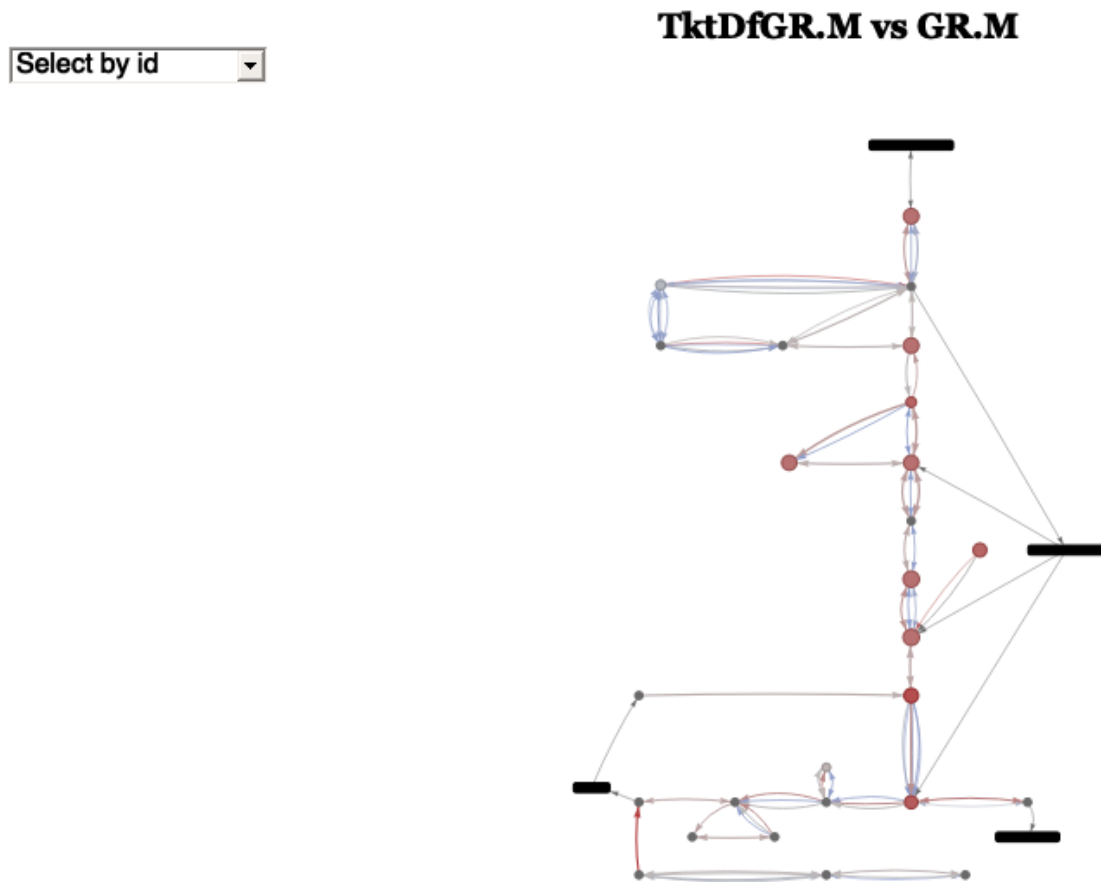


Figure 8: G85R control relative to G85R TKT-Df. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktDfWT.F vs WT.F

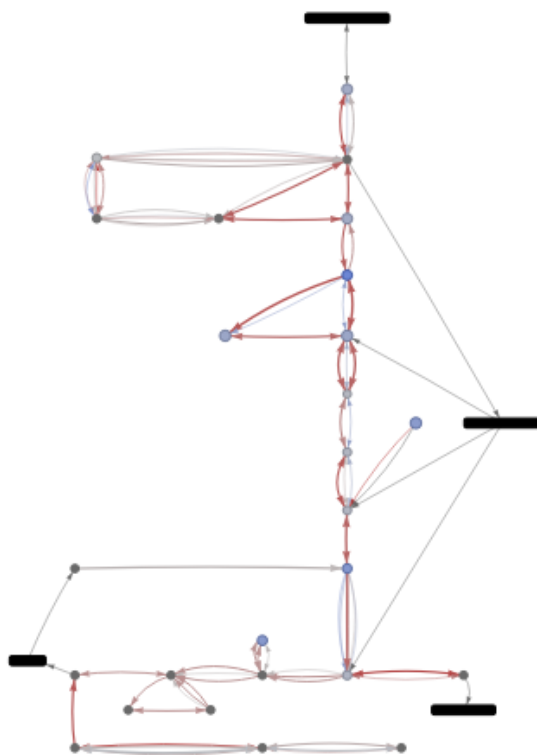


Figure 9: WT control relative to WT TKT-Df. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktDfWT.M vs WT.M

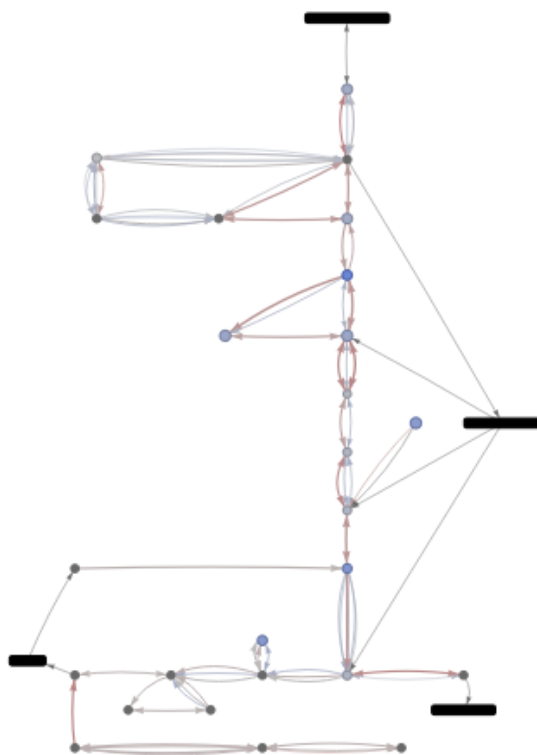


Figure 10: WT control relative to WT TKT-Df. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEGR.F vs GR.F

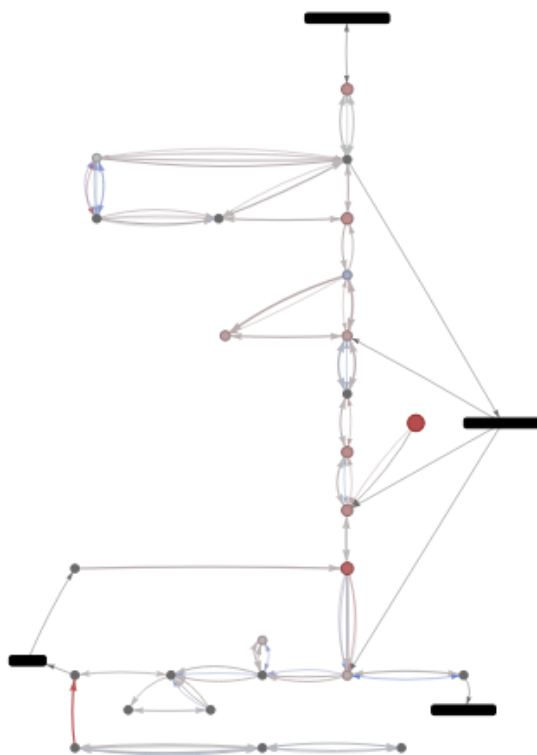


Figure 11: G85R control relative to G85R TKT-OE. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEGR.M vs GR.M

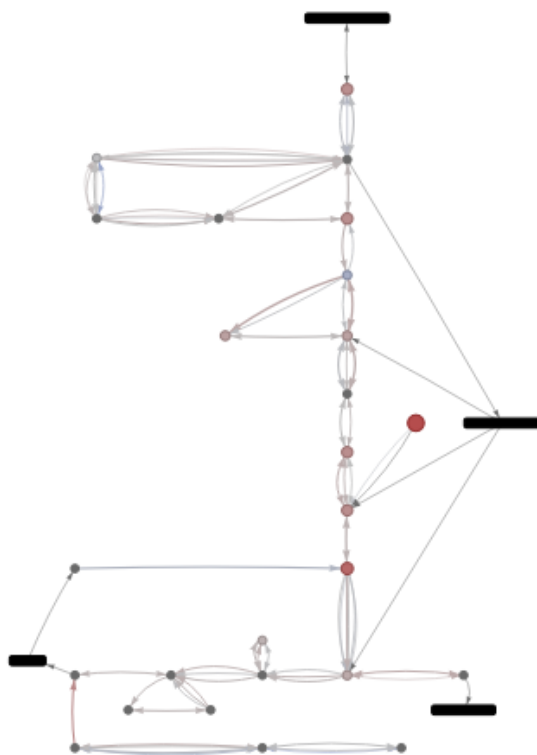


Figure 12: G85R control relative to G85R TKT-OE. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEWT.F vs WT.F

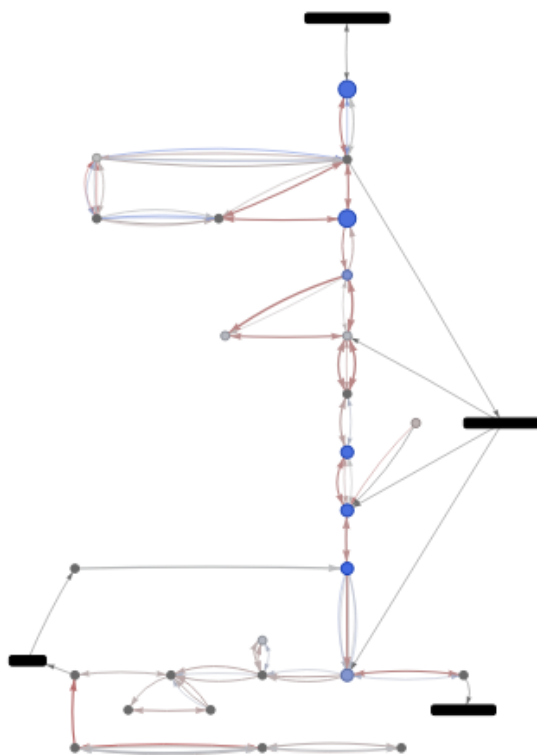


Figure 13: WT control relative to WT TKT-OE. Transcriptomic data is from females and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)

Select by id

## TktOEWT.M vs WT.M

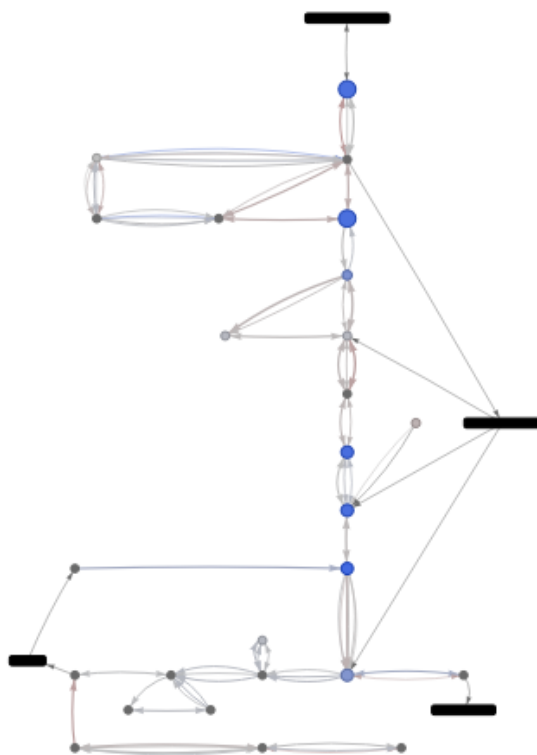


Figure 14: WT control relative to WT TKT-OE. Transcriptomic data is from males and metabolomic data is from both sexes. Grey is no data; Red is increase; Blue is decrease; Node size is relative to pval; Node color is relative to fold change (range: -1 to 1); Edge width is relative to FDR (max  $-\log_{10}(4)$ ); edge color is relative to fold change (range: -2 to 2)