ESM Fig. 6. Gene network analysis for gene-gene interaction of genes associated with MuTHER eSNPs in strong LD (r2 > 0.8) with rs10229583. Twenty-four tagSNPs in strong LD to rs10229583 with  $r^2 \ge 0.8$  were extracted. The maximum genomic distance to rs10229583 was 34kb. Highlighted circles in orange denote 4 genes identified from the eQTL analysis. Weight on edge, in form of thickness of the edge, was computed by GeneMania and reflects the degree of confidence of the relationships between any gene pair within the network. Blue coloured lines represent Pathway information from Pathway Commons. Cyan coloured lines represent interactions from BioGrid.

