**Figure S1. Manhattan plots summarizing distribution of eQTLs.** X-axis indicates positions (bp) by chromosomes and y-axis indicates the magnitude of associations i.e. -$\log_{10}$(P-value). Plots were generated for genes with highest number of trans-eQTLs including *HBM*, *CLEC1*, *MYL9*, and *ABCC*. eQTLs on adjacent chromosomes are colored differently and the y-axis has been capped at P=1 × $10^{-40}$ to aid viewing.