S5 Fig. Replication of trans-eQTLs that co-localize with disease-associated susceptibility allele. A: Top: Component 391 active in \( FF_{LPS24} \) (left) maps to Crohn’s disease associated variant \( rs503734 \) (Middle). The component contain genes from the members of the Zinc finger family (right). Bottom: The trans-eQTL is replicated in \( CG \). Component 431 in \( CG_{MP} \) (left) maps to the same Crohn’s variant (middle). Zinc finger genes shows up in both datasets (right). B: (Top:) \( FF \) Component 105 active in \( FF_{LPS2} \) (left) maps to Coronary Artery Disease variant \( rs589448 \) (middle) and component gene scores (right). Bottom: The trans-eQTL is replicated in \( CG \) (Component 417 in \( CG_{MP} \) for the same variant \( rs589448 \) is a cis-eQTL to both \( LYZ \) and \( YEATS4 \) in both \( FF \) and \( CG \).