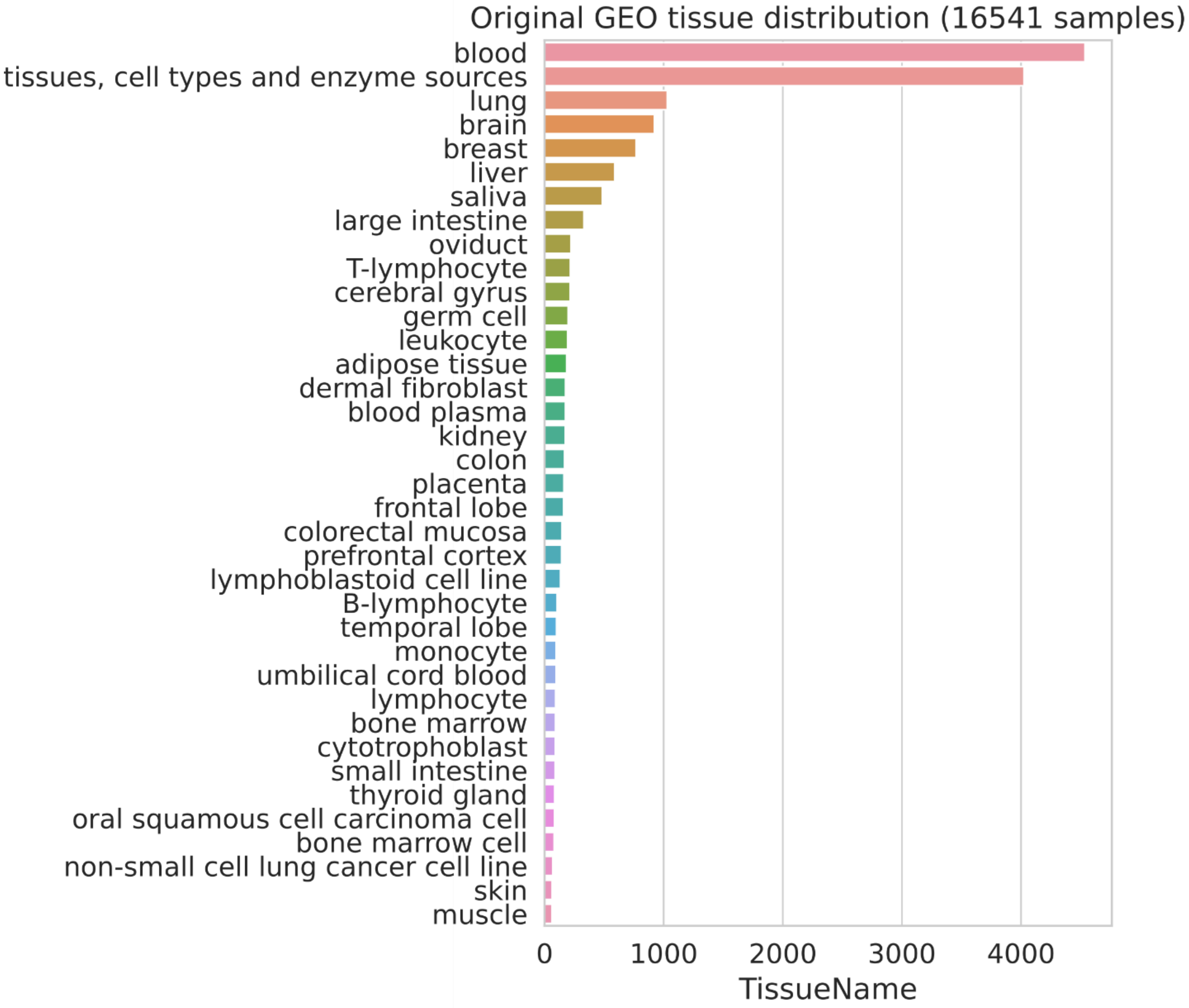
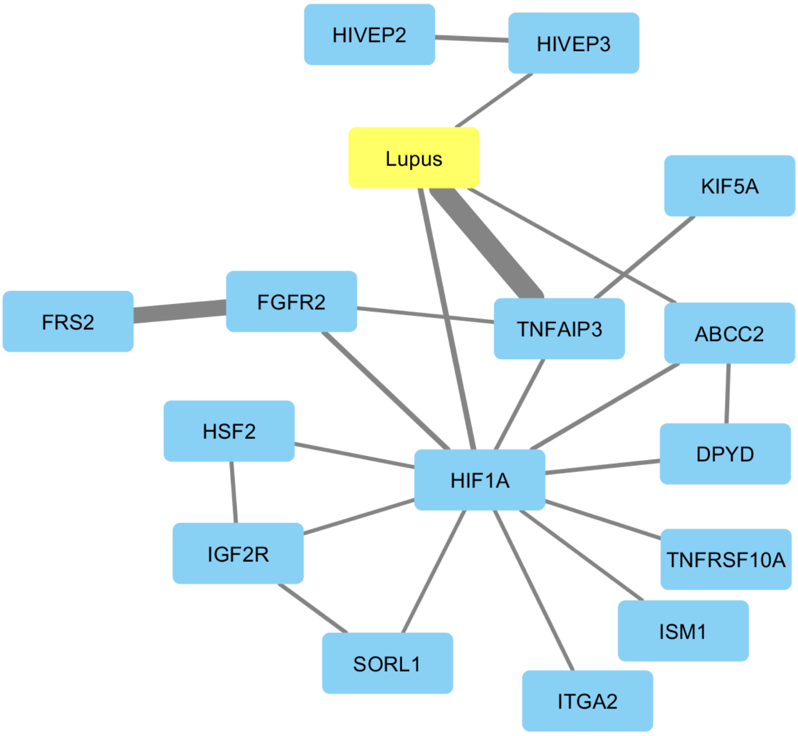
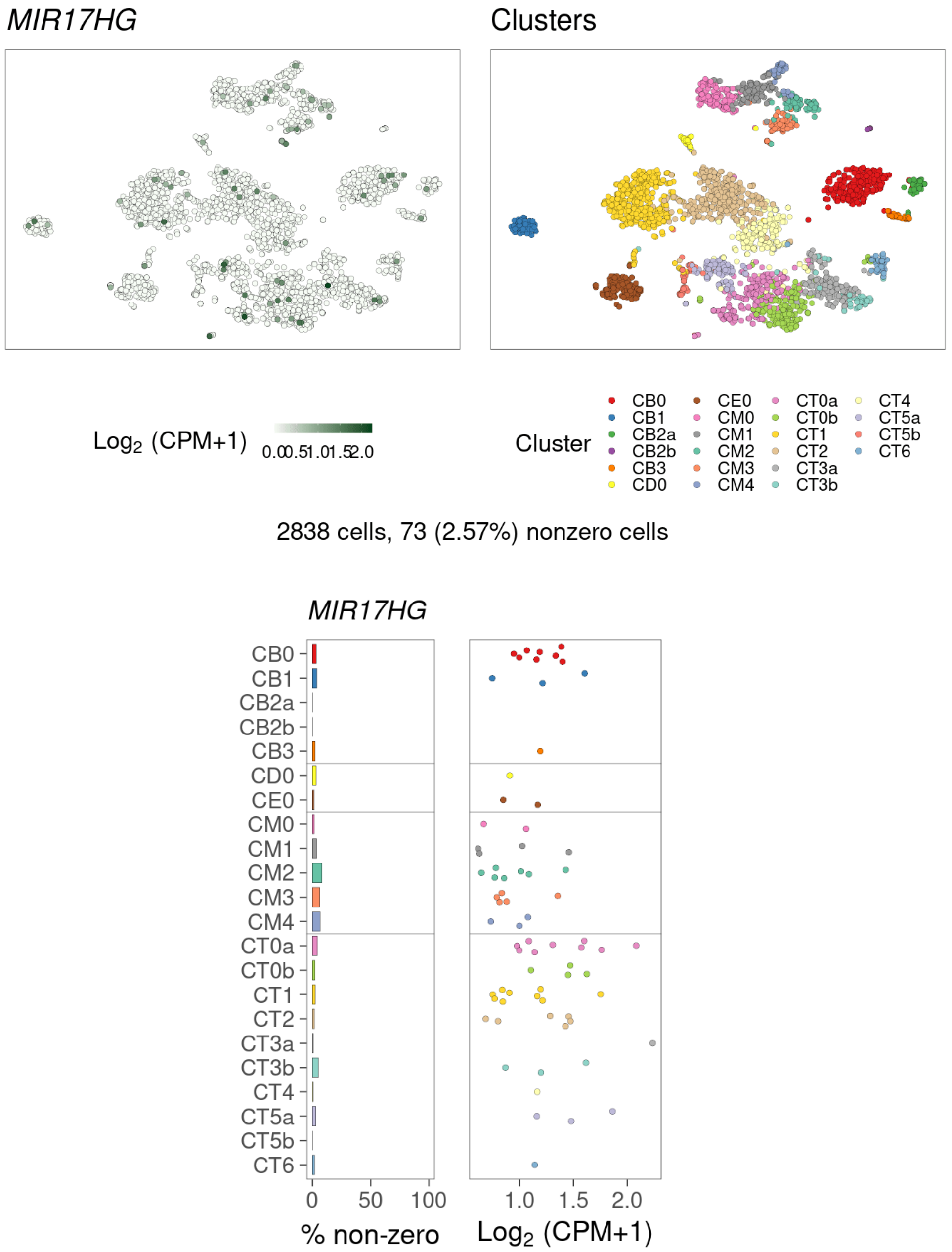
Supplementary Figure 1. Sample distribution of 16,541Infinium HumanMethylation450 array samples across 37 tissues sourced from the Gene Expression Omnibus (GEO). These samples were used to develop a multi-tissue correlation network used for trend deviation analysis.



Supplementary Figure 2. Literature-based network association analysis reveals relatedness to lupus between 15 out of 74 miR-18a target genes downregulated in lupus CD4+ T cells compared to healthy control. The thickness of the edges is proportional to the number of times the terms were co-mentioned in the literature.



Supplementary Figure 3. Expression of MIR17HG in kidneys of patients with lupus nephritis derived from the AMP project.



Cluster annotations:

CM0: CD16+ machrophage, inflammatory; **CM1:** CD16+ macrophage, phagocytic; **CM2:** Tissue-resident macrophage; **CM3:** cDCs; **CM4:** CD16+ macrophage, M2-like;

CT0a: Effector memory CD4+ T cells; **CT0b:** Central memory CD4+ T cells; **CT1:** CD56_dim CD16+ NK cells; **CT2:** CTLs; **CT3a:** Tregs; **CT3b:** TFH-like cells; **CT4:** GZMK+ CD8+ T cells; **CT5a:** Resident memory CD8+ T cells; **CT5b:** CD56_bright CD16- NK cells; **CT6:** ISG-high CD4+ T cells

CB0: Activated B cells; **CB1:** Plasma cells/Plasmablasts; **CB2a:** Naive B cells; **CB2b:** pDCs; **CB3:** ISG-high B cells;

CD0: Dividing cells; **CE0:** Epithelial cells