**Supplementary information**

**De novo identification of complex multimorbid conditions by integration of gene regulation and protein interaction networks with genome-wide association studies**

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**Supplementary Figure 1. Protein coding eGenes are significantly more intolerant to loss of function compared to protein coding non-eGenes.** A)Number of eQTL-eGene interactions in GTEx v8 compared to spatial eQTL-eGene interactions seen in whole blood, classified by interaction type. B) Proportion of eQTL-eGene interactions across chromosomes. C) Proportion of non-eGenes and statistically significant eGenes expressed in whole blood (median TPM >0.1) classified by biotype. D) expression level and E) tolerance to loss of function of protein coding eGenes and non-eGenes expressed in whole blood. In both D and E, the mean is shown in red while the median is shown in black. NS, not significant, t test (\*\*\*\*P <1 × 10−4).



**Supplementary Figure 2. Tissue-specific spikes in the ratio of eQTL-eGene interactions to SNPs seen in chromosomes 7, 18 and 19.** Ratio of whole blood, adult brain, and left ventricle spatial eQTL-eGene interactions to SNPs across A) chromosome 7, B) chromosome 18 and C) chromosome 19.



**Supplementary Figure 3. Asthma eGenes are enriched for immune-related processes and lipid metabolism**. GO enrichment analysis of asthma eGenes having significant enrichment of A) biological processes B) molecular functions and C) reactome pathways.



**Supplementary Figure 4. Blood GRN *de novo* identifies conditions that are multimorbid with ALL.** GWAS traits enriched in each of the four expanded PPIN neighbors of the ALL disease module. Circle size indicates the number of eQTLs, and circle color indicates statistical significance. ACPA; anti-citrullinated protein antibodies, OCB; oligoclonal band, EBNA-1; Antibodies against Epstein-Barr nuclear antigen 1, AQP4; Aquaporin 4, FEV1; forced expiratory volume in the first second, FVC; Forced vital capacity, COPD; chronic obstructive pulmonary disease.