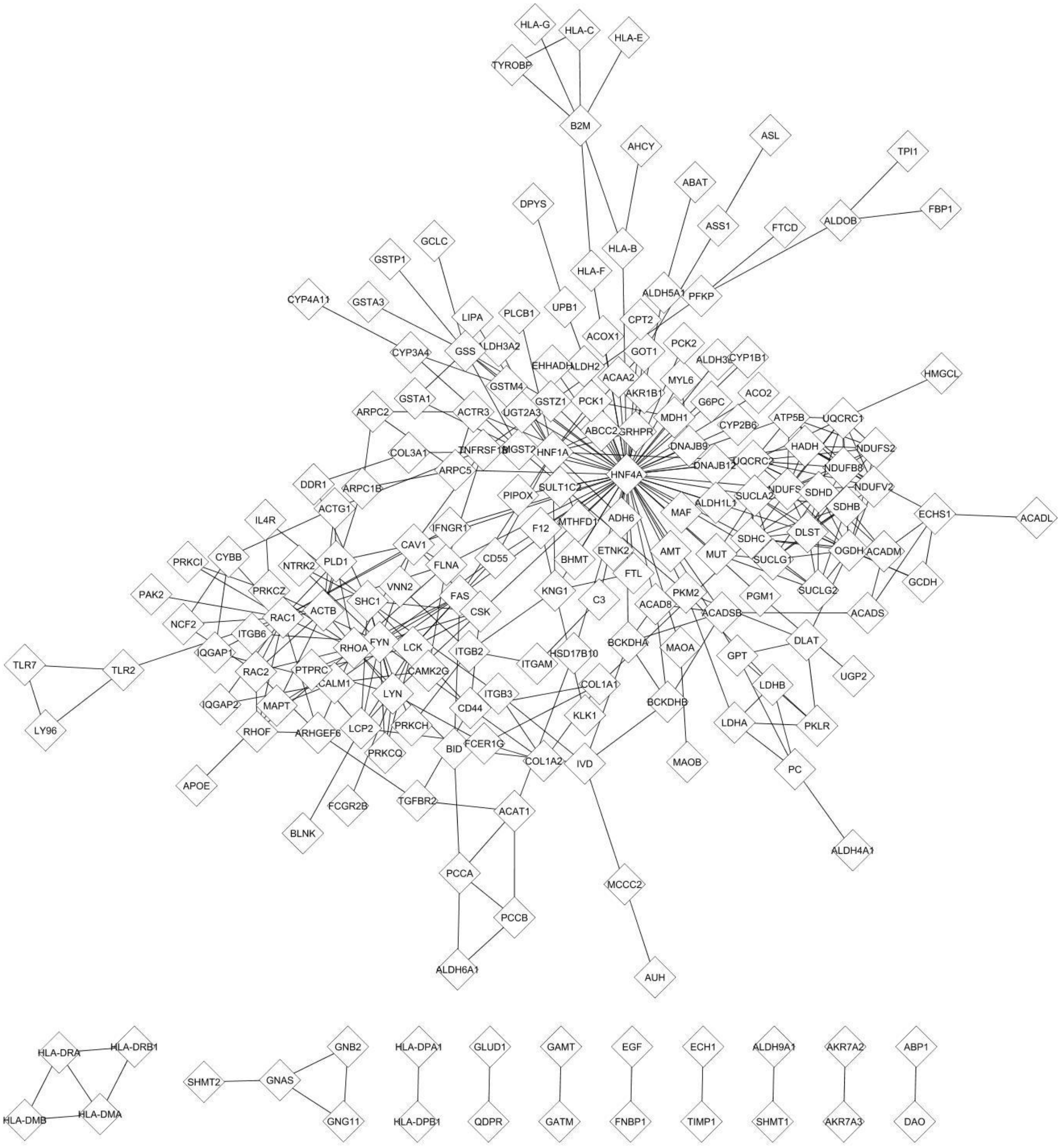
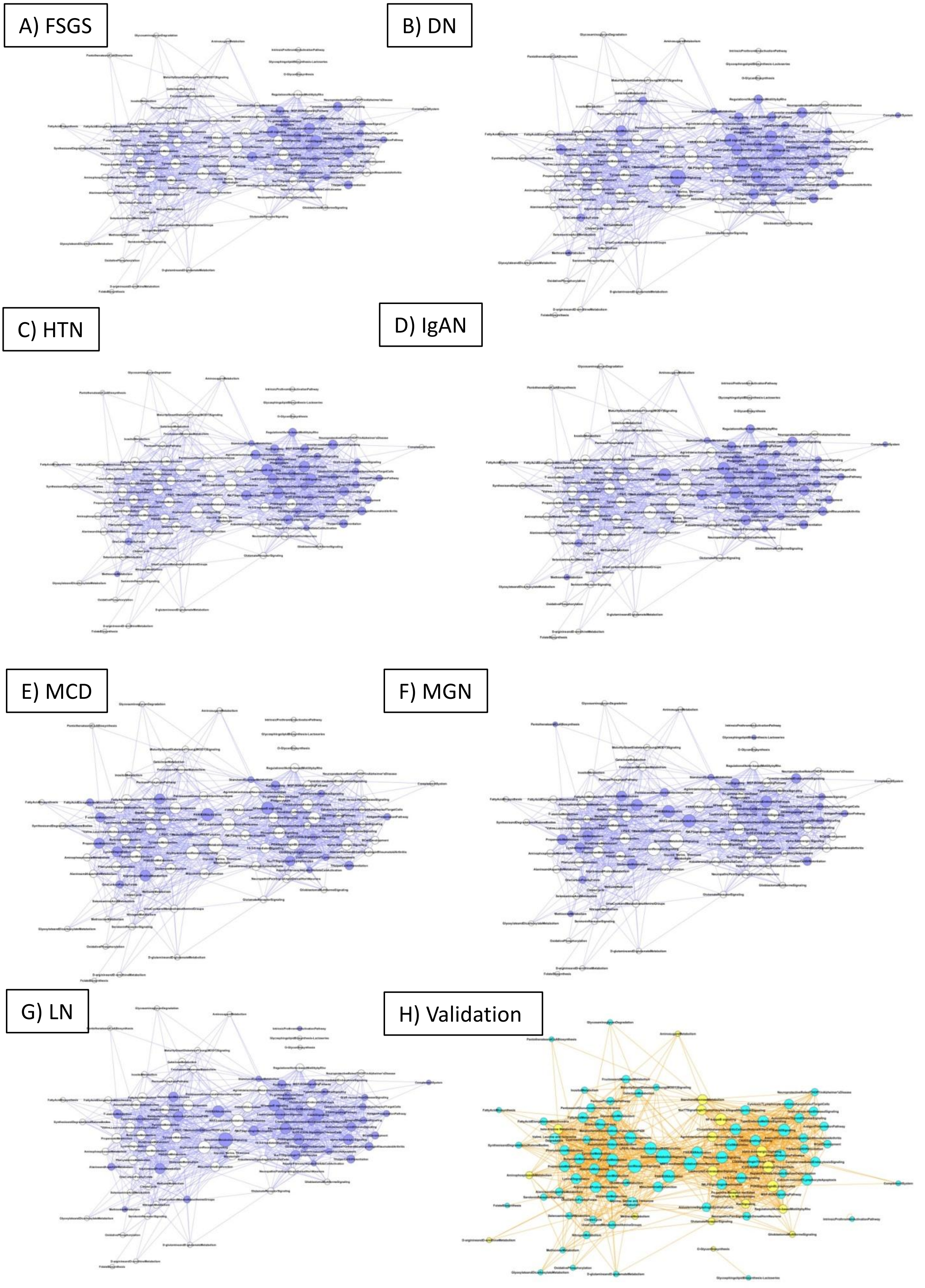
Suppl. Fig. 1: Protein-protein interaction network of the annotated connecting genes from the CKDGen pathway network *(Fig. 3).*



Suppl. Fig. 2: Differential expression for individual diseases mapped to the CKD-associated pathway network graph. Blue nodes in **A** to **G** indicate pathways that are enriched among differentially regulated genes (disease vs. living donor controls). For **H**, Green nodes represent the 78 pathways that were recapitulated in an independent CKD cohort applying the identical strategy steps.



A) FSGS

B) DN

C) HTN

D) IgAN

E) MCD

F) MGN

G) LN

H) Validation