

SIGNIFICANCE STATEMENT

Genome-wide association studies (GWASs) have identified a number of genetic regions correlated with development of CKD, but establishing causality remains challenging. This study applies a new approach to GWAS interpretation: to complement classic annotation on the basis of linear spatial proximity, the principle of transcriptional dysregulation is used to identify sites where CKD-associated variation colocalizes with DNA regulatory elements. The study describes the identification of 304 candidate genes that physically interact with regulatory elements that colocalize with 39 common variants associated with CKD. Future studies will be required to verify the findings of this screening pipeline, but the method could help to determine the causal roles that common variants play in complex diseases, such as CKD.