

COVID-eQTL: Genetic dissection of COVID-19 susceptibility

Abstract

A world-wide pandemic caused by SARS-CoV-2 virus provided an unprecedented opportunity to investigate the genetic susceptibility of virus infection and severity determination. For example, COVID-19 Host Genetics Initiative has released genome-wide associated variants from more than 100K infected individuals with COVID-19 severity. However, this study is not suited to analyze complex network of genomic variants and gene expression, which may eventually