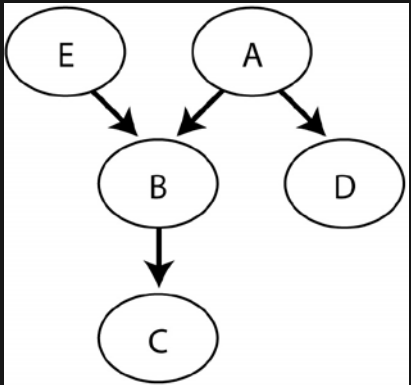


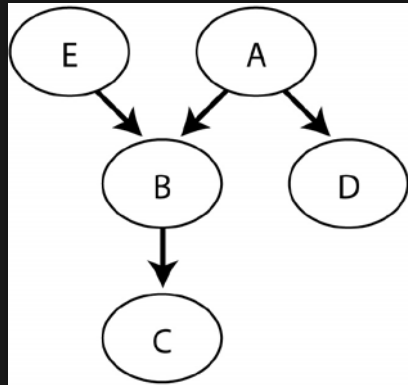
A functional genomics predictive network model identifies regulators of inflammatory bowel disease

Nature Genetics

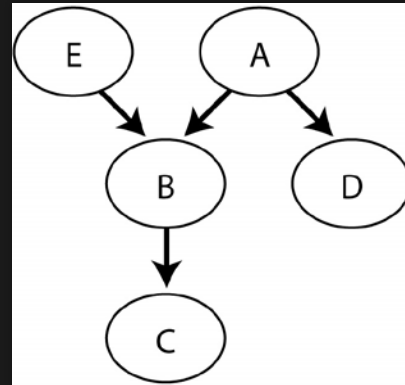
Three bayesian networks



Cohort 1 Network
Treatment-naive
pediatric patients

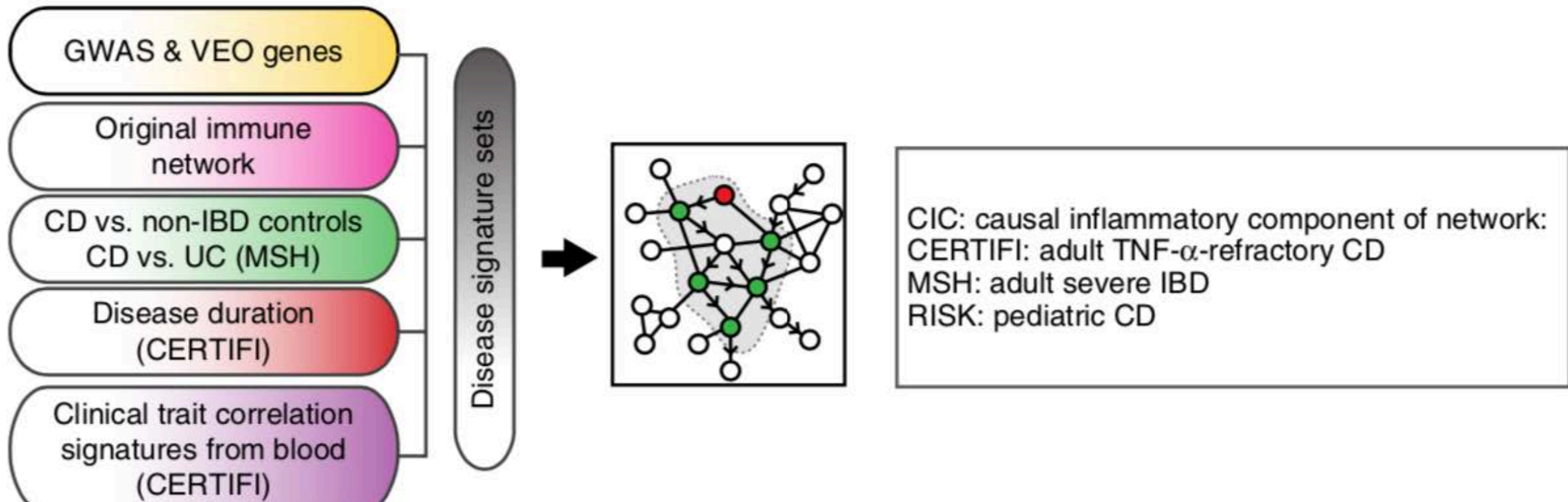


Cohort 2 Network
Refractory to anti-
tumor necrosis

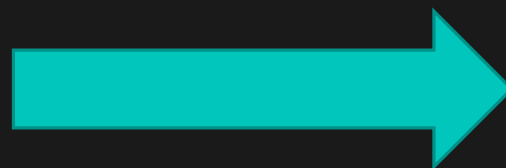


Cohort 3 Network
Advanced disease

Intersection of those 3
Bayesian networks with
core immune activation
module seed obtained
from previous domain
knowledge.

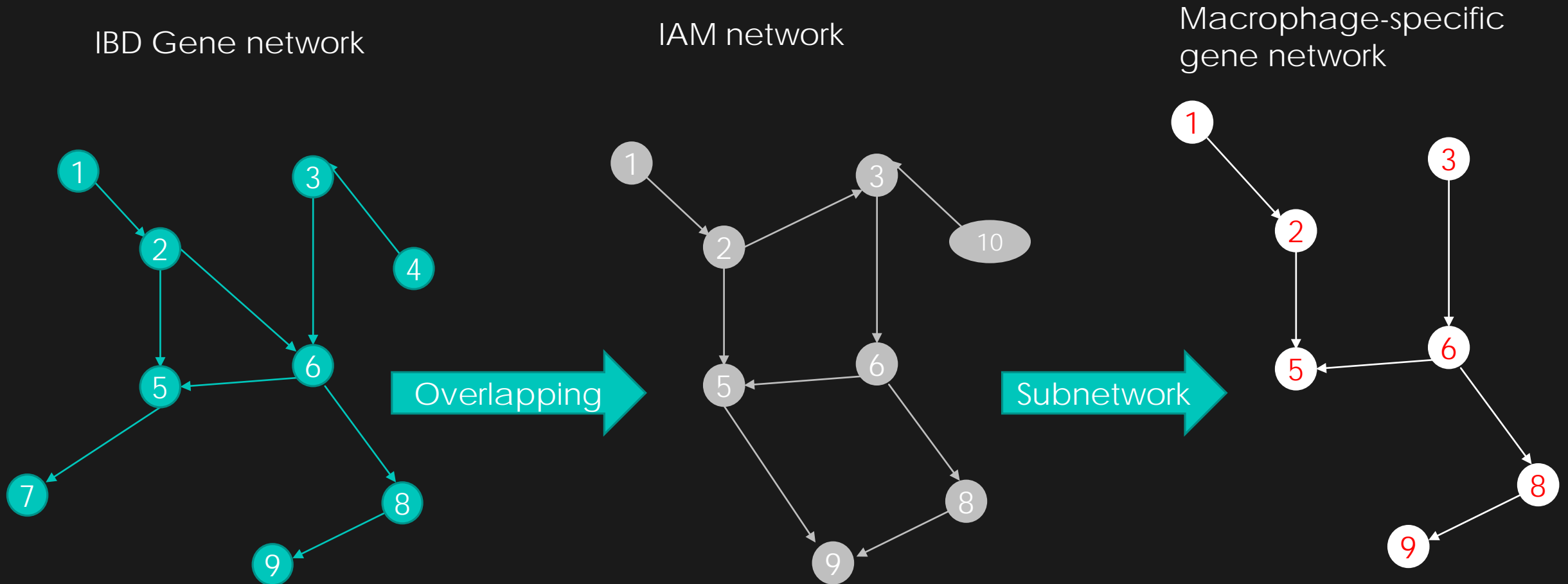


Find macrophage gene signature in the networks

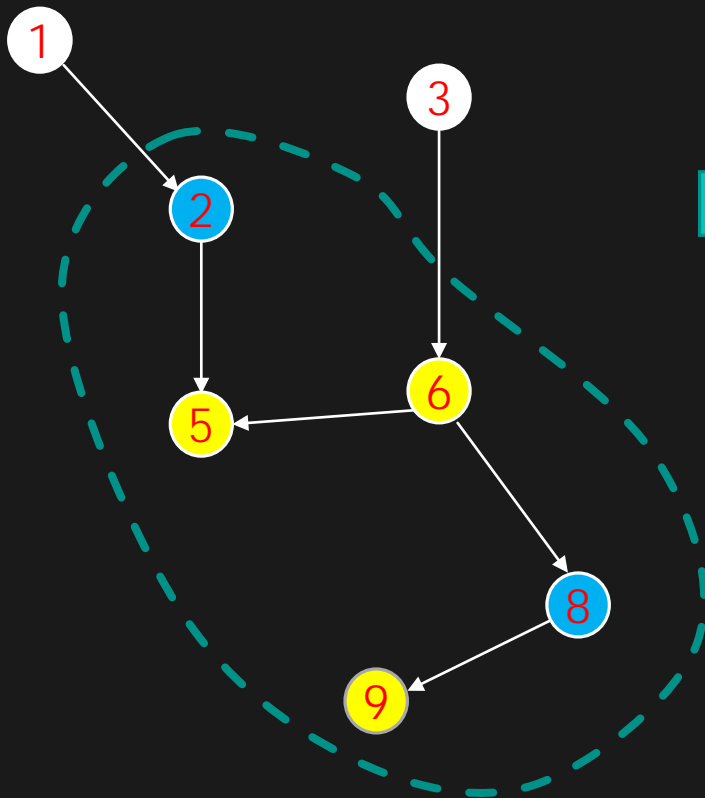


Identify Key driver genes by identifying the largest connected subnetwork comprising nodes within a path length of three of the genes.

Details about the overlapping of IBD gene networks and the domain knowledge core immune activation module



Validation



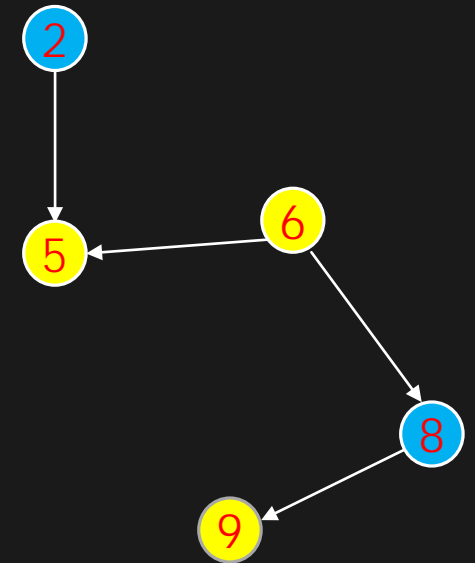
Identify IBD Networks

In vitro and in vivo validation

Rank KDG

Molecular network validation

KEY DRIVER
SUBNETWORKS



Final use

KDG molecular and network pathways.

Enable to identify rules between biological matter elements and inflammatory bowel disease.

