Figure S2. Analysis of allelically regulated loci with shared cis-associations between populations revealed enriched networks.


CY = CEU LCLs and YRI LCLs shared associations.

CYM = CY and monocytes shared associations.

CYFM = shared associations between all cell-populations (CEU LCLs, YRI LCLs, fibroblasts and monocytes).

Score is based on algorithm that aggregates genes based on known relationships in the Ingenuity Knowledge Base.

Focus molecules = # of genes in dataset involved in this network.