

Figure S12A

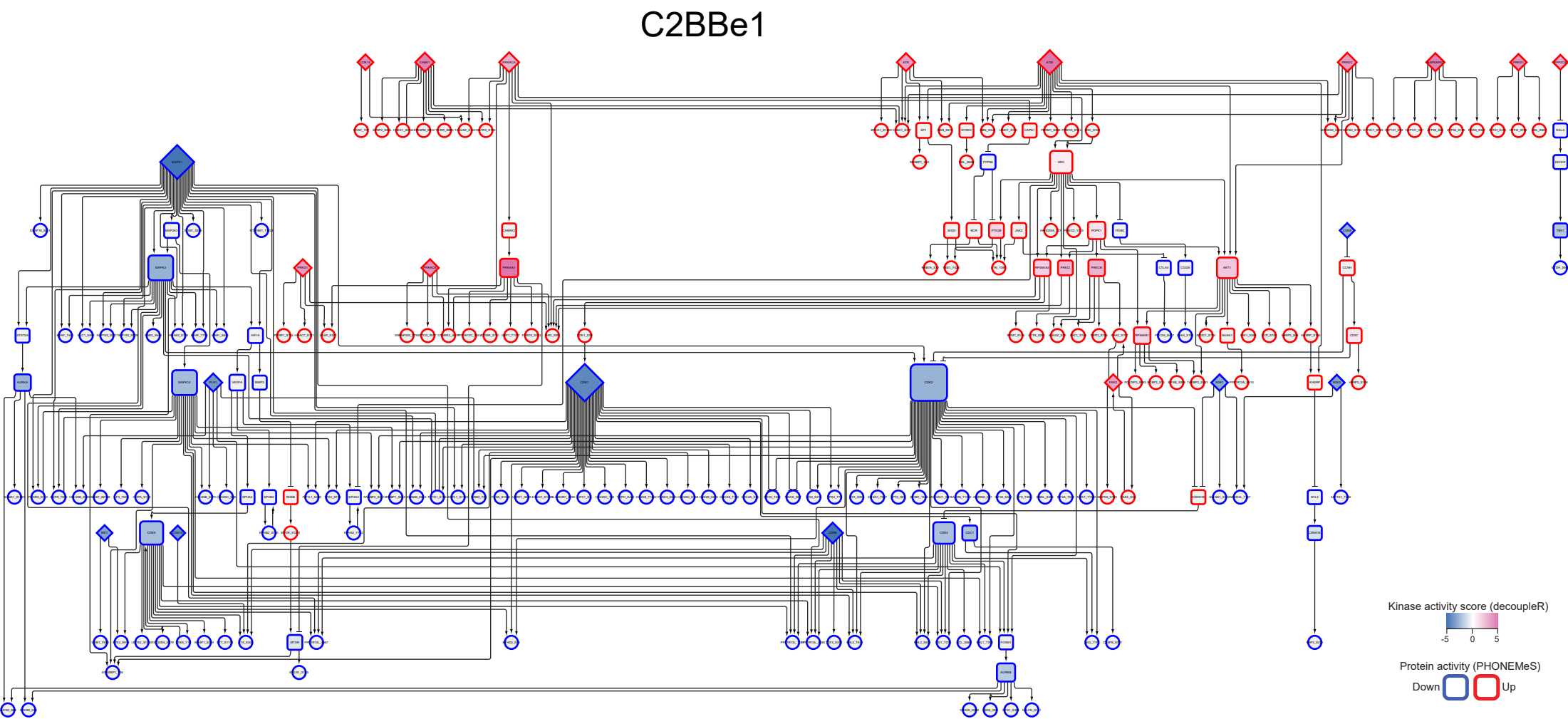


Figure S12: PHONEMeS reconstructed signaling networks in individual cell lines (related to Figure 6). (A-L) The border color corresponds to the protein activity scores calculated using PHONEMeS; the fill color mapping illustrated the decoupleR kinase activity score. The shape indicates whether the node is a P-site measured in our data (ellipse), kinase differentially perturbed in our data (diamond), or protein inferred by the algorithm to be a part of the signaling network (rectangle). The size corresponds to the number of out-going edges.

Figure S12B

COLO 205

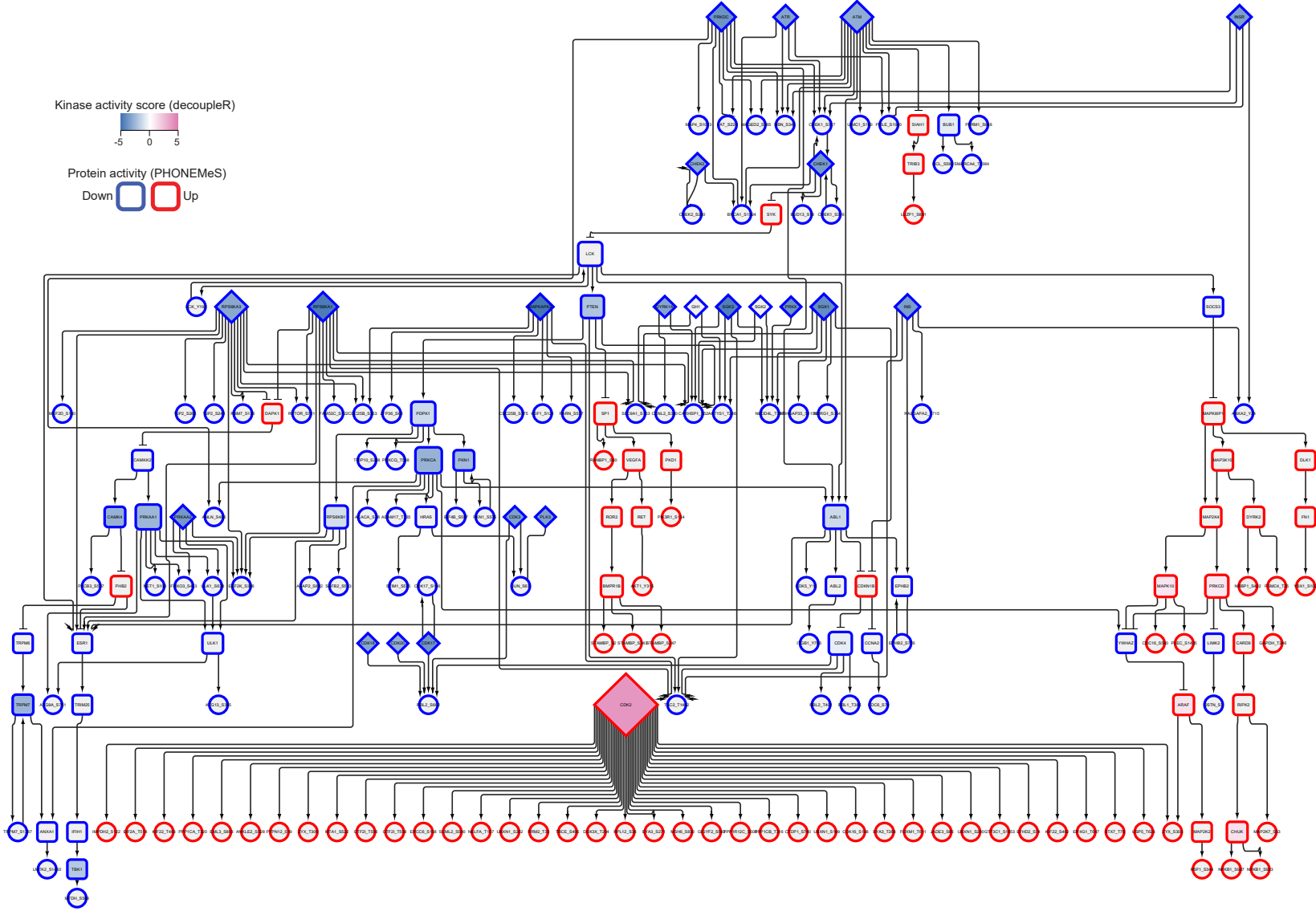


Figure S12C

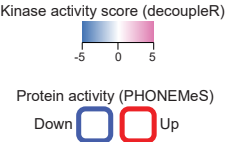
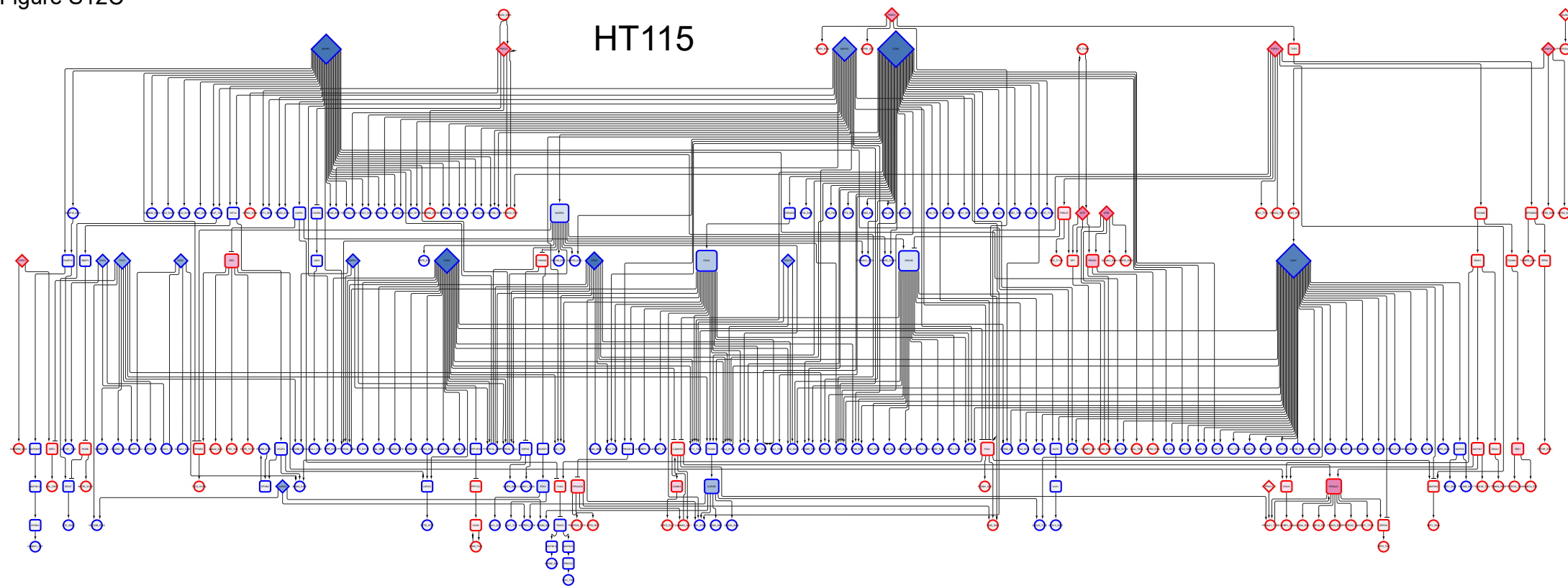


Figure S12D

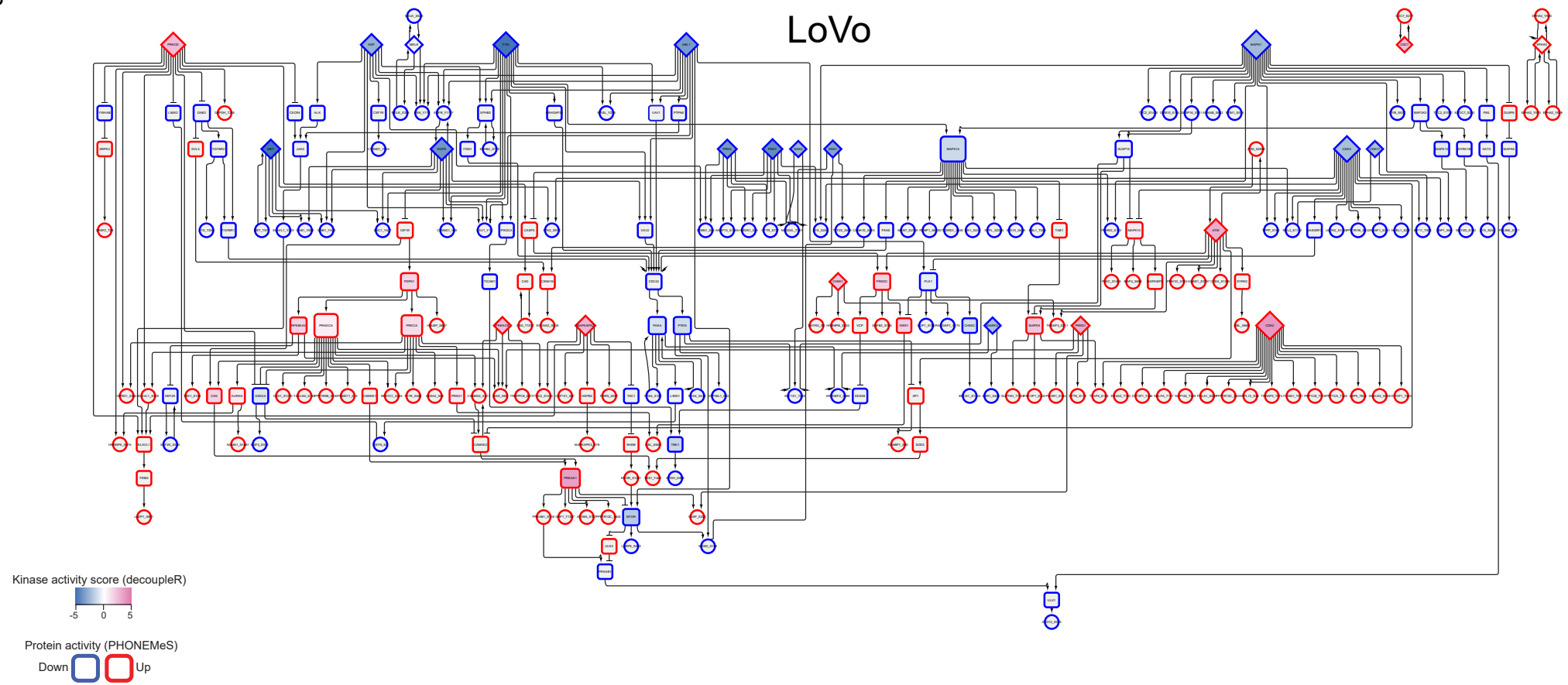


Figure S12E

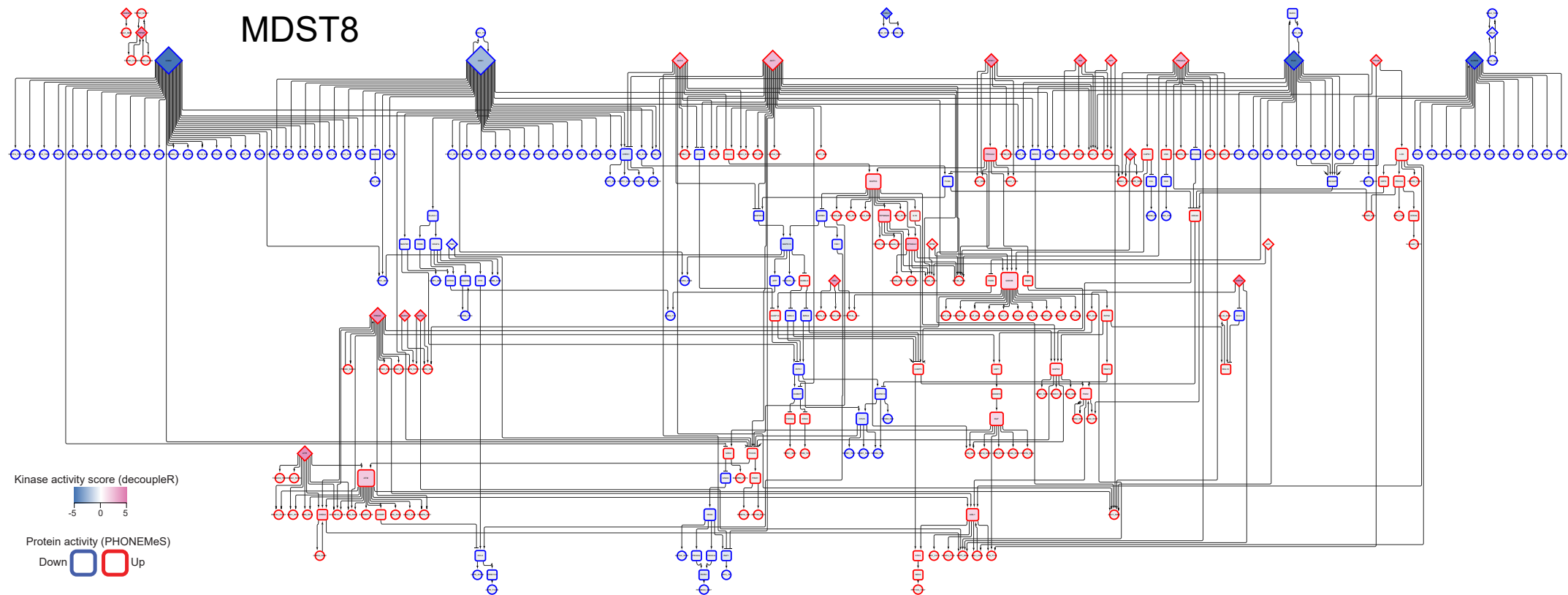


Figure S12F

NCI-H747

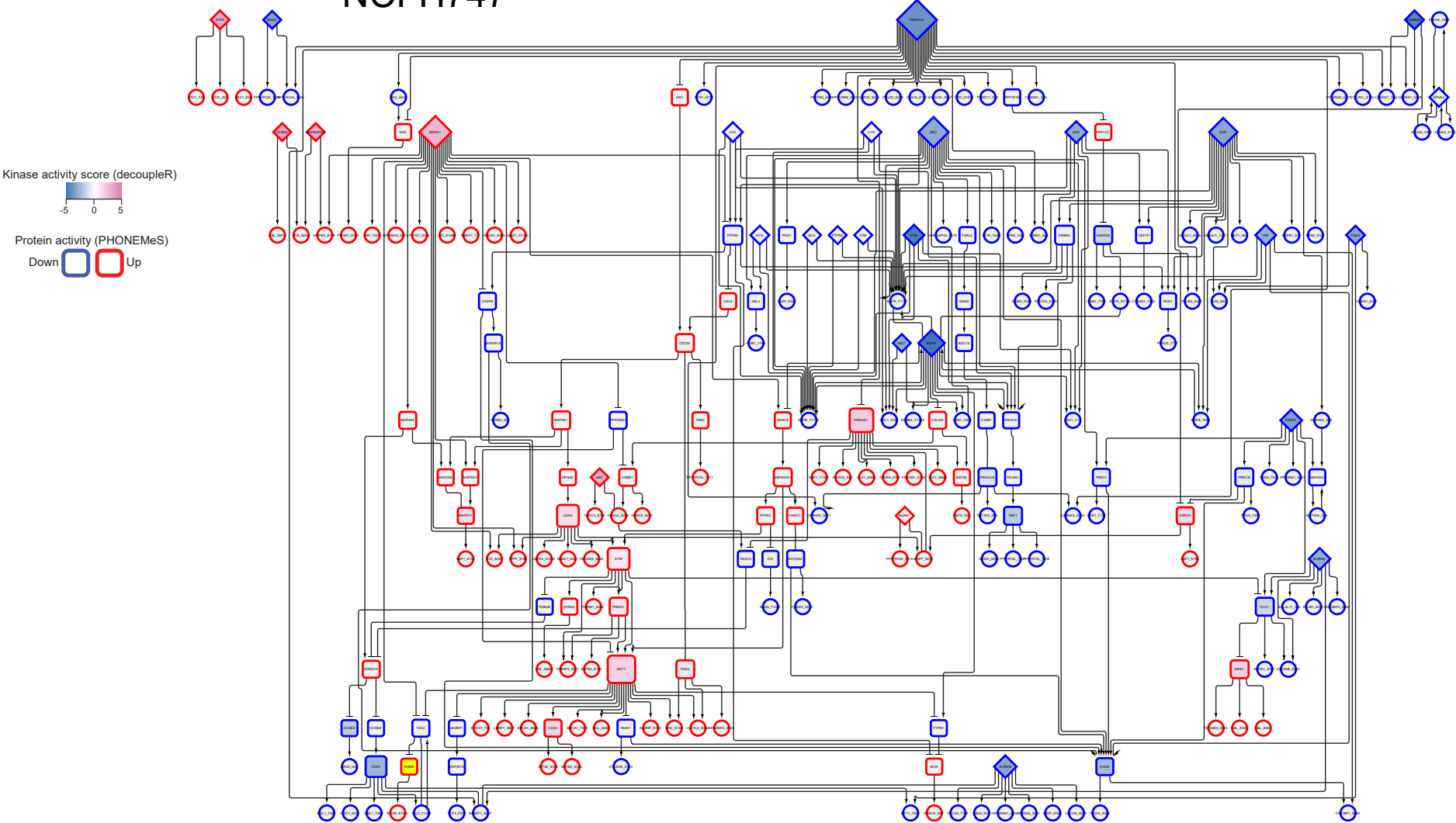
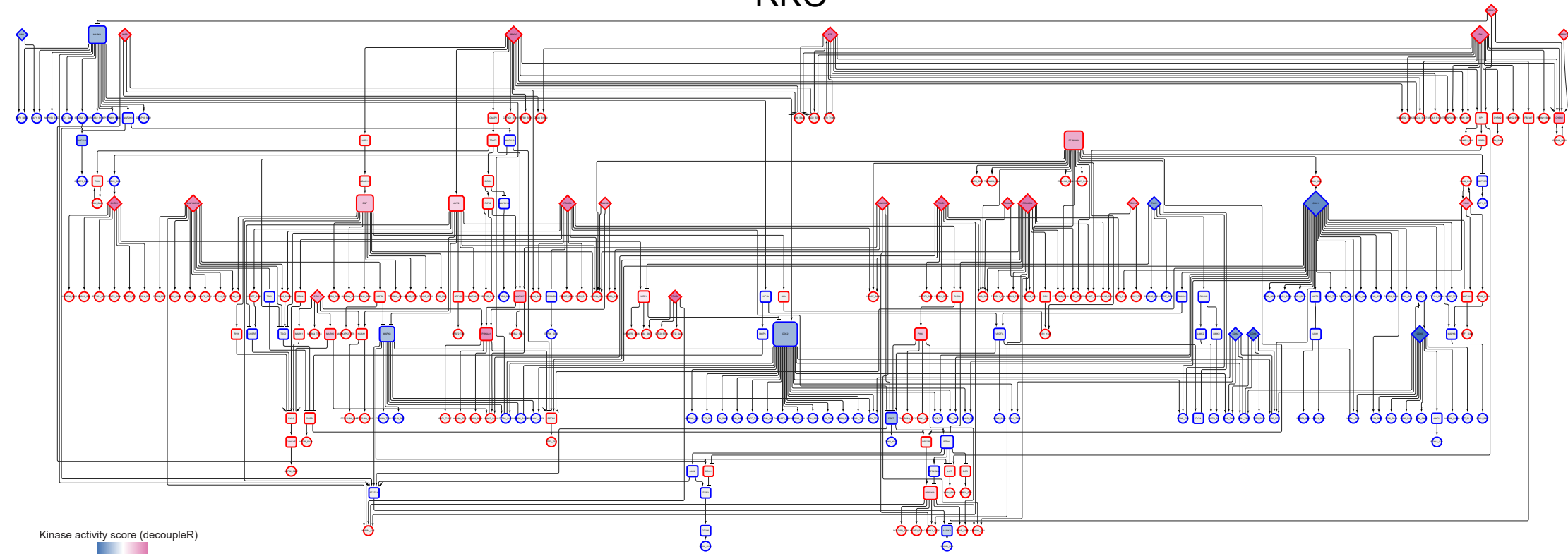


Figure S12G

RKO



Kinase activity score (decoupleR)



Protein activity (PHONeMeS)

Down Up



SNU-61

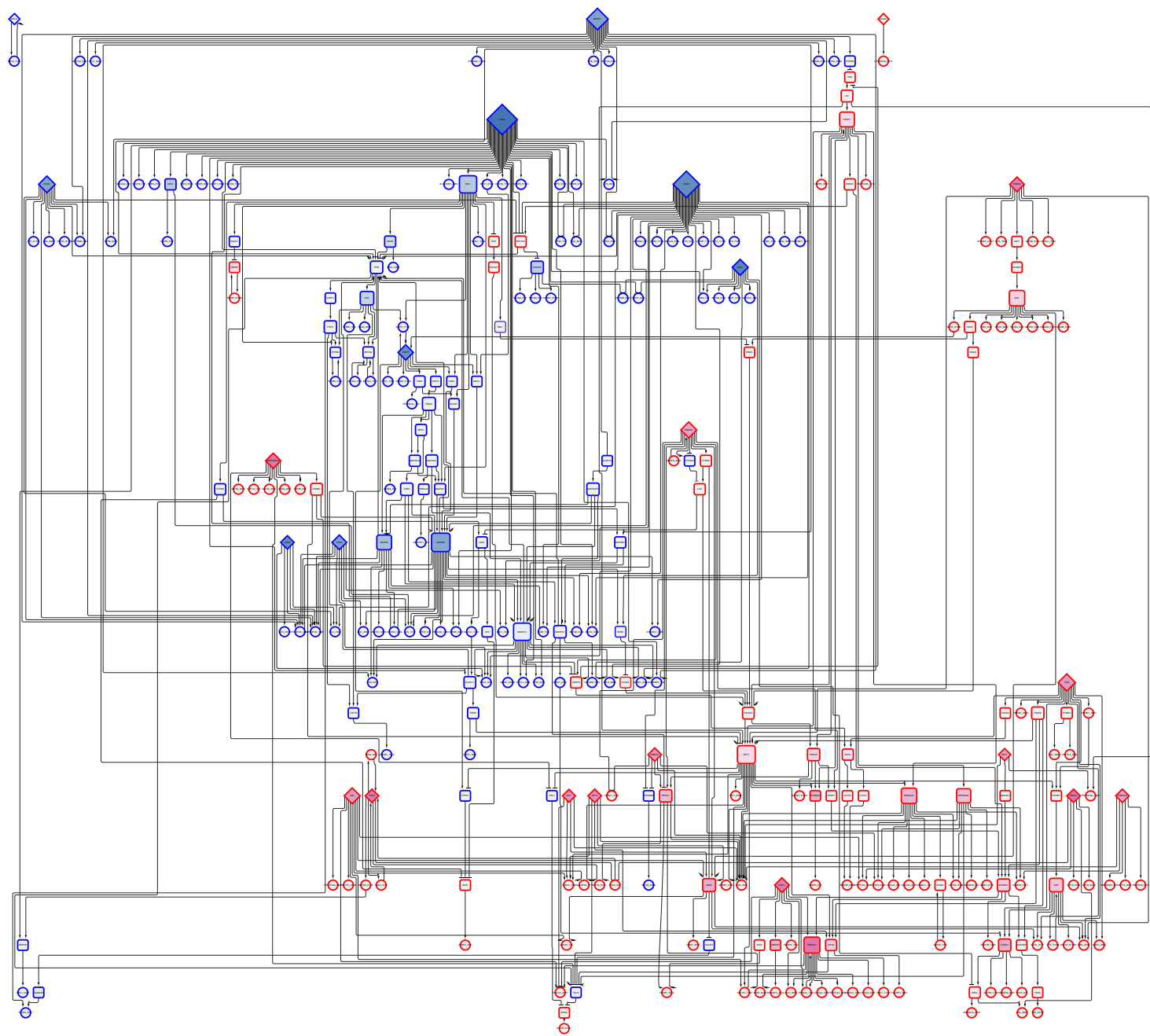


Figure S12I

SW48

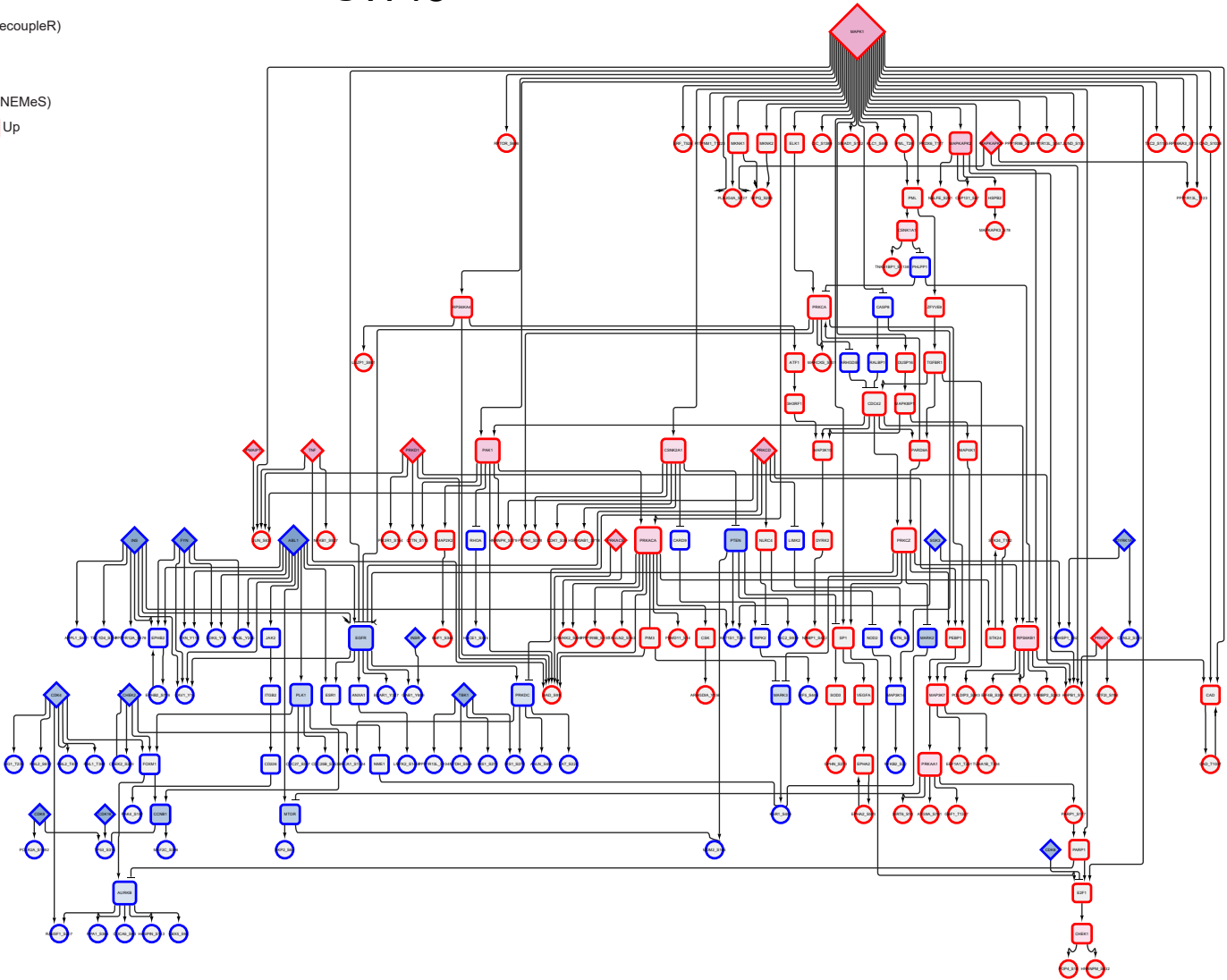
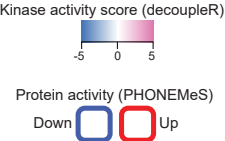


Figure S12J

SW837

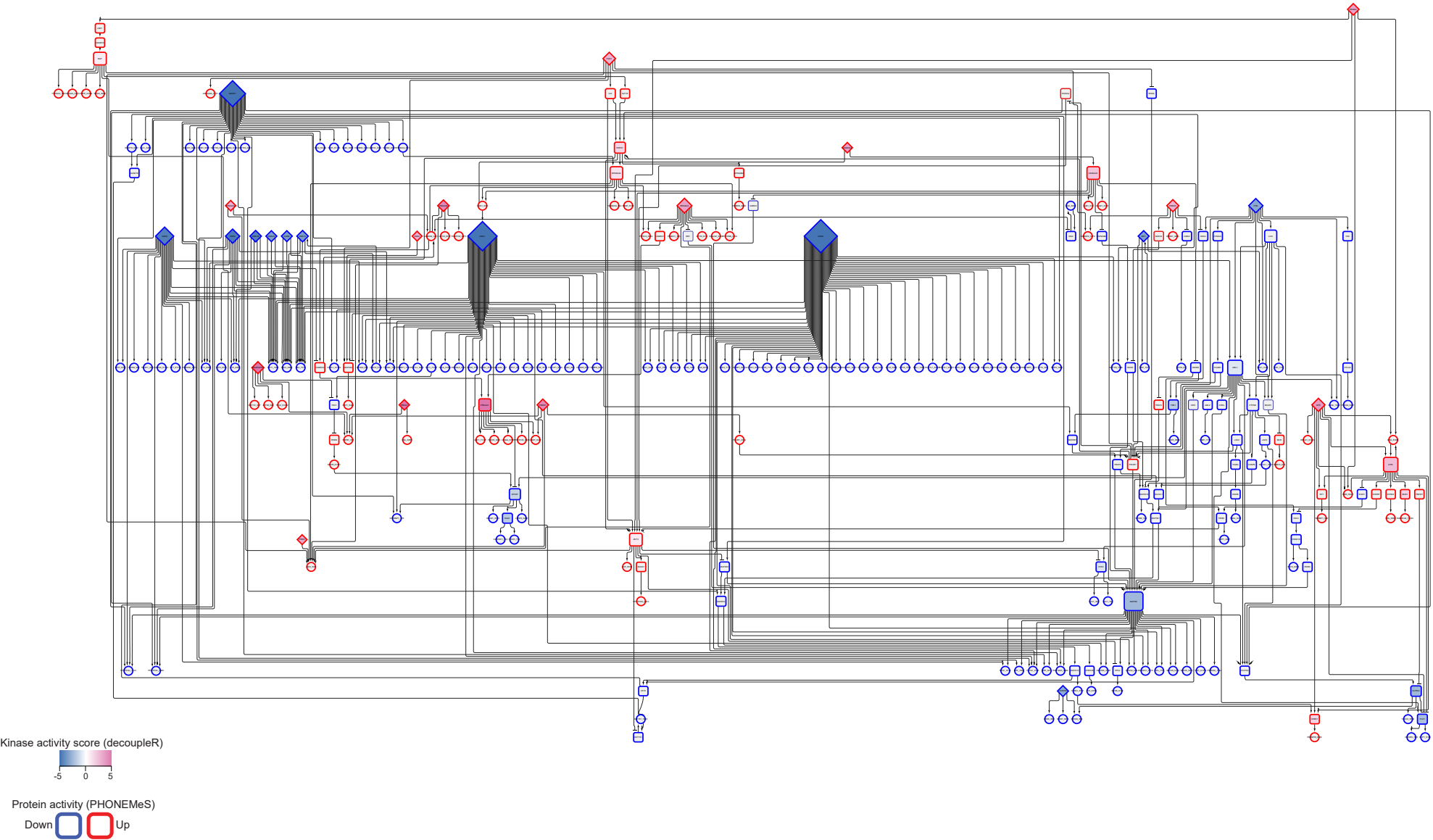


Figure S12K

SW948

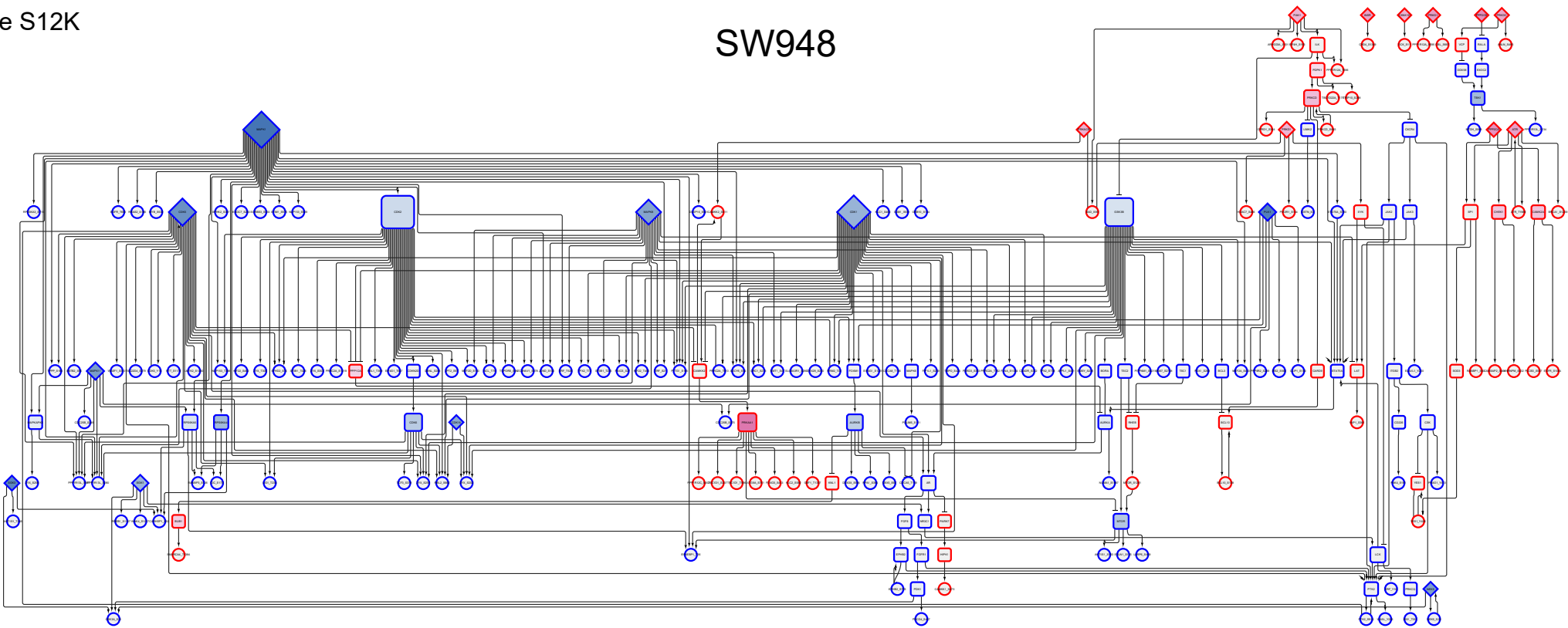
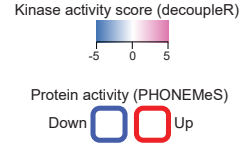


Figure S12L

T84

