

Table S4. All processed continuous data. This table is provided separately as a Microsoft Excel file. Data from receptor-specific cell lines are in separate spreadsheet tabs. Data are shown following the outlier flagging and condensing steps described in the Methods, such that only four biological replicates are shown for each time point (across each RTK-shRNA-phosphosite condition). Data are organized by phosphosite (rows), time points (columns), and shRNA conditions moving down the table. Biological replicate values are presented in adjacent rows.

Table S5. All discretized data used for network models. This table is provided separately as a Microsoft Excel file. Data from receptor-specific cell lines are in separate spreadsheet tabs. Data are shown following the outlier flagging and condensing steps described in the Methods. Following those steps, the median value was calculated across the four biological replicates and then discretized, such that only one discrete value is shown for each time point (across each RTK-shRNA-phosphosite condition). Data are organized by phosphosite (rows), time points (columns), and shRNA conditions moving down the table.