**Supplementary Data**

**Cell lines**

A549, AsPC-1, CAPAN-2, HPAF-ii, LS123, LS513, NCI-H1373, NCI-H1734, NCI-H1944, NCI-H2030, NCI-H23, NCI-H441, NCI-H747, SK-CO-1 and SW1990 were all purchased from ATCC (LGC Standards, Teddington, UK). CAPAN-1, CFPAC-1, COLO678, DAN-G, HuP-T4, MIA Paca-2, PANC-1, SNU-407 and SW1116 were all obtained from in house sources. LIM-1899 and LIM-2099 were purchased through Public Health England (Salisbury, UK). NCI-H1792, NCI-H358 and SK-LU-1 were kindly provided by The Francis Crick Institute Cell Services (London, UK). SW620 was purchased from Sigma-Aldrich (St. Louis, MO, USA).

**Culture medium**

All commercially purchased cell lines were grown in manufacturer-specified media. COLO678, DAN-G, NCI-H1792 and NCI-H358 were grown in RPMI-1640 (11835-063, Gibco, Burlington, ON, Canada). MIA Paca-2, PANC-1, SK-LU-1, SNU-407 and SW1116 were grown in Dulbecco’s Modified Eagle’s Medium (D5671, Sigma-Aldrich).CAPAN-1 (+20% FBS) and CFPAC-1 were grown in Iscove’s Modified Dulbecco’s Media (I3390, Sigma-Aldrich) and CFPAC-1 in Eagle’s Minimum Essential Medium (30-2003, LGC Standards). Additionally all media was supplemented with 20% FBS (unless otherwise stated, 10270-106, Gibco), 1mM L-Glutamine (25030-024, Gibco) and 1x MEM non-essential amino acid solution (Sigma-Aldrich, M7145). Cells were incubated at 37 oC with 5% CO2. All end point experiments were carried out in 20% FBS.

**Drug concentrations used**

The concentrations of drugs used were calculated from Cmax values in published literature of phase I studies AZD5363 (1), everolimus (2), gefitinib (3), luminespib/NVP-AUY22 (4), pictilisib/GDC-0941 (5), trametinib (6) and vemurafinib (7) adjusted for protein binding in the culture medium used.

The concentrations of drugs used in the screen include AZD5363 724.6 nM, everolimus 0.5 nM, gefitinib 27.8 nM, luminespib 116.4 nM, pictilisib 96.3 nM, trametinib 1.8 nM, vemurafinib 317606 nM.

**Cell culture**

All cell lines were grown to 80% confluence before exposing them to drugs.

**Methods for producing Figure 1**

This network was assembled using the canSAR v4 interactome (8) (excluding interactions between proteins in complex and transcriptional interactions) and visualised using Cytoscape 3.6.1 (9). Targets of drugs were identified using ChEMBL (10) bioactivity data accessed via canSAR.

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