Tumour	Cell line	AA mutation
Colorectal	COLO678	p.G12D
Colorectal	H747	p.G13D
Colorectal	LIM-1899	p.G12A
Colorectal	LIM-2099	p.G12C
Colorectal	LS123	p.G12S
Colorectal	LS513	p.G12D
Colorectal	SK-CO-1	p.G12V
Colorectal	SNU-407	p.G12D
Colorectal	SW1116	p.G12A
Colorectal	SW620	p.G12V
Lung	A549	p.G12S
Lung	H1373	p.G12C
Lung	H1734	p.G13C
Lung	H1792	p.G12C
Lung	H1944	p.G13D
Lung	H2030	p.G12C
Lung	H23	p.G12C
Lung	H358	p.G12C
Lung	H441	p.G12V
Lung	SK-LU-1	p.G12D
Pancreatic	ASPC-1	p.G12D
Pancreatic	CAPAN-1	p.G12V
Pancreatic	CAPAN-2	p.G12V
Pancreatic	CFPAC-1	p.G12V
Pancreatic	DAN-G	p.G12V
Pancreatic	HPAF-ii	p.G12D
Pancreatic	HuP-T4	p.G12V
Pancreatic	MIA paca-2	p.G12C
Pancreatic	PANC-1	p.G12D
Pancreatic	SW1990	p.G12D

Supplementary Table 1

KRAS mutations in colorectal, lung and pancreatic cell lines.

	VEGFR1	VEGFR2	cKIT	VEGFR3	MCSFR	TIE2	TIE1	PDGFRb	FLT3	PDGFRa
A2780	34.8	29.4	19.2	26.0	22.9	24.8	19.9	23.1	18.8	14.3
HT29	24.8	36.3	35.6	34.3	21.2	17.8	26.5	21.7	12.9	17.9
H520	35.3	29.3	17.8	21.7	17.6	12.6	22.2	38.0	19.4	32.6
	IGFR1pan	IRpan	HER3	HER4	GAPDH	ATF2	JNK	HSP27	AKT 308	p38
A2780	16.2	5.1	13.8	22.8	1.1	7.6	12.4	6.4	17.6	12.6
HT29	15.0	18.8	13.9	24.1	1.6	18.9	18.4	28.9	39.2	16.9
H520	16.8	7.2	8.7	21.6	1.7	14.5	20.1	18.2	23.7	10.1
	SRC	Total HSP27	NFkB	GSK3b	IGFR1	IRS1	AKT 473	mTOR	p70S6K	IR
A2780	19.3	2.9	23.8	12.7	22.4	28.1	13.2	10.2	14.0	13.4
HT29	12.3	11.1	17.2	8.7	28.1	16.8	15.0	10.2	15.0	13.6
H520	20.2	10.1	25.7	17.6	45.2	20.5	16.5	14.8	16.0	17.0
	ERK	LCK	p53	MEK1	MSK1	STAT1	STAT3	cJUN	EGFR	HER2
A2780	13.8	23.9	14.2	7.8	18.4	25.1	27.2	16.3	11.7	11.2
HT29	19.2	18.4	26.4	7.2	19.3	37.7	27.7	12.0	24.5	11.1
H520	12.4	14.2	21.0	8.8	13.1	24.9	12.1	16.5	31.7	13.4
	PTEN	GSK3a	TSC2	RPS6	cMET	CHK1	cRAF	Pras40	B-catenin	CHK2
A2780	27.7	13.4	20.2	10.5	37.9	15.5	14.9	15.7	15.0	32.1
HT29	16.1	12.7	16.1	12.1	16.1	24.1	16.0	27.2	32.6	25.6
H520	18.3	27.6	27.3	25.2	39.7	25.3	21.7	22.6	16.4	16.7
	AXL	RET	FAK	JAK1	Rb					
A2780	14.5	26.0	19.5	13.8	11.4					
HT29	6.0	29.4	8.6	12.9	11.5					
H520	20.5	20.5	21.6	10.8	28.8					

Supplementary Table 2

Assay variability

Coefficient of variance per analyte was calculated across three test cell lines (A2780, HT29 and NCI-H520). Each cell line was run in triplicate and each repetition was run across five separate 96 well plates. All plates were run in a single sitting to avoid inter-daily fluctuations. Values of coefficient of variance are displayed.

AZD5363		Everolimus		Gefitinib		Luminespib		Pictilisib		Trametinib		Vemurafenib	
Increased	Decreased	Increased	Decreased	Increased	Decreased	Increased	Decreased	Increased	Decreased	Increased	Decreased	Increased	Decreased
ERK	RPS6		p70S6K	ERK		MEK1		MEK1	p70S6K			ERK	GSK3B
MEK1			RPS6	MEK1		AKT308			RPS6			MEK1	AKT473
AKT473												MSK1	mTOR
AKT308													TSC2
													PRAS40
													p70S6K
													RPS6

Supplementary Table 3

Significant changes in phosphoproteins seen in more than 50% of cell lines

A significant change (either increased or decreased) was defined if the treatment values were above or below 2 standard deviations of the control. The changes in phosphoproteins seen in equal to or more than 50% of the 30 cell lines caused by individual drugs are shown.

		Pictilisib (nM)	Buparlisib (nM)
NSCLC	H1944	412	825
	H358	1029	989
	H1792	959	818
PANC	SW1990	909	1258
	CAPAN2	1024	1399
	HPAFii	737	1351
CRC	COLO678	1532	1615
	H747	814	1242
	LIM1899	710	1055

Supplementary Table 4

The GI_{50} concentrations of the two pan-PI3K inhibitors pictilisib and buparlisib used in validation experiments in Figure 4B.