Supplemental Methods:

Quantitative real time-polymerase chain reaction (qRT-PCR).

Pre-designed TaqMan gene specific primers (Life Technologies, Carlsbad, CA, USA): FGFR1 (forward: 5'-ACACCTTACACATGAACTCCAC-3', reverse: 5'-AGCATCAACCACACATACCAG-3'), FGFR2 (forward: 5'-GCTTGTCTTTGTCAATTCCCA-3', reverse: 5'-GTCTCCGAGTATGAACTTCCAG), FGFR3 (forward: 5'-CCAGCAGCTTCTTGTCCATC-3', reverse: 5'-GTACTGTGCCACTTCAGTGT-3').

Immunofluorescence Assay for LC3B.

Cells were plated in 8-well chamber slides at densities ranging from 5,000 to 9,000 cells/well. 24hrs after plating, they were treated with the indicated dose of AZD4547 or DMSO, irradiated with 3 Gy (Xstrahl RS225) after 1hr, and fixed with 70% methanol in PBS at indicated time points. Cells were permeabilized with 0.1% Triton-X 100 in TBST for 15 minutes, blocked with SuperBlockTM (Thermo Fisher #37515) for 1 hour in 25°C, and incubated with LC3B (D11) XP Rabbit mAb (Cell Signaling Technology #3868) antibody overnight at 4°C. Cells were then probed with Alexa Fluor 488 conjugated secondary antibody (CST #4413) for 1hr at 25°C in the dark, and cover-slipped with Fluoromount G containing DAPI. The next day, they were imaged at 60x magnification using a Nikon A1RS inverted point scanning confocal microscope system.

Supplementary Table 1. Short Tandem Repeat analysis of cell lines used in this study.

Cell Line	Source	Passage sent	Date sent	# of allelic match	% allelic match
NCI-H226	ATCC	P1	9/28/2017	29/29	100%
NCI-H520	ATCC	P1	9/28/2017	24/24	100%
NCI-H2228	ATCC	P1	9/28/2017	22/22	100%
NCI-H3122	ATCC	P1	9/28/2017	15/15	100%
NCI-H358	ATCC	P1	9/28/2017	26/26	100%
A549	ATCC	P1	9/28/2017	23/24	96%
NCI-H1581	ATCC	P1	9/28/2017	29/29	100%
BeasB2	ATCC	P1	8/20/2019	30/30	100%
HTE	Klingelhutz Lab, University of Iowa	P26	8/30/2017	See attached	

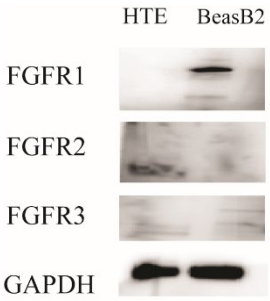
Supplementary Table 2. Antibodies used in this study.

Antibody	Source	Company	Catalog no.	Dilutions
AKT	Mouse	Cell Signaling Technology	2920	1:2000
α-Tublin	Mouse	Calbiochem	CP06	1:5000
Cleaved Caspase-3 (Asp175)	Rabbit	Cell Signaling Technology	9661	1:200
FGFR1	Rabbit	Cell Signaling Technology	9740	1:1000
FGFR2	Rabbit	Cell Signaling Technology	11835	1:1000
FGFR3	Rabbit	Cell Signaling Technology	4574	1:1000
GAPDH	Mouse	Cell Signaling Technology	97166	1:10000
phospho-AKT (Ser473)	Rabbit	Cell Signaling Technology	4060	1:1000
phospho-Histone H2AX (Ser139) (20E3)	Rabbit	Cell Signaling Technology	9718	In vitro 1:1000 In vivo: 1:200
phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204)	Rabbit	Cell Signaling Technology	4370	In vitro 1:1000 In vivo 1:200
phospho-p44/42 MAPK (Erk1/2)	Mouse	Cell Signaling Technology	4696	1:5000
phospho-S6 Ribosomal Protein (Ser235/236)	Rabbit	Cell Signaling Technology	4858	1:400

Supplemental Table 3: Dose Enhancement factors at survival fraction of 0.1 ($DEF_{0.1}$) and P-values for radiation clonogenic curves.

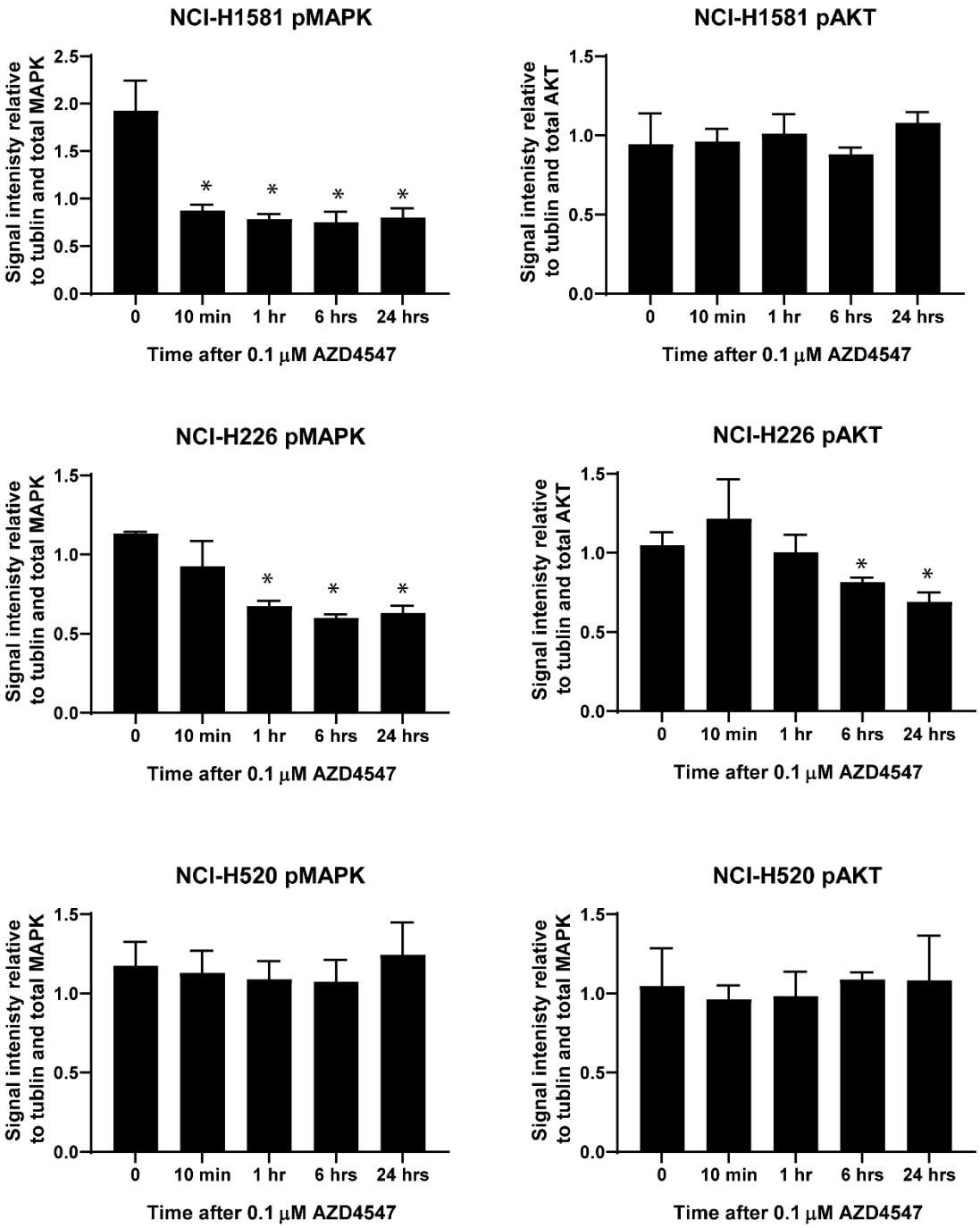
Cell line	$DEF_{0.1}$	P-value all points/curve (F-test)
NCI-1581	1.31	<0.0001
NCI-H226	1.29	<0.0001
NCI-H358	1.06	0.01
NCI-H520	1.11	0.36
NCI-H3122	1.08	0.077
A549	1.0	0.83
NCI-H2228	1.0	0.10
BeasB2	1.09	0.001
HTE	0.97	0.38

Supplemental Figure1



Western blot showing FGFR1, FGFR2 and FGFR3 protein levels in HTE and BeasB2 cell lines.

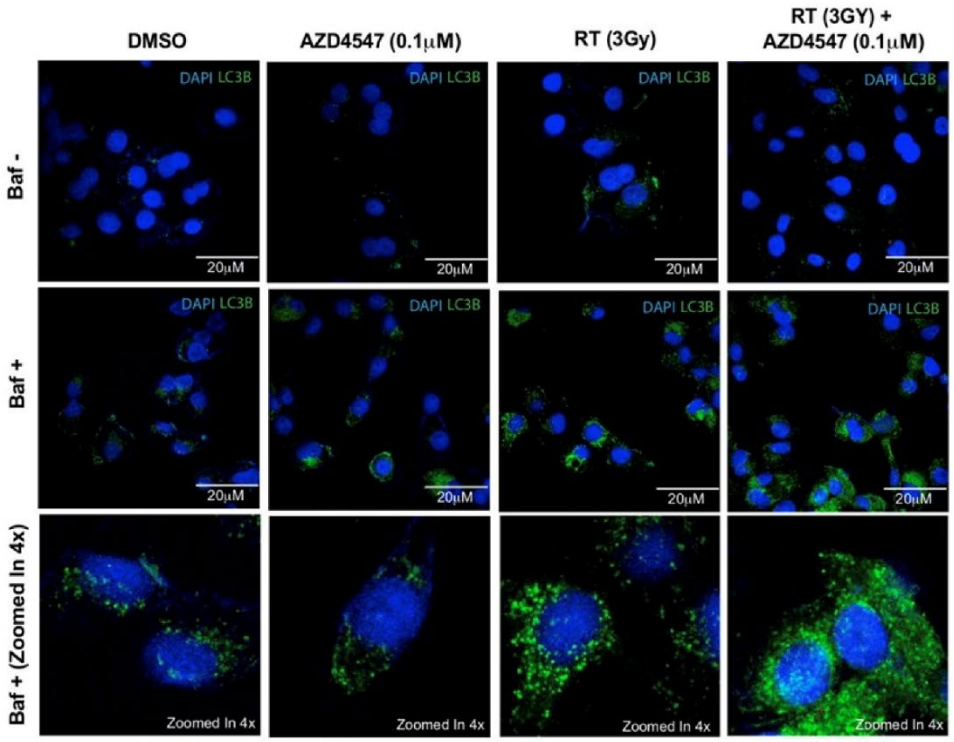
Supplemental Figure 2



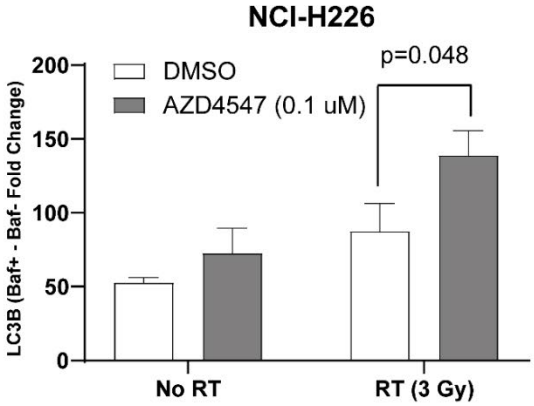
Normalized intensity quantification of pMAPK and pAKT proteins determined by western blot after treatment with AZD4547 in three NSCLC cell lines. NCI-H1581, NCI-H226 and NCI-H520 cells were treated for 10 minutes, 1 hour, 6 hours and 24 hours with 0.1 μM AZD4547. Intensity levels were first normalized to α-tublin and then either total MAPK or AKT, respectively. Columns, mean; bars, SEM (n=3), *, p-value <0.05 compared to no treatment.

Supplemental Figure 3

A



B



Combined radiation and AZD4547 induces autophagy. NCI-H226 cells were treated with DMSO, AZD4547 (0.1 μM), radiation (3 Gy), or combined AZD4547 (0.1 μM) and radiation (3 Gy) and analyzed at 72 hours post-treatment. (A) Representative immunofluorescence images tagged with LC3B antibody representing basal autophagy (Baf-) and autophagic flux (Baf+ minus Baf-) following treatments as indicated. (B) Quantification of Baf- and Baf+ fold change. Change in radiation plus AZD4547 compared to radiation alone was statistically significant with p-value of 0.048.

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Acct Ref 2:
Acct Ref 3:
MADISON, WI 53705

Cell Line Evaluation

LabCorp Case # **CX4-003942**

Sample	Label/Reference	LabCorp Id	Received
Cell Line Sample 1	**HTE (p.26)**	78U-9085-0	08/30/2017

DNA Analysis

	D3S1358	D7S820	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D16S539
SMP1	15, 17	8, 9	17, 18	20, 22	10, 13	30, 31	12, 16	10, 13	8, 11	9, 11

DNA Analysis

	TH01	TPOX	CSF1PO	AMEL	Penta D	Penta E	Mouse
SMP1	6, 8	11	11	X	9, 14	12, 16	NA*

Conclusion:

Sample number 78U-9085-0, labeled HTE (p.26) was submitted for identification. Fifteen autosomal short tandem repeat (STR) loci and the gender identity locus amelogenin were profiled using PowerPlex 16 HS (Promega Corporation). The electropherograms of analyzed data are attached.

NA* = No mouse DNA was detected for this sample.

Note: The information contained in this report does not constitute authentication of the submitted sample; further comparison to an appropriate reference sample (i.e. donor tissue/blood or low passage stock of in-house cell line) or database of cell line reference profiles is needed to designate the submitted sample as being related to a specific donor or reference cell line. A small amount of variation in the STR profiles of cell lines derived from the same donor is possible. It is recommended that an 80% match criteria be applied as detailed in the consensus standard ANSI/ATCC ASN-0002-2011. Authentication of human cell lines: Standardization of STR profiling.

Melanie S Trapani, PhD, F-ABC
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DNA Identification Testing Division
Laboratory Corporation of America
August 31, 2017