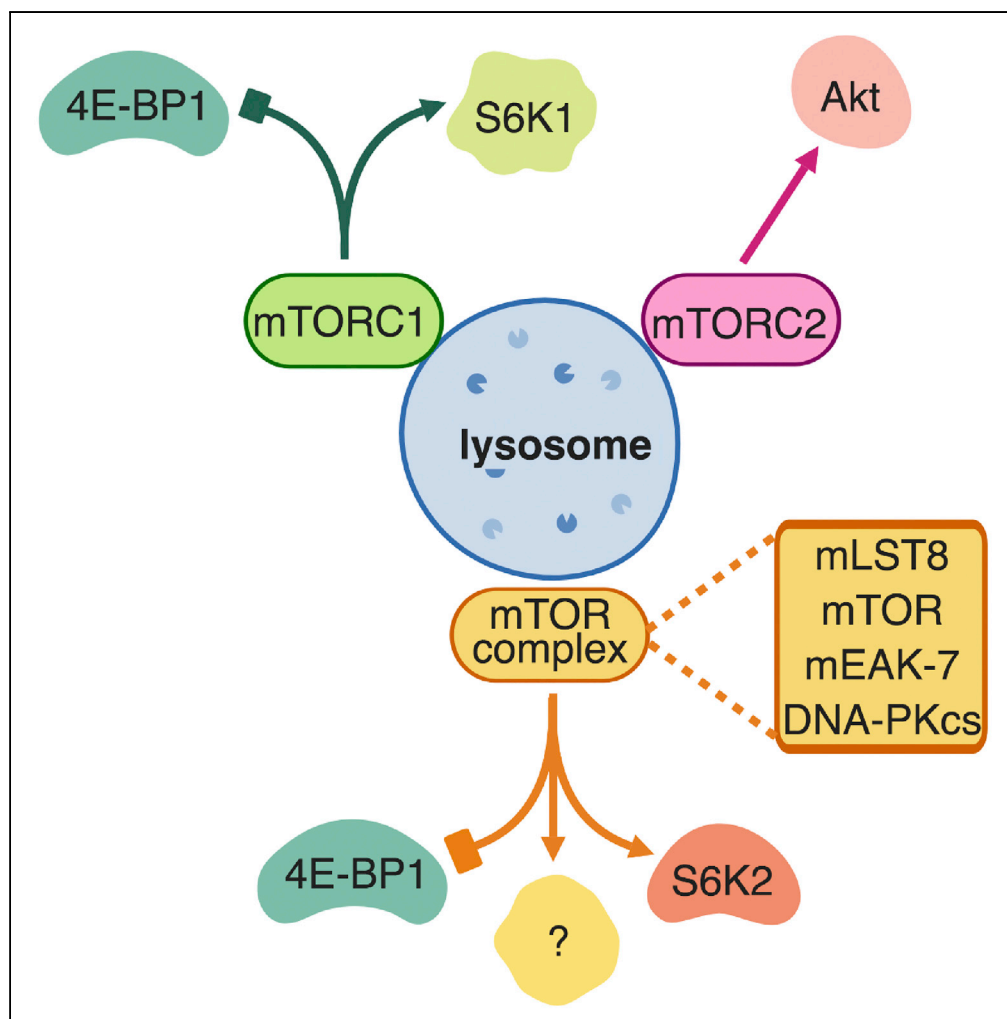


Article

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HIGHLIGHTS

mEAK-7 forms an
 alternative mTOR
 complex with DNA-PK
 in human cancer

mEAK-7 is upregulated in
 the metastasized lymph
 nodes of patients with
 NSCLC

DNA-PK is essential for
 mEAK-7-mTOR-S6K2
 signaling in human cancer

mEAK-7 is required for
 cancer cell clonogenicity
 and spheroid formation

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Article

mEAK-7 Forms an Alternative mTOR Complex with DNA-PKcs in Human Cancer

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SUMMARY

MTOR associated protein, eak-7 homolog (mEAK-7), activates mechanistic target of rapamycin (mTOR) signaling in human cells through an alternative mTOR complex to regulate S6K2 and 4E-BP1. However, the role of mEAK-7 in human cancer has not yet been identified. We demonstrate that mEAK-7 and mTOR signaling are strongly elevated in tumor and metastatic lymph nodes of patients with non-small-cell lung carcinoma compared with those of patients with normal lung or lymph tissue. Cancer stem cells, CD44+/CD90+ cells, yield elevated mEAK-7 and activated mTOR signaling. mEAK-7 is required for clonogenic potential and spheroid formation. mEAK-7 associates with DNA-dependent protein kinase catalytic subunit isoform 1 (DNA-PKcs), and this interaction is increased in response to X-ray irradiation to regulate S6K2 signaling. DNA-PKcs pharmacologic inhibition or genetic knockout reduced S6K2, mEAK-7, and mTOR binding with DNA-PKcs, resulting in loss of S6K2 activity and mTOR signaling. Therefore, mEAK-7 forms an alternative mTOR complex with DNA-PKcs to regulate S6K2 in human cancer cells.

INTRODUCTION

Aberrant mechanistic target of rapamycin (mTOR) signaling has been observed in many types of human cancer (Saxton and Sabatini, 2017). Recently, mEAK-7 (mammalian EAK-7 or MTOR associated protein, eak-7 homolog) was identified as a molecular activator of mTOR signaling in human cells (Nguyen et al., 2018). Interestingly, mEAK-7 exhibits a preferential expression pattern in human cancer cell lines (Nguyen et al., 2018). Although EAK-7 regulates dauer formation and lifespan in *C. elegans* (Alam et al., 2010), the extent to which EAK-7 functions similarly in nematodes and mammals to regulate TOR/mTOR function is unknown.

mEAK-7 uses the S6K2/4E-BP1 axis to regulate mTOR signaling (Nguyen et al., 2018). S6K2 signaling has not been adequately delineated from that of S6K1 signaling owing to their assumed functional redundancies (Pardo and Seckl, 2013). However, in breast cancer cells, loss-of-function studies demonstrate that S6K1 and S6K2 have several different protein targets (Karlsson et al., 2015). In addition, canonical models of mTOR complex 1 (mTORC1), the traditional S6K regulators, and mTORC2 may not exist similarly in all cell types. As examples of this phenomena, an mTOR complex that involves GIT1, which is distinct from mTORC1 and mTORC2, has been identified in astrocytes (Smithson and Gutmann, 2016), and ETS Variant 7 is capable of binding to mTOR and sustaining mTOR signaling in the presence of rapamycin (Harwood et al., 2018). These pivotal findings disrupt conventional ideas regarding the existence of only two mTOR complexes and therefore suggest the possibility of other, unidentified mTOR complexes.

Although it is largely believed that mTOR signaling is suppressed under genotoxic stress via AMPK regulation of TSC2 (Feng et al., 2007), studies have demonstrated aberrant activation of mTOR signaling in response to DNA damage. For example, mTORC1 signaling inhibits DNA damage response mechanisms *in vitro* and *in vivo* through RNF168 (Xie et al., 2018). S6K2, another crucial mTOR target, may also function in the DNA damage response, as S6K2 knockdown results in strong reduction of mTOR signaling, even in the presence of DNA damage (Xie et al., 2018). Furthermore, CHK1 function relies on mTORC1 signaling in response to DNA damage repair processes. These findings suggest that mTOR signaling supports DNA damage responses (Zhou et al., 2017). In examining the role of radiation in DNA damage, sustained radiation treatment to mice activates mTOR signaling and oxidative stress in the intestine (Datta et al., 2014), whereas normal tissues undergoing long-term radiation stress exhibit activated mTOR signaling in mini pigs (Zhu et al., 2016). Thus, there is a rationale to treat patients with a combination of chemotherapeutics that induce DNA damage and mTOR inhibitors, like rapamycin, due to additive cytotoxic effects in breast

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carcinoma cell lines (Mondesire et al., 2004). These studies suggest that mTOR signaling and DNA damage repair processes may function synergistically in specific biologic contexts, such as during the downregulation of p53 via S6K-mediated activation of MDM2 (Lai et al., 2010), or the phosphorylation of 4E-BP1 phosphorylation in response to DNA damage (Braunstein et al., 2009). Thus, we posit a mechanism supporting sustained mTOR signaling after genotoxic stress, which may allow enhanced cancer cell survival through radiation resistance.

Cancer stem cells (CSCs) are known to be radiation resistant and thrive under genotoxic stress, but the molecular mechanisms responsible for these adaptations remain unknown (Bao et al., 2006; Diehn et al., 2009). CSCs are a self-renewing population of cells within a tumor mass (Al-Hajj et al., 2003), and mTOR signaling has been implicated in regulating pancreatic CSC viability and self-renewal (Matsubara et al., 2013). This suggests that this population of cancer cells utilizes mTOR signaling to contribute to the survival and pathogenicity of human cancers. Data from a medulloblastoma *in vivo* model of CSCs suggest that phosphatidylinositol 3-kinase (PI3K) signaling is activated in response to DNA damage, as indicated by S6 regulation, a crucial readout of mTOR signaling (Hambardzumyan et al., 2008). This substantive evidence suggests that mTOR signaling plays an important role in CSC DNA damage response and self-renewal.

Given that genotoxic stressors are capable of activating mTOR signaling, select CSCs were found to demonstrate radiation resistance, and because CSCs require mTOR signaling, we sought to determine the extent to which mEAK-7 contributes to radiation resistance and self-renewal in cancer cells through an alternative pathway involving mTOR.

RESULTS

mEAK-7 Protein Levels Are Elevated in Metastatic Human Non-Small Cell Lung Carcinoma Lymph Nodes

Although mEAK-7 protein levels appear to be disproportionately high in human cancer cell lines when compared with non-cancerous cells (Nguyen et al., 2018), this limited observation does not exclude the possibility that mEAK-7 is present in healthy human tissues, because mTOR expression is found in many tissue types (Kim et al., 2002). To gain a better understanding of the expression pattern of mEAK-7 in healthy human tissues, we accessed the GTEx database and identified basal-level expression of *MEAK7* in many human tissues (Figure 1A). The BioGPS database also confirmed that *MEAK7* is expressed in diverse tissue types (Figure S1A) (Wu et al., 2009, 2013, 2016). Thus, future analyses of mEAK-7 in healthy tissues are essential to understanding the role of mEAK-7 in mammalian development and metabolism.

To identify *MEAK7* genomic alterations in human patients with cancer, we accessed the cBioPortal database. Genetic modifications to *MEAK7* included deletions, copy number amplifications, and mutations; yet these modifications were found to be cancer type dependent (Figures 1B and 1C). For example, many prostate cancers exhibit *MEAK7* deletions, whereas breast cancers often sustain substantial *MEAK7* gene copy number amplification (Figure 1B). Because of these different genetic profiles, the search parameters were narrowed to include only gain of expression and copy number amplification. The percentage of patients that demonstrated either of these anomalies ranged between 5% and 50% (Figure 1C) (Cerami et al., 2012; Gao et al., 2013), demonstrating that *MEAK7* genetic modifications are cancer type specific and can be observed in a diverse array of human cancers.

The TCGA cBioPortal revealed high expression of *MEAK7* in patients with non-small-cell lung carcinoma (NSCLC) (Figure 1C). In addition, the majority of our first report into the mechanistic function of mEAK-7 was done in NSCLC lines, H1299 and H1975 (Nguyen et al., 2018). Therefore, the OncoPrint database was accessed to analyze *MEAK7* expression patterns in lung carcinomas when compared with expression patterns in healthy lung tissue. Through two different lung cancer studies, *MEAK7* was found to be highly expressed in many NSCLCs and small cell lung carcinomas, when compared with normal lung tissue, suggesting that *MEAK7* may play a role in lung tumorigenesis (Figures 1D and 1E) (Rhodes et al., 2004). Also, an association was found between *MEAK7* expression and outcomes of patients with cancer. Patients who died from ductal breast carcinoma ($p = 2.72 \times 10^{-6}$, Fold Change: 2.136) and acute myeloid leukemia ($p = 7.99 \times 10^{-5}$, Fold Change: 2.655) had enhanced *MEAK7* expression (Figures S1B and S1C) (Rhodes et al., 2004). Thus the *MEAK7* expression profile of patients with cancer may provide insight into predicting patient prognosis and survival.

Figure 1. MEAK7 Gene Expression Is Detected in Normal Human Cells and Upregulated in Select Human Cancer Types

(A) Genotype-Tissue Expression (GTEx) database analysis of MEAK7 expression in normal human tissues.

(B and C) (B) The Cancer Genome Atlas cBioPortal analysis MEAK7 for all genomic alterations or (C) for only gain of mRNA expression or amplification of gene copy number. The results shown are based on data generated by TCGA Research Network: <http://cancergenome.nih.gov/>.

(D and E) OncoPrint analysis of MEAK7 gene expression of patients with normal lung and lung cancer via two different studies: (D) Garber Lung Study analysis by Student's t test 2-sample equal variance and (E) Hou Lung Study analysis by Mann-Whitney U test, $p < 0.01$, 2-tailed.

In a screen of human squamous cell carcinomas, the UM-SCC-17A cell line (Brenner et al., 2010), derived from the primary laryngeal cancer site of a 48-year-old female patient, did not express detectable levels of mEAK-7 protein (Nguyen et al., 2018). Interestingly, the UM-SCC-17B cell line, derived from a metastatic site from the same patient, did express mEAK-7 (Nguyen et al., 2018). These findings suggest that increased expression of mEAK-7 may be associated with tumor metastasis. To test the hypothesis that elevated mEAK-7 protein levels are associated with cancer metastasis, the protein expression patterns of primary tumors and confirmed metastases closest to lymph tissues of patients with cancer were compared with healthy lung and lymph tissues. An NSCLC tissue microarray containing 30 individual pathologist-graded, patient-matched sections of primary tumors, as well as their normal adjacent tissue, and metastatic lymph nodes were stained and analyzed. mEAK-7 and (Ser^{240/244}) p-S6 protein levels were significantly elevated in the primary human tumor when compared with the normal adjacent tissue (Figures 2A–2C). Furthermore, mEAK-7 and (Ser^{240/244}) p-S6 protein levels were significantly greater in the metastatic lymph nodes when compared with both primary tumor and normal adjacent tissue (Figures 2A–2C). However, healthy adult lymph tissue did not yield substantial mEAK-7 or (Ser^{240/244}) p-S6 protein levels (Figure S2A). Thus, mEAK-7 protein and activated mTOR signaling was found to be enhanced in primary NSCLC, and substantially detected in metastasized lymph nodes, suggesting that mEAK-7 could function as a biomarker for patients with metastasized cancers.

As OncoPrint databases demonstrate that higher MEAK7 expression is associated with poor patient prognoses (Figures S1B and S1C), we sought to investigate this via a lung adenocarcinoma tissue microarray detailing patient survival data. The microarray stained with antibodies targeting endogenous mEAK-7 and (Ser^{240/244}) p-S6 and a Kaplan-Meier Survival Curve analysis illustrated that mEAK-7 protein levels were strongly associated with poor patient prognosis, specifically in patients with relapse following surgical intervention (Figure 2D).

Because mEAK-7 protein levels were highly expressed in metastasized lymph nodes, we tested the extent to which mEAK-7 is required for cell invasion *in vitro*. To test this, H1975 cells were treated with control or mEAK-7 small interfering RNA (siRNA) for 48 h and 50,000 cells were seeded into invasion chambers for 24 h. Results demonstrated a statistically significant reduction in cell invasion after 24 h (Figure 2E). Thus, mEAK-7 may be a clinically relevant biomarker for predicting the prognosis of patients with metastatic NSCLC.

Cancer Stem Cells Exhibit High Protein Levels of mEAK-7 and mTOR Signaling

mEAK-7 is a strong, positive regulator of mTOR signaling (Nguyen et al., 2018), and several groups have demonstrated that mTOR signaling is essential for CSC self-renewal (Matsubara et al., 2013) and radiation resistance (Fang et al., 2013). Therefore, we hypothesized that mEAK-7 is differentially expressed in the CSC versus non-CSC populations. Because the majority of information on human mEAK-7 has been demonstrated in NSCLC cell lines H1975 and H1299, we sought to determine the expression profile of mEAK-7 and mTOR signaling in NSCLC CSCs. These cells are best identified as being CD44+ (Leung et al., 2010) and CD90+ (Wang et al., 2013). Therefore, H1299 cells were subjected to fluorescence-activated cell sorting for the aforementioned markers. CD44+/CD90+ cells, representing 1% of all cells sorted, were analyzed for mEAK-7 and mTOR signaling (Figure 3A). Immunoblot analysis demonstrated that CD44+/CD90+ H1299 cells, when compared CD44–/CD90–, yielded greater protein levels of mEAK-7 and S6K2, as well as activated mTOR signaling, as measured via p-S6 and p-4E-BP1 protein levels (Figure 3B). The CD44+/CD90+ cell population expressed n-cadherin (Figure 3B), which is known as an essential component of the epithelial-mesenchymal transition state in CSCs and suggests that high levels of mEAK-7 in cancer cells are more likely to metastasize (Liu et al., 2014). Similar results were observed in CD44+/CD90+ H1975 cells (Figures S2B and S2C). Collectively, these results demonstrate that there is a selective expression profile of mEAK-7 and S6K2 in self-renewing CSCs.

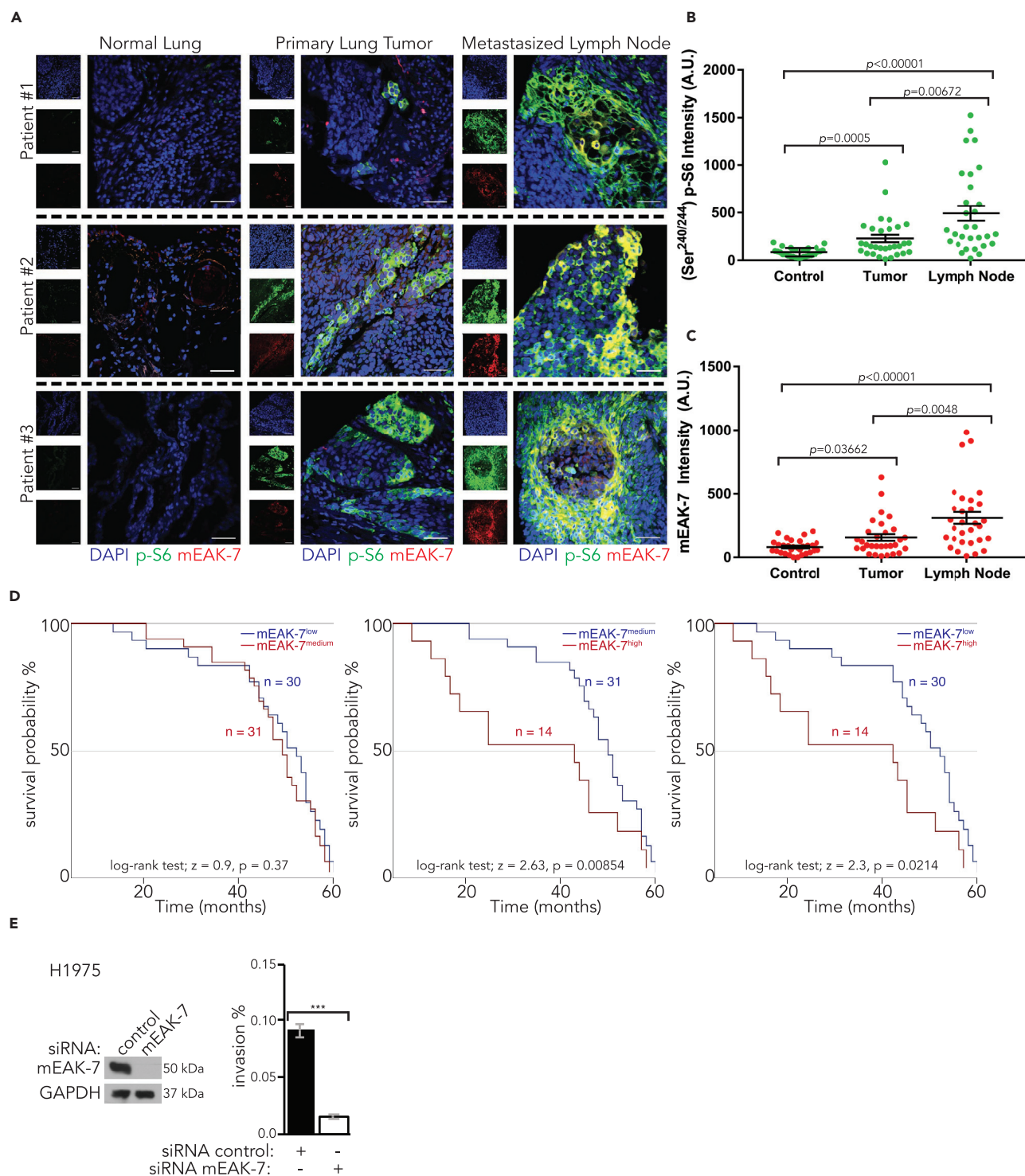


Figure 2. mEAK-7 Protein Levels Are High in Nearby Lymph Nodes of the Tumor Mass in Patients with NSCLC

(A) Three representative human patient tissue sections stained for (Ser^{240/244}) p-S6 and mEAK-7. Scale bar, 250 μ m.

(B) Statistical analysis of 30 paired patients with NSCLC with the normal lung, primary tumor, and metastasized lymph node for (Ser^{240/244}) p-S6 staining. Mann-Whitney U test was used.

Figure 2. Continued

(C) Statistical analysis of 30 paired patients with NSCLC with the normal lung, primary tumor, and metastasized lymph node for mEAK-7 staining. Mann-Whitney U test was used.

(D) NSCLC tissue microarray analysis of Kaplan-Meier survival curves. Log rank test was used.

(E) H1975 cells were treated with control or mEAK-7 siRNA for 48 h; 50,000 cells were seeded into *in vitro* Matrigel-based invasion chambers and allowed to grow for 24 h. Analyzed by Student's t test ($n = 6$). *** $p < 0.0001$. Experiments were repeated at least six times.

mEAK-7 Is Necessary for Clonogenic Potential and Spheroid Formation in Human Cancer Cells

To test the hypothesis that mEAK-7 affects cell survival following X-ray irradiation damage, a 2D clonogenicity assay was used to assess the surviving fraction of irradiated cancer cells (Franken et al., 2006; Puck and Marcus, 1956). H1299 and H1975 cells were treated with control or mEAK-7 siRNA for 48 h and then subjected to no treatment or X-ray irradiation of 2 or 6 Gy. These cells were then reseeded into new 60-mm tissue culture plates and allowed to grow for 10 days. In both H1299 and H1975 cells, clonogenic potential was significantly decreased after mEAK-7 knockdown, but little additional effects were found after exposure to 2- and 6-Gy X-ray irradiation in both H1299 and H1975 cells (Figures 3C–3H). This suggests that mEAK-7 alone is capable of regulating clonogenic potential to a dramatic extent. In H1299 and H1975 cells, similar results were observed at higher cell seeding densities (Figure S2D) or by utilizing a different siRNA mEAK-7 (Figures S3A and S3B), demonstrating that mEAK-7 enhances the clonogenic potential of human cancer cells in response to DNA damage.

Two-dimensional assays measuring clonogenic potential demonstrate the essential role of mEAK-7 in the DNA damage response, whereas 3D assays better simulate *in vivo* conditions. The spheroid-forming assay is a widely accepted experimental strategy to identify stem cell self-renewal in mammalian cell systems *in vitro* and *in vivo* (Pastrana et al., 2011). Furthermore, CSCs are the principal cancer cell population responsible for spheroid formation (Weiswald et al., 2015). Thus, to test the effect of mEAK-7 on spheroid size and formation, H1975 cells were treated with control or mEAK-7 siRNA for 48 h, subjected to no treatment or 2- or 6-Gy X-ray irradiation, and subsequently seeded in ultra-low attachment dishes for 1 week. mEAK-7 knockdown resulted in a dramatic reduction in spheroid size with no treatment, or 2- or 6-Gy treatment (Figure 4A). In addition, the gross number of spheroids formed was significantly reduced after mEAK-7 knockdown, and even further reduced following 2- or 6-Gy X-ray irradiation treatment (Figure 4B). Similar results were observed when H1975 cells were seeded at a lower density (Figure S3C) and when a different mEAK-7 siRNA was used in both H1299 and H1975 cells (Figures S3D and S3E). These results collectively indicate that mEAK-7 plays a significant role in cancer cell spheroid formation.

mEAK-7 Is Necessary for Chemoresistance, Radiation Resistance, and Sustained DNA Damage-Mediated mTOR Signaling in Human Cancer Cells

Although X-ray irradiation is a potent inducer of the DNA damage response pathway, we hypothesized that other forms of genotoxic stress may similarly regulate mEAK-7. Cisplatin is a chemotherapeutic drug often used to treat patients with cancer with solid tumors. Cisplatin is widely used for the treatment of solid tumors because it has the ability to activate the DNA damage response and allow cells to undergo apoptosis. Although the mechanism of action would take 20 years to unravel, it was clear that cisplatin produced DNA adducts and forced double-stranded breaks in the DNA. However, following initial tumor regression, a fraction of solid tumors become chemoresistant (Galluzzi et al., 2012). mTOR signaling can be activated during cisplatin treatment of ovarian cancer cells over time, as measured by enhanced (Thr³⁸⁹) p-S6K1 protein levels (Peng et al., 2010). As mEAK-7 is required for mTOR signaling, we tested the hypothesis that mEAK-7 is an essential modulator of mTOR signaling following genotoxic stress induced by cisplatin treatment. To test the extent to which genotoxic stress modifies mEAK-7 activity, H1299 cells were treated with mEAK-7 siRNA for 48 h. Next, these cells were treated with either DMSO or 10 μ M cisplatin for 4 or 8 h. mEAK-7 protein levels were increased in response to DNA damage by cisplatin treatment. Furthermore, mEAK-7 was required for regulation of (Ser⁶⁵) p-4E-BP1, an indicator of mTOR signaling (Figure 4C). Therefore, cisplatin is capable of regulating mEAK-7-mediated mTOR signaling.

mEAK-7 Knockdown Impairs the DNA Damage Response and Enhances Noxa Levels after X-Ray Irradiation

Cancer cells utilize many mechanisms to promote radioresistance in response to cancer therapies (Kim et al., 2009). To determine the role of X-ray irradiation on mEAK-7 and the DNA damage response,

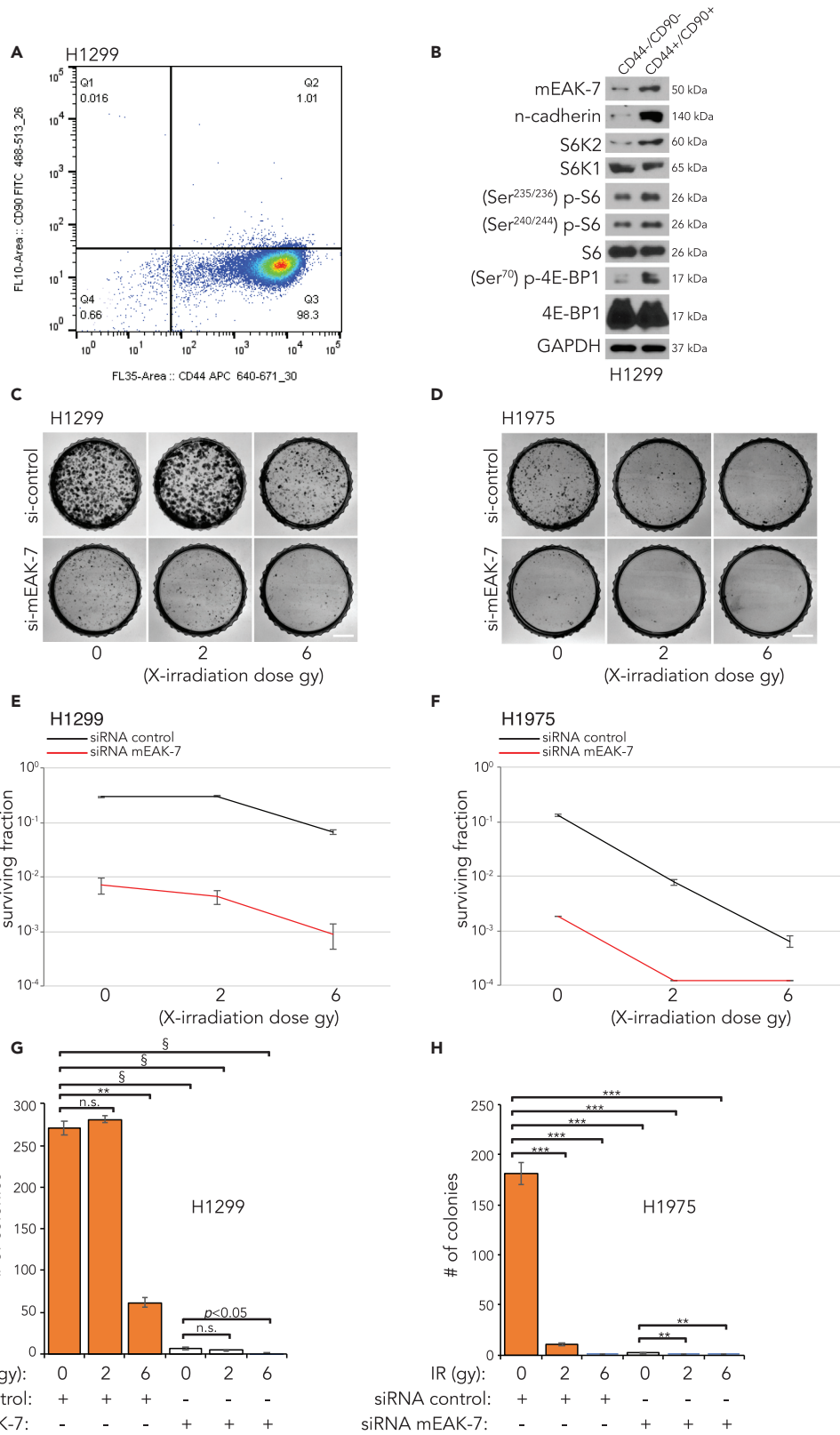


Figure 3. mEAK-7 Is Expressed in CD44+/CD90+ Group and Required for Clonogenic Potential and Radiation Resistance

(A) Flow sort diagram depicting the CD44+/CD90+ cell population in H1299 cells.

(B) Immunoblot analysis of CD44–/CD90– and CD44+/CD90+ H1299 cells for mEAK-7 and mTOR signaling.

(C) H1299 cells were treated with control or mEAK-7 siRNA for 48 h, X-ray irradiated at 2 or 6 Gy, and 2,500 cells were seeded into 60-mm tissue culture plates (TCPs) and grown for 10 days.

(D) H1975 cells were treated with control or mEAK-7 siRNA for 48 h and subjected to no treatment or 2- and 6-Gy X-ray irradiation, and 5,000 cells were seeded into 60-mm TCPs and grown for 10 days. Scale bars, 2.5 mm.

(E) H1299 surviving fraction analysis for (C).

(F) H1975 surviving fraction analysis for (D).

(G) H1299 colony number graphs for (C).

(H) H1975 colony number graphs for (D).

Analysis of clonogenic assay via Student's *t* test. ***p* < 0.001, ****p* < 0.0001, §*p* < 0.000001. All experiments were repeated at least three times, and (C–H) was repeated six times.

H1975 cells were treated with control or mEAK-7 siRNA, and X-ray irradiated with 20 Gy for up to 2 h. H1975 cells treated with mEAK-7 siRNA exhibited a dramatic increase in Noxa levels (Figure 4D). We also found similar results in H1299 cells treated with mEAK-7 siRNA and subjected to X-ray irradiation (Figure S3F). Upregulation of Noxa occurs in response to DNA damage after mEAK-7 knockdown (Figure 4D), which ultimately leads to cellular apoptosis (Ploner et al., 2008), suggesting that mEAK-7 plays a role in the DNA damage response and cancer cell survival. Noxa is known to be regulated by p53-dependent mechanisms through oncogene-independent apoptosis induced by genotoxic stressors, where p53 activates both survival and apoptotic pathways through p21WAF1/Cip1 (Shibue et al., 2003). However, Noxa has also been shown to function through p53-independent mechanisms, where ATF3 and ATF4 are induced by cisplatin, a DNA-damaging agent, and downregulation of ATF3 or ATF4 reduces Noxa expression because ATF3 and ATF4 bind to and cooperatively activate the Noxa promoter (Sharma et al., 2018). As H1975 is a p53 wild-type NSCLC line and H1299 is a p53-null NSCLC line, mEAK-7 may regulate Noxa expression through a p53-independent mechanism.

The comet assay is used to quantify intracellular DNA damage resulting from an insufficient DNA damage repair response in eukaryotic cells (Collins, 2004). H1299 and H1975 cells were independently embedded in an agarose gel and lysed, thereby releasing intracellular DNA. During gel electrophoresis, DNA fragments migrate toward the anode, resulting in a “comet” pattern with a trail of DNA fragments, such that a longer trail signifies more fragments, and therefore more DNA damage (Ostling and Johanson, 1984). Owing to the dramatic results from radiation treatment with mEAK-7 knockdown in the clonogenicity (Figures 3C–3H) and spheroid assays (Figures 4A and 4B), we hypothesized that mEAK-7 plays a crucial role in the DNA damage repair pathways. The visualization of DNA strand migration via the comet assay, and subsequent quantification of that migration, allowed us to predict the relative levels of the DNA repair response. H1299 and H1975 cells were treated with control or mEAK-7 siRNA and subjected to no treatment or 2- or 6-Gy X-ray irradiation for 30 min. Comet pattern formations, quantified as tail DNA %, were enhanced in H1299 and H1975 cells treated with mEAK-7 siRNA and X-ray irradiation (Figures 4E–4H), suggesting mEAK-7 is necessary for the DNA repair response in these cancer cells.

mEAK-7 Interacts with DNA-PKcs in Response to X-Ray Irradiation Damage

To determine the extent to which mEAK-7 regulates genotoxic activation of mTOR signaling, we sought to identify interacting partners of mEAK-7 by transducing H1299 cells with a lentivirus expressing pLenti-GIII-HA(c-term)mEAK-7. Through hemagglutinin (HA)-mEAK-7 immunoprecipitation (IP) and mass spectrometric (MS) analysis, a list of proteins that potentially interact with mEAK-7 was generated (Table S1). DNA-dependent protein kinase catalytic subunit isoform 1 (DNA-PKcs) scored the highest with 241 exclusive spectral counts and 36% protein coverage (Figure 5A). As with the canonical role of DNA-PKcs in the DNA damage response, ataxia mutated (ATM) and ataxia telangiectasia- and Rad3-related (ATR) also play essential and redundant roles in repairing damaged DNA, because all three share similar targets in response to DNA damage (Ciccio and Elledge, 2010; Nguyen et al., 2018). These data suggest that other phosphatidylinositol 3-kinase-related kinase (PIKK) members, like DNA-PKcs and mTOR, could also work in concert to regulate metabolism. Thus, we posited that mEAK-7 regulates mTOR signaling, in part, through the interaction with DNA-PKcs.

To confirm our IP/MS results, protein lysates were harvested from H1299 cells stably transduced with HA-mEAK-7. Exogenous mEAK-7 interacted with endogenous DNA-PKcs (Figures 5B and 5C). Under UV B

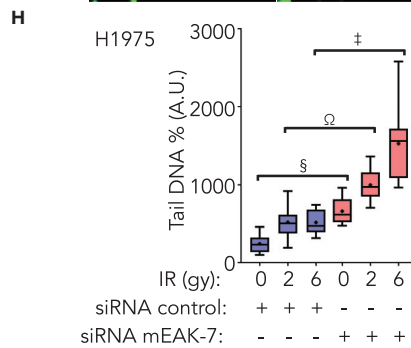
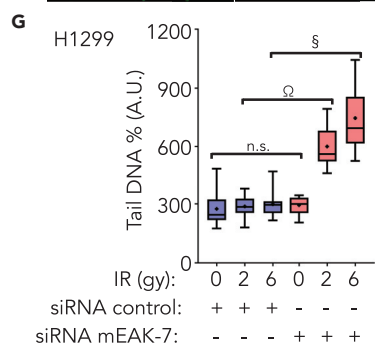
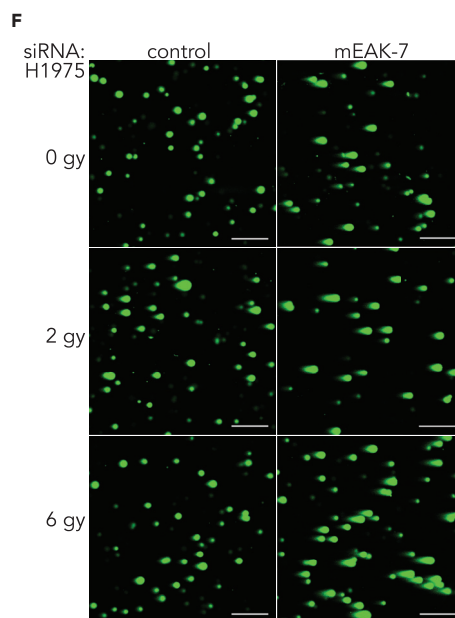
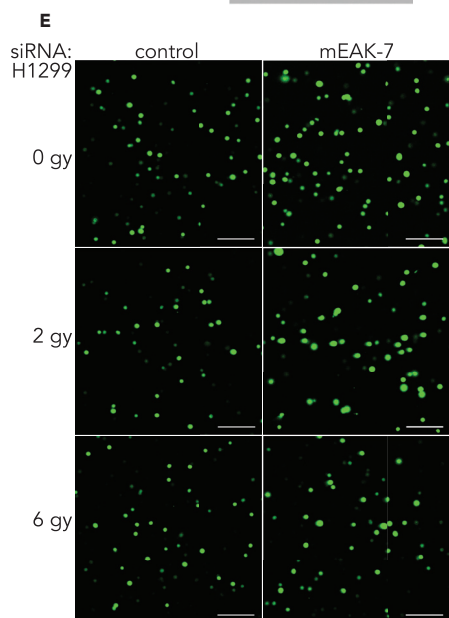
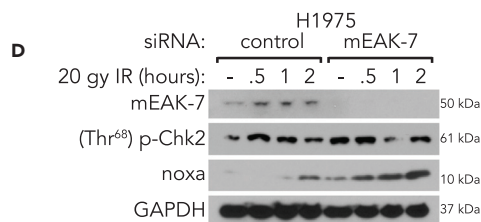
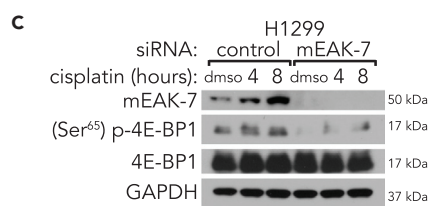
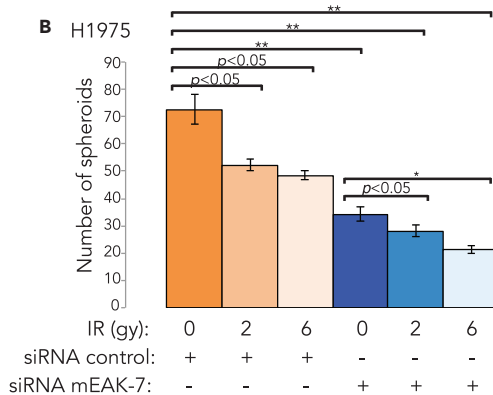
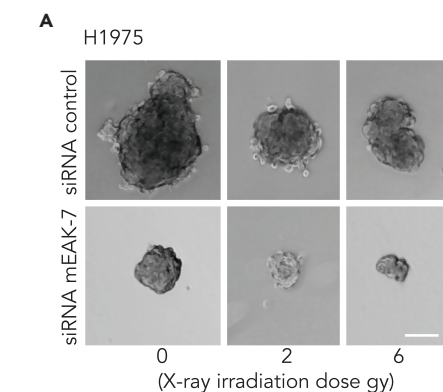


Figure 4. mEAK-7 Is Required for Spheroid Formation and Is Necessary for an Effective DNA Damage Response

(A) Images of spheroids. H1975 cells were treated with control or mEAK-7 siRNA, X-ray irradiated at 2 or 6 Gy, and 10,000 cells were seeded into 60-mm ultra-low attachment plates and grown for 10 days. Scale bar, 125 μ m.

(B) Quantification of spheroid formation and analysis via Student's t test ($n = 6$) of (A). * $p < 0.01$, ** $p < 0.001$.

(C) H1299 cells were treated with control or mEAK-7 siRNA and with DMSO or 10 μ M cisplatin for 4 or 8 h, and mTOR signaling was analyzed.

(D) H1975 cells were treated with control or mEAK-7 siRNA and X-ray irradiated at 20 Gy for 30 min, 1 h, or 2 h and analyzed for Noxa expression by DNA damage response.

(E and F) H1299 and H1975 cells were treated with control or mEAK-7 siRNA and X-ray irradiated at 2 or 6 Gy for 30 min and assessed via the comet assay to detect damaged DNA. Scale bar, 250 μ m.

(G and H) Statistical analysis via Student's t test ($n = 15$) of (E and F) represented as box plots. * $p < 0.01$, ** $p < 0.001$, † $p < 0.00001$, ‡ $p < 0.000001$, § $p < 0.0000001$, ¶ $p < 0.0000001$. All experiments were repeated at least three times.

irradiation, DNA-PKcs has been shown to interact with mTOR kinase and SIN1 to affect mTORC2 signaling in epithelial skin keratinocytes, but the molecular rationale for this interaction remains elusive (Tu et al., 2013). Furthermore, nuclear DNA-PKcs translocates to the cytosol in response to DNA damage (Tu et al., 2013). This ability to travel to the cytoplasm, combined with evidence that DNA-PKcs can activate metabolism-related genes, suggests a role for DNA-PKcs in metabolic signaling.

Because mEAK-7 interacts with mTOR in increasing amounts of amino acid, insulin, or nutrient conditions (Nguyen et al., 2018), we sought to determine the extent to which mEAK-7 increases its binding to DNA-PKcs after DNA damage. H1299 cells stably expressing HA-mEAK-7 were subjected to no treatment or X-ray irradiated with 10 Gy for 30 or 60 min, and results revealed that mEAK-7 increasingly interacted with DNA-PKcs over time in response to DNA damage (Figure 5D). These data suggest that mEAK-7 associates with DNA-PKcs and mTOR to form a third mTOR complex (mTORC3), distinct from mTORC1 and mTORC2.

First, to determine the extent to which S6K2 is required for mTOR signaling following X-ray irradiation, H1975 and H1299 cells were treated with controls or two unique S6K1 or S6K2 siRNAs. Results revealed that p-S6 levels were abrogated after S6K2 knockdown in H1975 and H1299 cells (Figures S4A and S4B), suggesting that S6K2 is necessary for sustained S6 phosphorylation in response to DNA damage. S6K2 is capable of binding to mTOR in the presence of nutrient stimulation (Nguyen et al., 2018), but it is unknown whether S6K2 binds to DNA-PKcs. As mEAK-7 is required for the mTOR-S6K2 axis (Nguyen et al., 2018), DNA-PKcs and S6K2 binding was tested to determine the extent to which mEAK-7 and DNA-PKcs form a complex that regulates mTOR signaling through S6K2. To test whether S6K2 interacts with DNA-PKcs in the presence of DNA damage, H1299 cells were transiently transfected with pcDNA3-HA-S6K2-WT; subsequently, they were X-ray irradiated with 10 Gy for 1 h and HA-S6K2 was immunoprecipitated. X-ray irradiation considerably increased the interaction between DNA-PKcs and HA-S6K2, whereas it had little to no influence on mTOR and HA-S6K2 interaction (Figure 5E). Conversely, HA-S6K1 binding to DNA-PKcs was observed, but there was a severe reduction in binding after DNA damage, suggesting that S6K1 is not the main downstream target of DNA-PKcs after DNA damage (Figure S4C). These findings were reproduced under nutrient stimulation as well, where DNA-PKcs enhances binding to HA-S6K2 and DNA-PKcs diminishes binding to HA-S6K1 (Figure S4D). DNA-PKcs is capable of interacting with S6K2 to regulate its function in response to DNA damage. To determine if mTOR is required for mEAK-7-mediated DNA-PKcs function and interaction, mTOR was knocked down with two different mTOR siRNAs, which resulted in a dramatic reduction of DNA-PKcs interaction with endogenous mEAK-7 (Figure 5F). This collective evidence links mEAK-7 to the major metabolic sensor, mTOR, and the crucial DNA damage repair regulator, DNA-PKcs.

Although we previously established the function of mEAK-7 in mTOR signaling under nutrient conditions (Nguyen et al., 2018), its role in mTOR signaling under genotoxic stressors remains unknown. To test the hypothesis that mEAK-7 is required for mTOR activation after DNA damage, H1299 and H1975 cells were treated with control or mEAK-7 siRNA for 48 h in DMEM with 10% fetal bovine serum (FBS). Two different conditions were compared: 1-h nutrient starvation with 30-min nutrient replenishment was compared with 10-Gy X-irradiation for 30 min. Under these conditions, mEAK-7 was also capable of regulating sustained activation of mTOR signaling after X-ray irradiation in NSCLC (Figure 5G). Thus, mEAK-7 is capable of regulating nutrient-dependent mTOR signaling, as well as X-ray irradiated activation of mTOR signaling.

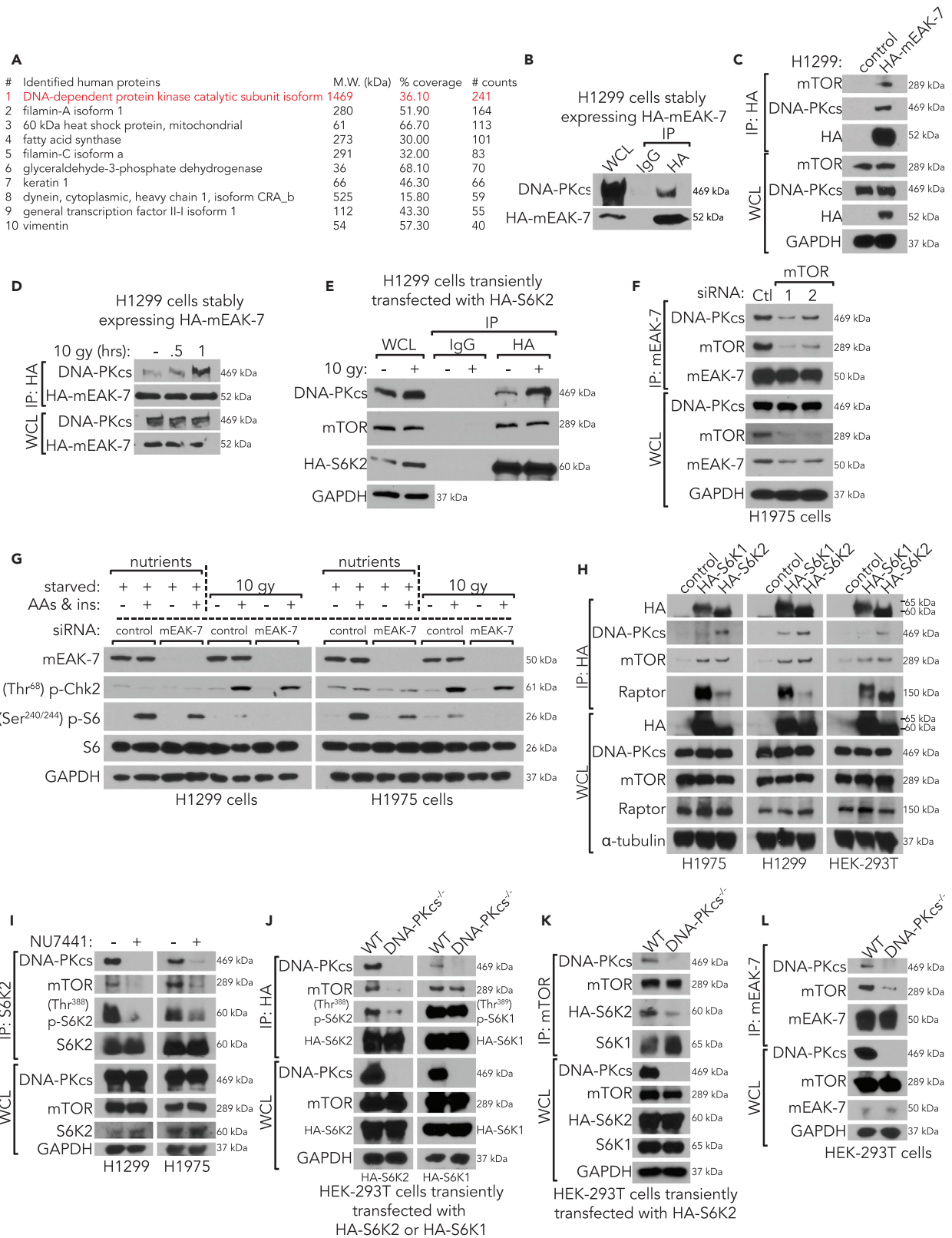


Figure 5. mEAK-7 Forms a Third mTOR Complex with DNA-PKcs to Regulate S6K2 Activity

- (A) H1299 cells stably expressing HA-mEAK-7 were lysed in 3-((3-cholamidopropyl) dimethylammonio)-1-propanesulfonate (CHAPS) buffer, HA-mEAK-7 was immunoprecipitated, and co-immunoprecipitated proteins were analyzed for mass spectrometry quantitative profiling.
- (B) H1299 cells stably expressing HA-mEAK-7 were lysed in NP40 lysis buffer and using IgG control antibody or HA-tag antibody, HA-mEAK-7 was immunoprecipitated to check DNA-PKcs interaction.
- (C) Non-transduced H1299 cells or H1299 cells stably expressing HA-mEAK-7 were lysed in CHAPS lysis buffer, and HA-tag antibody was used for immunoprecipitation to check DNA-PKcs or mTOR interaction.
- (D) H1299 cells stably expressing HA-mEAK-7 were untreated or X-ray irradiated at 10 Gy for 30 min and 1 h and lysed in NP40 lysis buffer. HA-mEAK-7 was immunoprecipitated to check DNA-PKcs interaction.
- (E) H1299 cells were transiently transfected with pcDNA3-HA-S6K2 and then untreated or X-ray irradiated at 10 Gy for 1 h. HA-S6K2 was immunoprecipitated to check DNA-PKcs or mTOR interaction.
- (F) H1975 cells were transiently transfected with control or mTOR #1 or mTOR #2 siRNA for 48 h. Cells were collected in CHAPS, and endogenous mEAK-7 was immunoprecipitated to check DNA-PKcs interaction.
- (G) H1299 and H1975 cells were transiently transfected with control or mEAK-7 siRNA for 48 h. Cells were subsequently starved of nutrients for 1 h and replenished with DMEM⁺AAAs and 10 μ M insulin for 30 min or cultured normally and treated with 10-Gy X-ray irradiation for 30 min. Immunoblot analysis was conducted for mTOR signaling proteins.
- (H) H1975, H1299, and HEK293T cells were transfected with no plasmid, pRK7-HA-S6K1-WT, and pcDNA3-HA-S6K2. HA-tag antibody was immunoprecipitated and probed for DNA-PKcs, mTOR, and Raptor.
- (I) H1299 and H1975 cells were treated with either DMSO or NU7441 (DNA-PKcs inhibitor) at 5 μ M for 2 h and mixed in fresh DMEM with 10% FBS. Cells were collected in CHAPS, S6K2 was immunoprecipitated, and immunoblots were utilized to assess mTOR signaling. GAPDH was used for loading controls.
- (J) DNA-PKcs^{WT} and DNA-PKcs^{-/-} HEK293T cells were transfected with pcDNA3-HA-S6K2 or pRK7-HA-S6K1-WT. Before protein isolation, cells were fed fresh DMEM with 10% FBS for 1 h before collection in CHAPS. HA-tag antibody was immunoprecipitated and probed for mTOR and activated S6K2 signaling.
- (K) Experimental protocols were repeated from (J), and mTOR antibody was immunoprecipitated and probed for mTOR, HA-S6K2, and S6K1.
- (L) DNA-PKcs^{WT} and DNA-PKcs^{-/-} HEK-293T cells were collected in CHAPS lysis buffer. Endogenous mEAK-7 was immunoprecipitated and probed for mTOR and DNA-PKcs. All experiments were repeated at least three times.

Next, to determine the relative binding affinities of S6K1 and S6K2 to their most relevant complex, we transfected H1299, H1975, and HEK-293T cells with HA-S6K1 or HA-S6K2 and immunoprecipitated HA-S6K1 or HA-S6K2 to probe for mTOR, raptor, and DNA-PKcs binding. Interestingly, we discovered that HA-S6K1 is capable of binding to DNA-PKcs, but HA-S6K2 binds to DNA-PKcs to a significantly larger extent (Figure 5H). Furthermore, we found that raptor binding to HA-S6K1 was strong, whereas HA-S6K2 binding to raptor was weaker (Figure 5H). This suggests that S6K1 and S6K2 have preferential binding affinities to mTORC1, or alternative mTOR complexes. Finally, to test the extent to which DNA-PKcs activity is required for S6K2 function, H1299 and H1975 cells were treated with either DMSO or 5 μ M NU7441, a highly specific chemical inhibitor of DNA-PKcs, for 2 h under freshly stimulated 10% FBS medium. NU7441 is 1,000 \times more specific for DNA-PKcs than PI3K and 200 \times more specific for DNA-PKcs than mTOR. DNA-PKcs inhibition resulted in a substantial decrease in S6K2/mTOR/DNA-PKcs binding, as well as S6K2 functional activity (Figure 5I). These results suggest that mEAK-7 structurally links DNA-PKcs and S6K2 to mTOR signaling.

Although pharmacologic agents are potent molecules to dissect the downstream pathways within cells, they still may yield non-specific targeting. To rule out non-specific interactions of DNA-PKcs inhibitors with other kinases, we obtained validated DNA-PKcs^{-/-} HEK293T cells (Neal et al., 2016). In DNA-PKcs^{-/-} cells, IP demonstrated that HA-S6K2 phosphorylation was diminished and HA-S6K2 binding to mTOR was reduced, but HA-S6K1 phosphorylation and HA-S6K1 binding to mTOR were minimally affected (Figure 5J). IP of mTOR in DNA-PKcs^{-/-} cells transfected with HA-S6K2 resulted in abrogated binding to HA-S6K2 and increased binding to HA-S6K1, demonstrating that mTOR utilizes DNA-PKcs to form a new complex to target S6K2 (Figure 5K). Finally, loss of DNA-PKcs inhibited the ability of mEAK-7 to bind to mTOR, suggesting that mEAK-7, DNA-PKcs, and mTOR form a stable complex to regulate S6K2 (Figure 5L).

mEAK-7 Is Required for Sustained IR-Mediated mTOR Signaling in Human Cancer Cells and Loss of mEAK-7 Results in Enhanced PARP Cleavage

As we determined that mEAK-7 knockdown combined with X-ray irradiation resulted in strong Noxa upregulation, we posited that other markers of cell apoptosis would also be affected by mEAK-7. PARP cleavage has been shown to be an essential mediator of cell apoptosis and cell death (Morales et al., 2014). To determine the extent to which mEAK-7 regulates PARP cleavage, H1299 cells treated with mEAK-7 siRNA resulted in enhanced levels of cleaved PARP (Figure 6A). These results suggest mEAK-7 is required for radiation resistance and that the loss of mEAK-7 results in severe reduction of mTOR signaling and enhanced PARP cleavage.

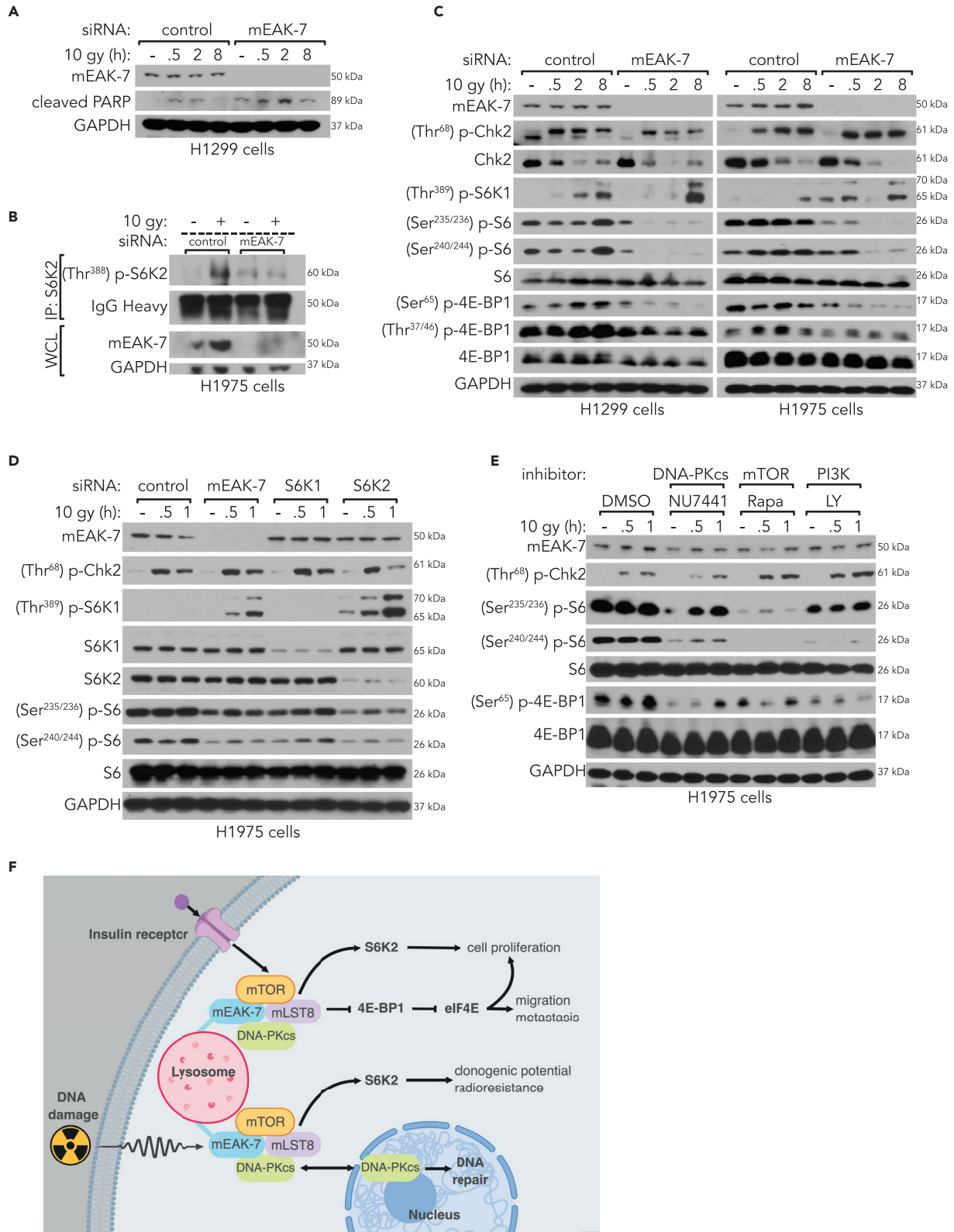


Figure 6. mEAK-7 and DNA-PKcs Are Required for X-Ray Irradiation-Mediated mTOR Signaling

- (A) H1299 cells were treated with control or mEAK-7 siRNA for 48 h; X-ray irradiated at 10 Gy for 30 min, 2 h, and 8 h; and analyzed for PARP cleavage.
- (B) H1975 cells were transiently transfected with control or mEAK-7 siRNA for 48 h. Next, cells were treated with 10-Gy X-ray irradiation for 30 min, followed by IP of endogenous S6K2, and probed for activated S6K2 signaling.
- (C) H1299 and H1975 cells were treated with control or mEAK-7 siRNA for 48 h; X-ray irradiated at 10 Gy for 30 min, 2 h, and 8 h; and analyzed for mTOR signaling.
- (D) H1975 cells were treated with control, mEAK-7, S6K1, and S6K2 siRNA for 48 h; X-ray irradiated at 10 Gy for 30 min and 1 h; and analyzed for mTOR signaling.
- (E) H1975 cells were treated with DMSO, DNA-PKcs inhibitor (5 μ M NU7441 IC50 = 14 nM), mTOR inhibitor (100 nM rapamycin, IC50 = 1 nM), and PI3K inhibitor (50 μ M LY249002, IC50 = 2.3 μ M) for 1 h before being treated with X-ray irradiation at 10 Gy for 30 min and 1 h and analyzed for mTOR signaling.
- (F) Working model for a mEAK-7-mTOR-DNA-PKcs complex. All experiments were repeated at least three times. GAPDH was used for loading controls.

Next, we posited that mEAK-7 was required for S6K2 phosphorylation and activation after X-ray irradiation. H1975 cells were treated with control or mEAK-7 siRNA for 48 h and 10-Gy X-ray irradiation for 30 min. IP of endogenous S6K2 demonstrated that mEAK-7 knockdown resulted in a dramatic decrease in X-ray irradiation-mediated S6K2 phosphorylation (Figure 6B). Use of a different mEAK-7 siRNA also resulted in a decrease in S6K2 phosphorylation after DNA damage (Figure S4E). Moreover, the literature details examples of sustained mTOR signaling following DNA damage as a modulator of self-renewal and radiation resistance (Silvera et al., 2017). To test the hypothesis that mEAK-7 is necessary for sustained X-ray irradiation-mediated mTOR signaling, H1299 and H1975 cells were treated with control or mEAK-7 siRNA for 48 h in DMEM with 10% FBS and then with 10-Gy X-irradiation for 30 min, 2 h, or 8 h. H1299 and H1975 cells treated with mEAK-7 siRNA exhibited abrogated mTOR signaling over time (Figure 6C). These results were also confirmed in MDA-MB-231 cells, a triple-negative breast carcinoma cell line (Figure S5). Therefore, these results suggest that mEAK-7 is required for sustained mTOR signaling as well as cell survival after DNA damage, and that the loss of mEAK-7 results in severe reduction of mTOR signaling and enhanced PARP cleavage.

Both S6K1 and S6K2 are essential components of mTOR signaling that are described to have similar, but distinct, cellular roles in human development and disease (Pardo and Seckl, 2013). To elucidate the roles of S6K1 and S6K2 following X-ray irradiation damage, (Ser^{240/244}) p-S6 levels were measured in response to siRNA-mediated knockdown of mEAK-7, S6K1, or S6K2 and treatment with 10-Gy X-ray irradiation. H1975 cells were treated with control, mEAK-7, S6K1, or S6K2 siRNA for 48 h in DMEM with 10% FBS. Subsequently, the cells were treated with 10-Gy X-ray irradiation for 30 min or 1 h. mEAK-7 and S6K2 knockdown each markedly reduced (Ser^{240/244}) p-S6 levels, but S6K1 knockdown did not have a substantial effect on (Ser^{240/244}) p-S6 levels (Figure 6D). These results mirrored the nutrient conditions, as previously published (Nguyen et al., 2018). Furthermore, mEAK-7 or S6K2 knockdown dramatically increased (Thr³⁸⁹) p-S6K1 levels following X-ray irradiation-induced damage, suggesting a specific role for S6K2 and mEAK-7 during X-ray irradiation-mediated mTOR signaling (Figure 6D).

Although some reports suggest a possible intersection of DNA-PKcs and mTOR signaling, these ideas have not yet been fully validated across a spectrum of cell types and experimental conditions. In an effort to test the hypothesis that DNA-PKcs and mTOR signaling depend on mEAK-7 to carry out a shared function, we treated H1299 and H1975 cells with NU7441. NU7441 treatment significantly reduced infrared (IR)-mediated mTOR signaling in a dose-dependent manner, but had little effect on (Ser²⁴⁴⁸) p-mTOR levels (Figure S6A). To determine whether NU7441 significantly inhibits IR-induced activation of mTOR signaling compared with other mTOR inhibitors, we used specific inhibitors of DNA-PKcs (NU7441), mTOR (rapamycin), and PI3K (LY249002). Inhibition of DNA-PKcs, mTOR, or PI3K significantly decreased mTOR signaling in H1975 cells (Figure 6E). These results were also consistent in H1299 cells (Figure S6B). In conclusion, DNA-PKcs is a fundamental component of a novel mTOR complex that regulates the mEAK-7/mTOR signaling axis and targets S6K2.

DISCUSSION

Surgical intervention and radiation therapy are common treatment modalities for patients with solid tumors. However, in many patients the condition relapses as tumors acquire resistance through intratumoral evolution (McGranahan and Swanton, 2017). CD44+/CD90+ cells have been identified as a unique population of cancer cells that may be required for the regulation of chemo- and radioresistance through PI3K and mTOR signaling (Chang et al., 2013). Furthermore, the literature demonstrates that S6K2 inhibits apoptosis in lung cancer (Pardo et al., 2006) and that S6K2 amplification is associated with more aggressive

forms of breast cancer (Pérez-Tenorio et al., 2011). Similarly, a retrospective study conducted on patients with breast cancer demonstrated that 4E-BP1 and S6K2 were correlated with poor prognosis and endocrine resistance (Karlsson et al., 2013). This evidence, combined with our findings that mTOR signaling, mEAK-7, and S6K2 are upregulated in CD44+/CD90+ cancer cell populations, suggests that mEAK-7 is involved in mTOR signaling in CSCs.

Although CD44+/CD90+ cells demonstrate radiation resistance and self-renewal capacity that correlate with elevated mEAK-7 protein levels, loss of mEAK-7 alone does not result in enhanced cell apoptosis in human cancer cells (Nguyen et al., 2018). The combination of DNA damage and loss of mEAK-7 is capable of enhancing cell apoptosis. This is likely because the mechanisms that support cell survival and self-renewal are different. As PI3K and mTOR signaling are crucial regulators of radiation resistance and self-renewal in many carcinomas, including cervical carcinoma (Kim et al., 2010), head and neck squamous cell carcinoma (Leiker et al., 2015), and breast carcinoma (Steelman et al., 2011), it is important to note that mEAK-7 is also a strong effector of these processes. Specifically, CSCs have been identified as a cell population that modulates radiation resistance and self-renewal in solid tumors (Pajonk et al., 2010).

Alternative mTOR signaling appears to be upregulated in human patients with cancer, specifically in patients with metastatic disease (Figures 2A–2C). Here, DNA-PKcs was identified as a new interacting partner of mEAK-7 (Figures 5A–5H) and may participate in the regulation of this alternative mTOR signaling. DNA-PKcs is a member of the PIKK family that includes mTOR, ATM, ATR, suppressor of morphogenesis in genitalia (SMG1), and transformation/transcription domain-associated protein (TRRAP) (Lovejoy and Cortez, 2009). DNA-PKcs has been extensively studied in the context of non-homologous end joining and homologous recombination, both of which are DNA damage repair pathways (Smith and Jackson, 1999). PIKKs typically have redundant cellular roles, depending on their cellular localization and biologic context. For example, DNA-PKcs, ATM, and ATR all have similar cellular targets in response to DNA damage (Ciccio and Elledge, 2010). Intriguingly, DNA-PKcs was found to play a critical role in metabolic gene regulation in response to insulin (Wong et al., 2009). However, DNA-PKcs predominantly resides in the nucleus, so it was initially unclear how DNA-PKcs could exit the nucleus to affect nutrient metabolism. The literature supports the observation that pockets of DNA-PKcs exist in lipid rafts outside of the nucleus, suggesting the existence of a different role for DNA-PKcs in cytoplasmic cellular signaling (Lucero et al., 2003). In support of these diverse findings, we demonstrate that DNA-PKcs interacts with mEAK-7 to regulate mTOR signaling, predominantly through S6K2.

In mini pigs, mTOR signaling is enhanced in salivary glands 5 days after treatment with X-ray irradiation (Zhu et al., 2016). In addition, PI3K and mTOR are essential regulators of radiation resistance in prostate cancer cells (Chang et al., 2014) as dual PI3K-mTOR inhibitors re-sensitize cancer cells to radiation treatment (Mukherjee et al., 2012). Here, we demonstrate that mEAK-7 is required for the sustained activity of mTOR signaling following X-ray irradiation damage. Continued investigation of mEAK-7 and other molecular machinery that regulates IR damage-mediated activation of mTOR signaling will allow for the creation of targeted inhibitors promoting radiation re-sensitization.

As the role of mEAK-7 is further studied in the context of human disease, its unique role in nutrient-sensing and DNA damage response (Figure 6F) will likely expand. S6K2 is a crucial component of mTOR signaling that has been overlooked (Pardo and Seckl, 2013). Yet, many studies demonstrate that S6K2 is associated with human diseases, including non-small-cell lung cancer (Pardo et al., 2006) and late-stage breast cancer (Karlsson et al., 2015). We determined that there are high mEAK-7 protein levels in the tumors and lymph nodes of patients with metastatic cancer, that mEAK-7^{high} patients have poor prognoses, and that mEAK-7 is essential for self-renewal and radioresistance. To determine the evolutionary benefit that cancer cells gain from upregulating mEAK-7, future research should be focused on elucidating the mechanisms allowing tumorigenesis in a broader range of cancers. Likewise, development of mEAK-7 inhibitors may benefit patients with metastatic cancers that demonstrate aberrant mTOR signaling associated with high levels of mEAK-7.

Limitations of the Study

Here, we report that DNA-PKcs is a binding partner of the mEAK-7-mTOR complex. Some pitfalls of these studies are that we lack animal models that could recapitulate human disease. As most of our work is to identify novel binding partners and the detailed mechanism by which they interact, future studies will be

required to examine the role of mEAK-7 *in vivo*. Also, our inhibitor studies against DNA-PKcs, although severalfold more specific to DNA-PKcs versus mTOR, could yield some off-target effects and DNA-PKcs knockout cell lines may not recapitulate all of physiology, suggesting that genetic approaches *in vivo* are required to understand the role of DNA-PKcs binding to mTOR to form mTORC3. Thus the role of this alternative complex to canonical mTOR signaling requires further study in animal models where mTOR signaling is required for eukaryotic development and disease progression.

METHODS

All methods can be found in the accompanying [Transparent Methods supplemental file](#).

SUPPLEMENTAL INFORMATION

Supplemental Information can be found online at <https://doi.org/10.1016/j.isci.2019.06.029>.

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AUTHOR CONTRIBUTIONS

J.T.N., F.S.H., A.L.F., C.R., D.B.M., J.K.K., and P.H.K. designed experiments and analyzed results. J.T.N., F.S.H., A.L.F., and C.R. carried out experiments. J.T.N. and P.H.K. are responsible for the major ideas. J.T.N. and P.H.K. wrote the paper. J.T.N., F.S.H., C.R., D.B.M., A.L.F., J.K.K., and P.H.K. edited the manuscript.

DECLARATIONS OF INTERESTS

The authors declare no competing interests.

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Supplemental Information

mEAK-7 Forms an Alternative mTOR

Complex with DNA-PKcs in Human Cancer

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1 SUPPLEMENTAL INFORMATION

- 2 • Transparent Methods
- 3 • Figure S1, related to Figure 1: *MEAK7* expression patterns in normal human tissues
4 and cancer patients.
- 5 • Figure S2, related to Figure 2 and Figure 3: Normal lymph tissue analysis, H1975
6 cancer stem cell analysis, and differential cell density clonogenicity assay.
- 7 • Figure S3, related to Figure 3 and Figure 4: Colony formation assay with second
8 mEAK-7 siRNA, spheroid formation assay with differential cell density or second
9 mEAK-7 siRNA, and mEAK-7 effect of Noxa expression by X-ray irradiation in
10 H1299 cells.
- 11 • Figure S4, related to Figure 5 and Figure 6: DNA damage mediated S6K1/2
12 signaling, and DNA-PKcs binding to S6K1, and second mEAK-7 siRNA effect on
13 DNA damage or nutrient induced S6K2 activation
- 14 • Figure S5, related to Figure 6: MDA-MB-231 cell data on mEAK-7 and X-ray
15 irradiation-mediated mTOR signaling.
- 16 • Figure S6, related to Figure 6: Dose-dependent analysis of NU7441 on IR-mediated
17 mTOR signaling and DNA-PKcs, mTOR, and PI3K inhibitor study after X-ray
18 irradiation.
- 19 • Table S1, related to Figure 5: Immunoprecipitation-mass spectrometry analysis of
20 mEAK-7.
- 21 • Table S2, related to Figure 2: Detailed patient information from US Biomax Tissue
22 Microarrays.

23 **TRANSPARENT METHODS**

24

25 **Cell lines**

26 H1299 and H1975 are non-small cell lung carcinoma cell lines obtained from ATCC.

27 MDA-MB-231 is a triple negative breast carcinoma cell line obtained from ATCC. DNA-

28 PKcs^{WT} and DNA-PKcs^{-/-} HEK-293T cells were kindly gifted from Dr. Kathryn Meek, a

29 Professor at Michigan State University. H1299 cells (ATCC® CRL-5803™) were derived

30 from a 43 year old male, Caucasian. H1975 cells (ATCC® CRL-5908™) were derived

31 from an unknown aged, female. MDA-MB-231 (ATCC® HTB-26™) cells were derived

32 from a 51 year old female Caucasian. HEK-293T cells (ATCC® ACS-4500™) were

33 derived from an unknown aged, human embryonic kidney tissue. All cell lines are of

34 human origin.

35

36 **Statement of regulatory oversight and approval**

37 The University of Michigan Institutional Review Boards is the committee approving the

38 cell line experiments, approving the use of human samples from US Biomax, and

39 confirming that all experiments conform to the relevant regulatory standards. It is not

40 clear to what extent that sex, gender, and age affected data presented in human tissue

41 microarrays obtained from US Biomax. The influence or association between these

42 characteristics would require further assessment, with regards to the conclusions of this

43 manuscript. Detailed information regarding patient samples from US Biomax can be

44 accessed in Table S2.

45

46 Cell culture

47 *Cell culture:* Cell lines were grown in Dulbecco's minimal essential medium (DMEM,
48 Thermo Fisher Scientific (TFS): cat# 11995-073), without antibiotics/antimycotics and
49 supplemented with a concentration of 10% fetal bovine serum (FBS, TFS: cat# 10437-
50 036, Lot # 1399413) at 37°C in 5.0% CO₂ incubator. Cells were grown in Falcon™
51 Tissue Culture Treated Flasks T-75 (Fisher Scientific (FS): cat# 13-680-65) until 75%
52 confluent and split with Trypsin-EDTA 0.25% (TFS: cat# 25200-056) for 5 min in the
53 37°C cell incubator. Cells were washed 1x with PBS and resuspended in 10% FBS
54 containing DMEM. Cells were counted with the LUNA™ Automated Cell Counter (Logos
55 Biosystems (LB): cat# L10001) utilizing LUNA™ Cell Counting Slides (LB: cat# L12003)
56 and AO-PI dye (LB: cat# F23001).

57

58 Small interfering RNA or plasmid transfection

59 Cells were seeded at a density of 500,000 cells per 60 mm TCP and grown for 24
60 hours. For siRNA transfection, Lipofectamine® RNAiMAX Transfection Reagent (TFS:
61 cat# 13778-150) was incubated with Opti-MEM® I Reduced Serum Medium (TFS: cat#
62 31985-070) and 100 nM siRNA was incorporated before introduction to cells at 100 nM
63 concentration. For plasmid transfection, FuGENE® 6 Transfection Reagent (Promega:
64 cat# E2691) was incubated with Opti-MEM I Reduced Serum Medium and 2 µg
65 plasmids were incorporated before introduction into cells. For dual transfection, we
66 added both solutions. siRNAs used were as follows: mEAK-7 #1 siRNA (TFS: ID#
67 s33640). mEAK-7 #2 siRNA (TFS: ID# HSS126697). S6K1 #1 siRNA (TFS: ID#

68 s12282). S6K1 #2 siRNA (TFS: ID# s12283). S6K2 #1 siRNA (TFS: ID # s12287). S6K2
69 #2 siRNA (TFS: ID # s12286). Control siRNA (TFS: cat# 4390843). Plasmids were
70 purchased from Addgene. HA-S6K2 plasmid: pcDNA3-S6K2-WT was a gift from John
71 Blenis (Addgene plasmid # 17729).

72

73 **X-ray irradiation protocol**

74 After appropriate treatment of cells with siRNA, plasmids, chemical compounds,
75 nutrients, etc, we subjected the cells to X-ray irradiation. The machine is a Polaris IC-
76 320 SC-500 series 2 from Kimtron. The dose rate is set at 4.5223Gy/min. X-ray
77 irradiation of cells was done via the 1.5mm Aluminum filter, with a cone which has a
78 20x20cm beam pattern and a 50 cm FSD (radiation distance). X-ray irradiation applied
79 is either 10 gy or 20 gy.

80

81 **Immunofluorescence**

82 Deparaffinization and rehydration steps were as follows: xylene for 10 minutes, 100%
83 ethanol for 5 minutes, 95% ethanol for 5 minutes, 70% ethanol for 5 minutes, Milli Q
84 water for 10 minutes, and 1x PBST for 10 minutes. Antigen retrieval steps were as
85 follows: slides were placed in the slide holder to pressure cooker immersed in 10 mM
86 citric acid (pH 6.0). Then, slides were placed in the microwave and cooked at full power
87 for 12.5 minutes, finishing when pressure valve has been up for 1 min. Pressurized
88 steam was exhausted from the pressure cooker. The pressure cooker and slides were
89 cooled under running water for 15 minutes. Slides were washed with 1x PBS for 10

90 minutes. Slides were permeabilized for 10 minutes with 1x PBS with 0.4% Triton-X.
91 Slides were blocked with 2.5% bovine serum albumin and 1% Tween20 in 1x TBS.
92 Slides were incubated overnight at 4°C with primary antibody. Next, slides were washed
93 with PBS and incubated in secondary antibodies for 1 hour at room temperature. Slides
94 were washed with PBS with DAPI for 10 minutes. Prolong Gold Antifade with DAPI was
95 used to mount slides (Fisher cat# P36935). Nikon Ti Eclipse Confocal Microscope (60x
96 with oil magnification) was used to capture images. Images were captured with or
97 without 3x digital zoom, 1/32 frames per second, 1024x1024 image capture, 1.2 Airy
98 Units, 2x line averaging, appropriate voltage and power settings optimized per antibody.
99 No image modification was performed, except image sizing reduction for figure
100 preparation. Quantitative analyses were completed via Nikon Analysis Software, with
101 the data analysis and images representing the average of 3 fields of view and more
102 than 50% of the tissue core. NSCLC tissue microarray used for protein level detection of
103 mEAK-7 and p-S6 was purchased from US Biomax (cat# HLug-Squ090Lym-01).
104 Healthy lymph tissue microarray used for protein level detection of mEAK-7 and p-S6
105 was purchased from US Biomax (cat# LN802A). NSCLC tissue microarray used for
106 patient survival was purchased from US Biomax (cat# HLug-Squ150Sur-02). Primary
107 antibodies for immunofluorescence were as follows: mEAK-7 (Santa Cruz
108 Biotechnology (SCB) cat# sc-247321) and (Ser^{240/244}) p-S6 ribosomal protein (D68F8)
109 XP® (Cell Signaling Technologies (CST): cat#5364S). All antibodies were used at
110 1:1,000 with a working volume of 1.5 mL in 5% BSA in PBS, unless noted otherwise.
111 Secondary antibodies for immunofluorescence were as follows: Donkey anti-Goat IgG

112 Alexa Fluor® 647 (TFS: cat# A-21447), Anti-rabbit IgG (H+L), and F(ab')₂ Fragment
113 Alexa Fluor® 488 Conjugate (CST: cat# 4412S). All antibodies were used at a
114 concentration of 1:1,000, with a working volume of 1.5 mL in 5% BSA in PBS. DAPI
115 stain was used for DNA staining.

116

117 **Immunoblot analysis**

118 Cells were lysed in cold NP40 lysis buffer (50 mM Tris, 150 mM NaCl, and 1.0% NP-40
119 at pH 8.0). 50 µg of protein lysate was separated with Novex® Tris-Glycine SDS
120 Running Buffer 10X (TFS: cat# LC2675-4) and Novex™ WedgeWell™ 4-20% Tris-
121 Glycine Gels (TFS; cat# XP04205BOX), NuPAGE™ 3-8% Tris-Acetate Protein Gels
122 (TFS; cat# EA03785BOX). Proteins were transferred to PVDF membranes. 4-20% gels
123 were used for proteins 100 kDa and below, while 3-8% gels were used for proteins 100
124 kDa and above. Primary antibodies were incubated with membranes overnight at 4°C,
125 and secondary antibodies were incubated with membranes at room temperature for 1
126 hour. Membranes were incubated with SuperSignal™ West Pico Chemiluminescent
127 Substrate (TFS; cat# 34078) or Femto (TFS; cat# 34095) for film capture on HyBlot CL
128 autoradiography film (Denville Scientific: cat# e3018). Primary antibodies were as
129 follows: α-mEAK-7 (KIAA1609) mouse monoclonal antibody clone OT112B1 (formerly
130 12B1) was obtained from Origene Technologies (OT; cat# TA501037, lot A01). All
131 antibodies from Cell Signaling Technologies (CST) are rabbit: α-glyceraldehyde-3-
132 phosphate dehydrogenase (CST: cat# 2118S), α-tubulin (CST: cat# 2144S), α-
133 phospho-S6 ribosomal protein (Ser^{240/244}) (CST: cat# 2215S), α-phospho-S6 ribosomal

134 protein (Ser^{235/236}) (CST: cat# 2211S), α -S6 ribosomal protein (CST: cat# 2217S), α -
135 phospho-p70 S6 kinase (Thr³⁸⁹) (CST: cat# 9234S), α -S6K1 (CST: cat# 2708S), α -
136 S6K2 (CST: cat# 14130S), α -mTOR (CST: cat# 2983S), α -HA-tag mouse (CST: cat#
137 2367S), α -HA-tag rabbit (CST: cat# 3724S), α -(Ser⁶⁵) p-4E-BP1 (CST: cat# 9451S), α -
138 (Thr^{37/46}) p-4E-BP1 (CST: cat# 9459S), α -(Thr⁷⁰) p-4E-BP1 (CST: cat# 13396S), α -4E-
139 BP1 (CST: cat# 9452S), α -N-cadherin (CST: cat# 13116S), α -noxa (CST: cat#
140 14766S), α -Cleaved PARP (CST: 5625S), α -(Thr⁶⁸) p-Chk2 (CST: cat# 2197S), α -Chk2
141 (CST: cat# 3440S), α -(Ser²⁴⁴⁸) p-mTOR (CST: cat# 2971S). Concentration of
142 antibodies: p-S6, S6, and 4E-BP1 used at 1:3,000 dilution and remainder at 1:1,000
143 dilution in 5% BSA in 1X TBST buffer with 0.04% sodium azide. Secondary antibodies
144 for immunoblot analysis: 1:4,000 dilution for α -mouse IgG (Promega; cat# W4021).
145 1:7,500 dilution for α -rabbit (Promega; cat# W4011), and 1:2,000 dilution for α -rabbit
146 light chain specific antibody (Abcam: cat# ab99697) only for S6K2 IP experiments.

147

148 **Chemical Inhibitors**

149 All chemical were resuspended in DMSO, according to manufacturer recommendations.
150 Rapamycin (CST; cat# 9904S), LY293002 (CST; cat# 9901S), NU7441 (Tocris
151 Biotechne; cat# 3712). All inhibitors were applied to cells for at least 2 hours, unless
152 stated otherwise in the manuscript.

153

154 **Immunoprecipitation (IP) analysis and mass spectrometry**

155 After siRNA and/or plasmid transfection, cells were harvested in 1% NP40 lysis buffer or
156 CHAPS lysis buffer (FIVEphoton Biochemicals (FB): cat# CIB-1) supplemented with
157 protease inhibitors (FB: cat# PI-1) and phosphatase inhibitors (FB: cat# PIC1). For
158 antibody-bead conjugation, 1 to 2 μg of antibodies and 50 μL of mixed Protein A/G
159 PLUS-Agarose (SCB; Cat # sc-2003) were incubated for 1 hour on vertical shaker at
160 4°C. Afterwards, the antibody-bead mix was washed 3 times with 1x PBS. Next, 250 μg
161 of protein in CHAPS buffer were incubated with the antibody-bead mix for 1.5 hours on
162 vertical shaker at 4°C. After incubation, the antibody-bead conjugates were washed 3
163 times with 1x PBS. Beads were washed 3 times with 1x PBS, and 3x loading buffer with
164 SDS was added to the bead mix, boiled, spun down, and utilized for immunoblot
165 analysis. Immunoprecipitation-mass spectrometry: Samples were processed by the
166 University of Michigan Proteomics core for IP/MS analysis and protocols can be found
167 on their webpage. Samples submitted to the core were pooled from 3x reactions of HA-
168 mEAK-7 in H1299 cells, as described above. Full excel sheet supplied as Table S1.
169 Antibodies used for immunoprecipitation reactions were as follows: Anti-HA epitope tag
170 polyclonal goat IgG Antibody (Novus Biologicals: cat# NB600-362), polyclonal goat IgG
171 antibody (SCB: cat# sc-2028), α -S6K2 (CST: cat# 14130S), α -mTOR (CST: cat#
172 2983S), mEAK-7 (SCB, cat# sc-247321).

173

174 **Cell Invasion assay**

175 After siRNA transfection and X-ray irradiation, cells were trypsinized and 50,000 cells
176 were seeded onto Corning® Matrigel® Invasion Chamber 24-Well Plate 8.0 Micron

177 (Corning: cat# 354480), with 1 mL of DMEM^{-AAs} without FBS within the top chamber,
178 and 1 mL of 10% FBS-containing DMEM medium on the bottom of the plate. After 24
179 hours, we processed the samples with Hema 3™ Stat Pack (Fisher: cat# 123-869),
180 according to manufacturer specifications. Images were captured with a stereoscope,
181 attached to a digital camera. Brightness and contrast were adjusted, as needed.
182 Analysis was conducted via student's t-test. % invasion was counted on 6 individual
183 experiments per condition as: # cells adhered to the bottom chamber divided by # cells
184 seeded total.

185

186 **Comet Assay**

187 Lysis Buffer, Alkaline Solution, and Electrophoresis Running Solution were prepared
188 according to manufacturer's instructions. Solutions were stored at 4°C. Oxiselect Comet
189 Agarose (Cell Bio Labs (CBL): #235002) was heated to 95°C for 20 minutes, then
190 placed in 37°C water bath until use. Cells were grown according to experimental
191 procedures for siRNA treatment. Two days post siRNA treatment, cells were subjected
192 to no treatment, 2 gy, and 6 gy X-ray irradiation. Cells were trypsinized and
193 resuspended at a concentration of 1×10^5 cells/mL in cold PBS. Then, 10 μ L of cell
194 suspension was mixed with 90 μ L of comet agarose. After mixing thoroughly, 75 μ L of
195 this mixture was transferred to the OxiSelect Comet Slide (CBL: #STA-352). Slides
196 were placed in the dark at 4°C for 15 minutes. Slides were transferred to a small basin
197 containing pre-chilled Lysis buffer and placed at 4°C for 60 minutes in the dark. Lysis
198 solution was aspirated from the basin, replaced with pre-chilled Alkaline solution, and

199 placed at 4°C in the dark for 30 minutes. Then, Alkaline solution was aspirated and
200 replaced with pre-chilled TBE Electrophoresis solution. After 5 minutes, TBE
201 Electrophoresis solution was aspirated and replaced with new TBE Electrophoresis
202 solution. Slides were transferred to a horizontal electrophoresis chamber and the well
203 was filled with enough TBE Electrophoresis solution to fully cover the slides. Voltage
204 was applied for 45 minutes at 20 volts. After electrophoresis, slides were transferred to
205 a small basin containing pre-chilled DI H₂O, and the slides were fully immersed. After 2
206 minutes, the DI H₂O was aspirated and replaced. This rinse was repeated twice. After
207 the third rinse, slides were immersed in cold 70% ethanol for 5 minutes, then removed
208 from the basin and allowed to air dry. Once the agarose was dried fully, 100 µL of
209 diluted Vista Green DNA dye (CBL: cat# 235003, diluted 1:10,000 in TE buffer) was
210 added to each well and allowed to incubate at room temperature for 15 minutes. Slides
211 were imaged with Nikon Ti Eclipse Confocal Microscope at 10x magnification lens to
212 capture images. Images were captured at 1/8 frames per second, 1024x1024 image
213 capture, 1.2 Airy Units, 2x line averaging, appropriate voltage and power settings for
214 FITC (488 nm). No image modification was performed, except image sizing reduction
215 for figure preparation.

216

217 **Cancer Stem Cell sorting**

218 Cells were trypsinized and resuspended in DMEM medium with 10% FBS and counted
219 on Luna cell counter (Logos Biosystems (LB): cat# L10001) using Acridine
220 Orange/Propidium Iodide dye (LB: cat# F23001) for viability. 1×10^7 cells were filtered

221 into each of 5 labeled 50 mL falcon tubes, through a 40 μm filter. 1×10^7 cells were
222 filtered into each of 5 labeled 5 mL round bottom tubes (Falcon: cat# 352235) to be
223 used as single-color controls. Tubes were centrifuged at 1,000 rpm for 4 minutes at 4°C
224 and supernatant was discarded. One 5 mL single color control tube was resuspended
225 with 200 μL PBS with 10% FBS to be used as a negative control. Three of the other
226 single-color control tubes were resuspended with 200 μL PBS with 10% FBS, and
227 single color dyes were added as detailed: 2 μL DAPI (Thermo Fisher: cat# D1306), 25
228 μL CD90 (Biolegend: cat# 328107), and 10 μL CD44 (BD Biosciences: cat# 559942).
229 The final single-color tube was used for Isotype control. This pellet was resuspended
230 with 191 μL PBS with 10% FBS and 2 μL DAPI, 2 μL APC Isotype (BD Biosciences:
231 cat# 340442), and 5 μL FITC Isotype (BD Bioscience: cat# 555909) were added. Cells
232 in the 50 mL tubes were resuspended with 10 mL PBS with 10% FBS. The stain master
233 mix was added to each tube to be sorted. Tubes were placed on a rack and incubated
234 at 37°C for 30 minutes. Cells were rinsed with 1x PBS and resuspended 1x PBS
235 containing 3% FBS. Place all tubes on ice until samples will be run on Flow Cytometer
236 (Sony: Cat# SH800).

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238 **Clonogenicity Assay**

239 Cells were grown according to experimental procedures for siRNA treatment.
240 Two days post siRNA treatment, cells were subjected to no treatment, 2 Gy, and 6 Gy X-
241 ray irradiation. 10,000 H1975 cells or 2,500 H1299 cells were plated into 60 mm dishes
242 with 2 mL DMEM with 10% FBS. Cells were cultured in the incubator for 10 days (until

243 control colonies contained >50 cells), and new media and new siRNA were added every
244 4 days. Cells were fixed with 2 mL of fixation mix (glacial acetic acid (Sigma-Aldrich
245 537020) and methanol (Sigma-Aldrich 67-56-1), at a 1:7 ratio) for 2-3 minutes at room
246 temperature and incubated with 2 mL Crystal Violet (Sigma-Aldrich C6158-50G, diluted
247 to 0.5% in Milli-Q water) for 2 hours at room temperature. After 2 hours, the Crystal
248 Violet was removed and the dishes were rinsed with 2 mL of media (no FBS added),
249 pipetting vigorously to dislodge cells. Dishes were rinsed carefully in DI water and
250 placed on paper towel to dry for 2-3 days. Once plates were dry, colonies were counted
251 and recorded.

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253 **Spheroid Formation Assay**

254 Cells were grown according to normal experimental procedures for siRNA treatment
255 (n=6). Two days post siRNA treatment, cells were subjected to no treatment, 2 Gy and 6
256 Gy X-ray irradiation. 10,000 H1975 cells or 5,000 H1299 cells were plated into ultralow
257 attachment plates (Costar: cat# 3471). 2 mL of Serum Free Medium (435 mL MEBM
258 Medium (Lonza: cat# CC-3151), 10 mL B27 (Gibco: cat# 17504-044), 5 mL Pen/Strep
259 (Gibco: cat# 15070), 5 mL Lipid Concentrate (Gibco: cat# 11905-031), 2.5 mL Insulin
260 (Sigma-Aldrich: cat# I6634), 10 µg EGF (BD Biosciences: cat# 354052), 10 µg bFGF
261 (BD Bioscience: cat# 354060), 500 µg Hydrocortisone (Sigma-Aldrich: cat# H4001), 500
262 µL 100 mM β-mercaptoethanol (Sigma-Aldrich: cat# M3148), 2 mg Cholesterol (Sigma-
263 Aldrich: cat# C4951)) were added to each well. Cells were grown for 2 weeks, adding
264 500 µL of Serum Free Medium every 4 days to ensure cells have adequate nutrients.

265 After 2 weeks, the number of spheres growing in each well (spheres must have defined,
266 circular edges and be made of at least 10 cells) was counted, and representative
267 images of spheres from each treatment group were taken.

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269 **Statistical analysis and reproducibility**

270 GTEX data acquisition, processing, and statistical analysis information can be found on
271 “gtexportal.org”. cBioportal was accessed by searching for “*MEAK7*” or “*MEAK7*: gain
272 amp”. Patient derived data from Oncomine were analyzed via unpaired student’s t-test.

273 Patient derived tissue microarray data were analyzed via paired Mann-Whitney’s U-test.

274 2D/3D clonogenicity assay, comet assay, cell proliferation, cell migration, and cell size
275 were analyzed via paired student’s t-test. Immunoblot and immunoprecipitation assays
276 were repeated at least thrice in all cell lines.

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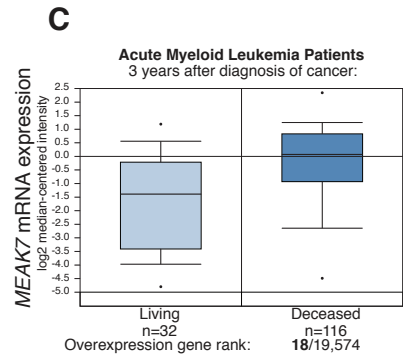
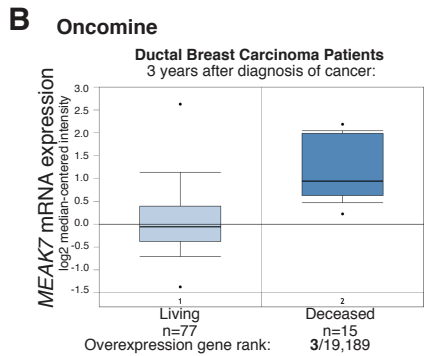
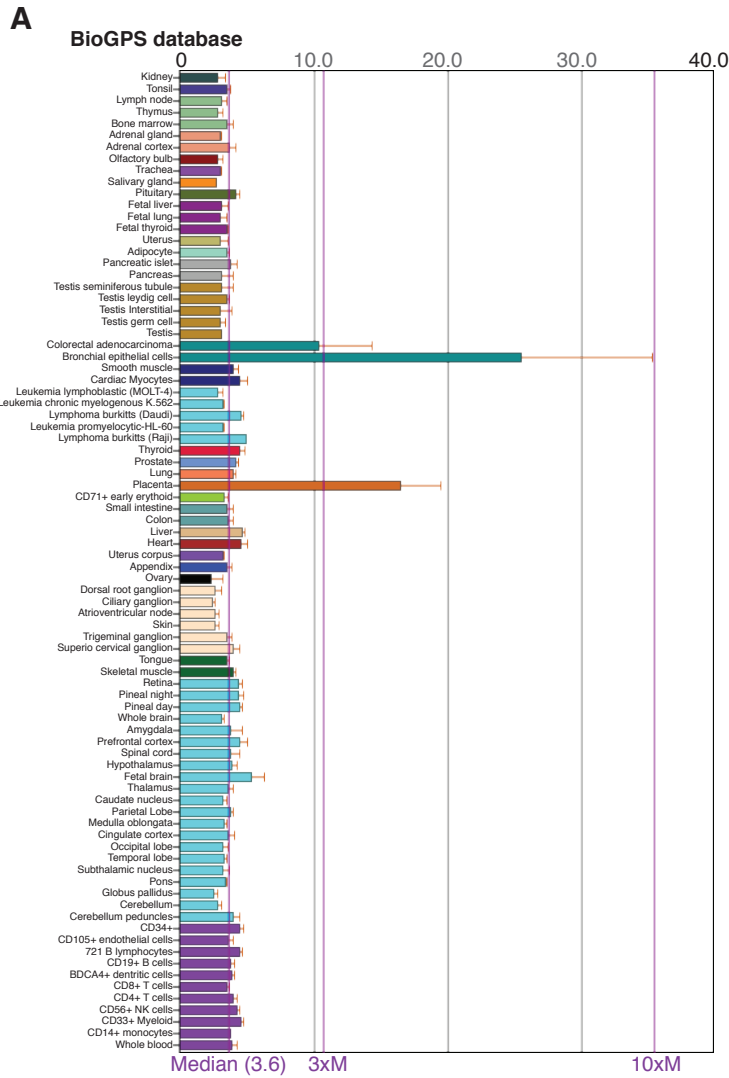
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288 **Figure S1, related to Figure 1. *MEAK7* is expressed at basal levels in many normal**
289 **human tissues, but significantly overexpressed in human cancer patients with**
290 **mortality. (A) BioGPS analysis of *MEAK7* in human tissues and cells. (B, C) OncoPrint**
291 **analysis of *MEAK7* gene expression of patients with (b) ductal breast carcinoma**
292 **($P=2.72 \times 10^{-6}$, Fold Change: 2.136) and (c) acute myeloid leukemia ($P=7.99 \times 10^{-6}$, Fold**
293 **Change: 2.655).**

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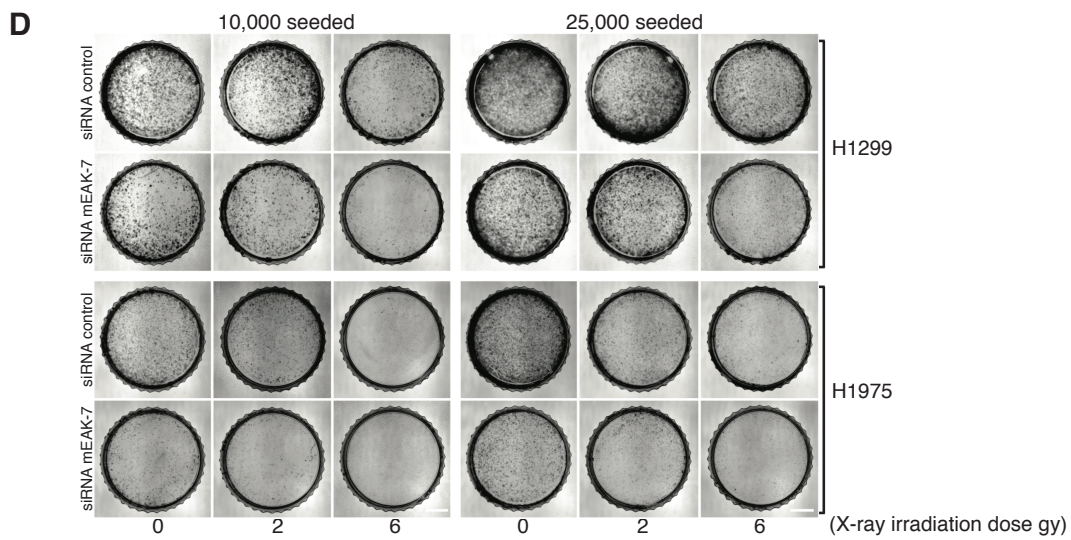
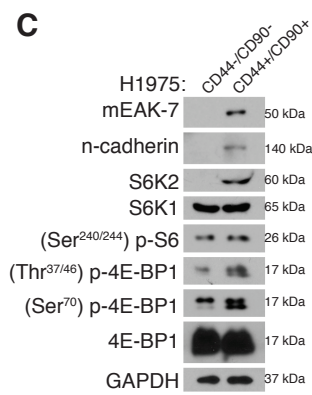
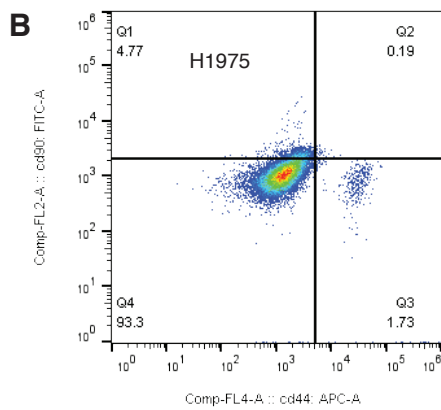
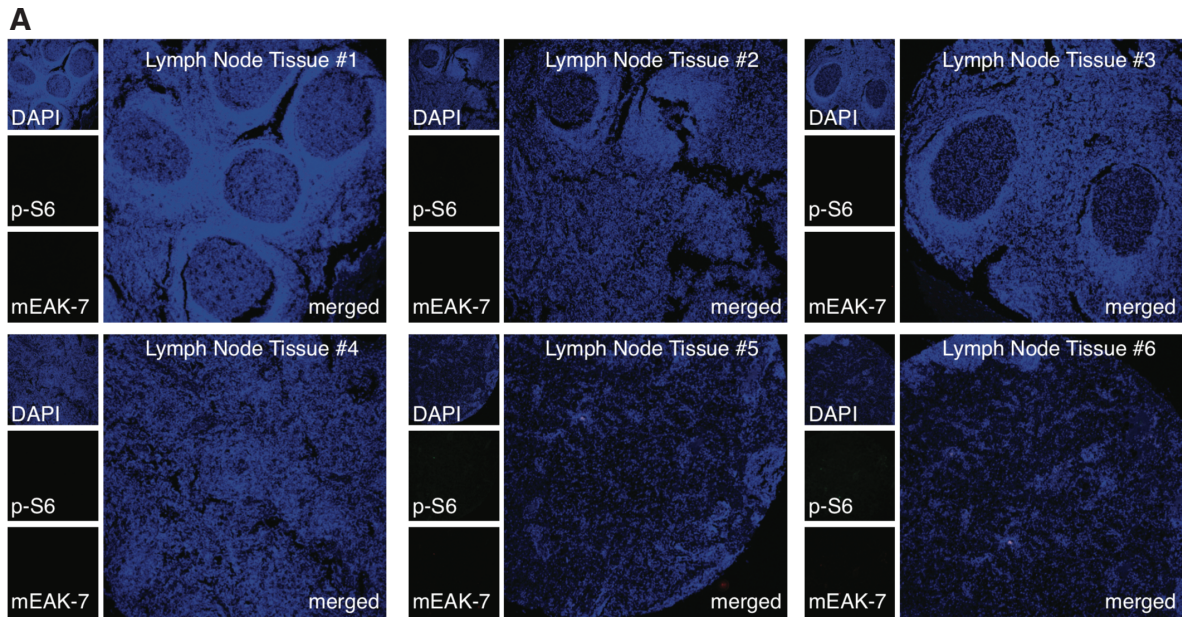
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311 **Figure S2, related to Figure 2 and Figure 3. Normal lymph tissue analysis, H1975**
312 **cancer stem cell analysis, and differential cell density clongenicity assay. (A)** 6
313 representative sections of US Biomax tissue microarray LN802a was analyzed using
314 the antibodies against mEAK-7 and p-S6. **(B)** Flow sort diagram depicting the
315 CD44+/CD90+ cell population in H1975 cells. **(C)** Immunoblot analysis of CD44-/CD90-
316 and CD44+/CD90+ H1975 cells for mEAK-7 and mTOR signaling. **(D)** H1299 and
317 H1975 cells were treated with control or mEAK-7 siRNA, X-irradiated at 2 or 6 gy, and
318 10,000 or 25,000 cells were seeded into 60 mm TCPs and grown for 10 days. White
319 bars denote 2.5 mm. This experiment was repeated at least 6 times.

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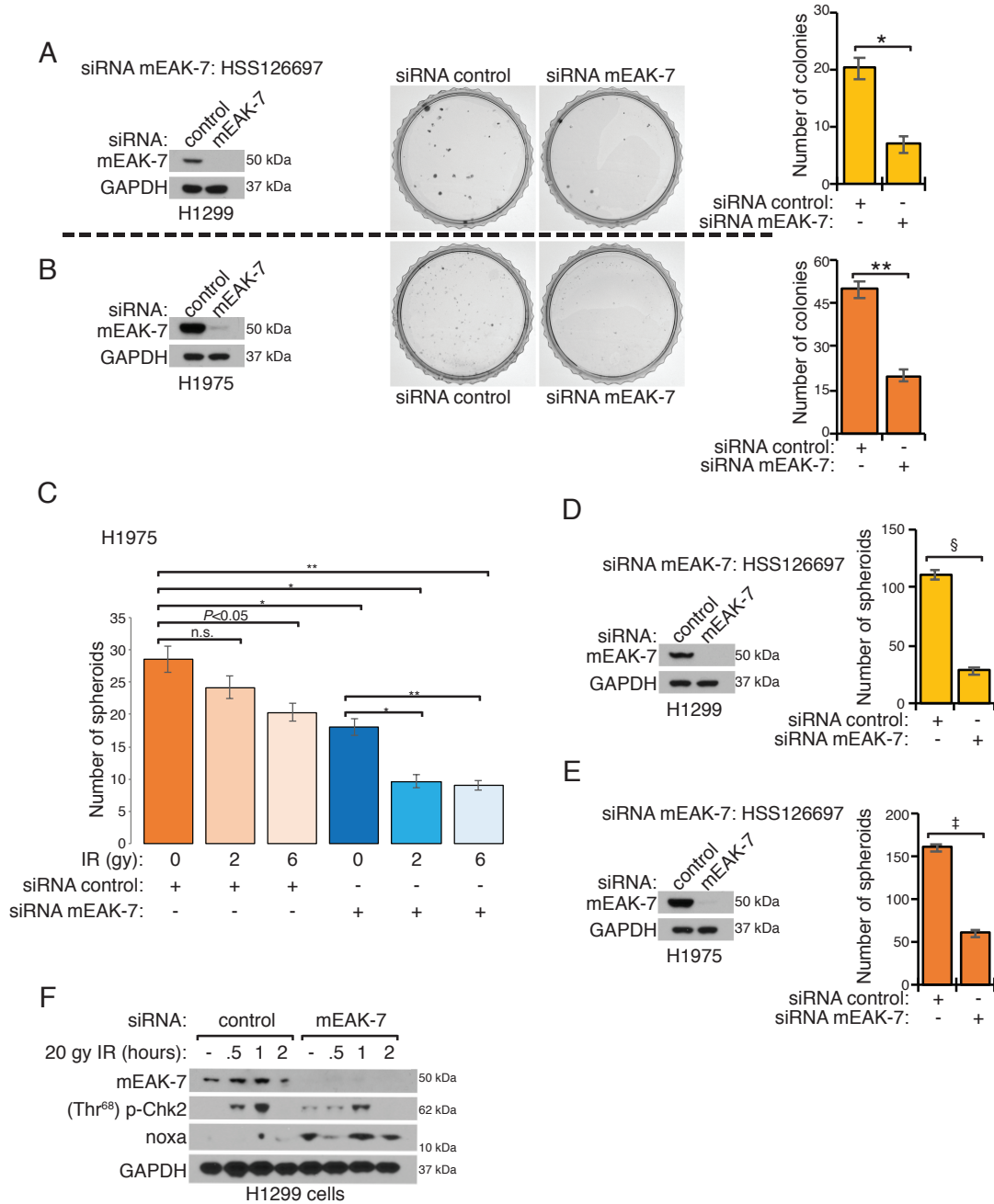
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Figure S3, related to Figure 3 and Figure 4. Colony formation assay with second mEAK-7 siRNA, spheroid formation assay with differential cell density or second mEAK-7 siRNA, and mEAK-7 effect of Noxa expression by X-ray irradiation in H1299 cells. (A) H1299 cells were treated with control or mEAK-7 siRNA (ID: HSS126697) for 48 hours, and 500 cells were seeded into 60 mm TCPs and grown for

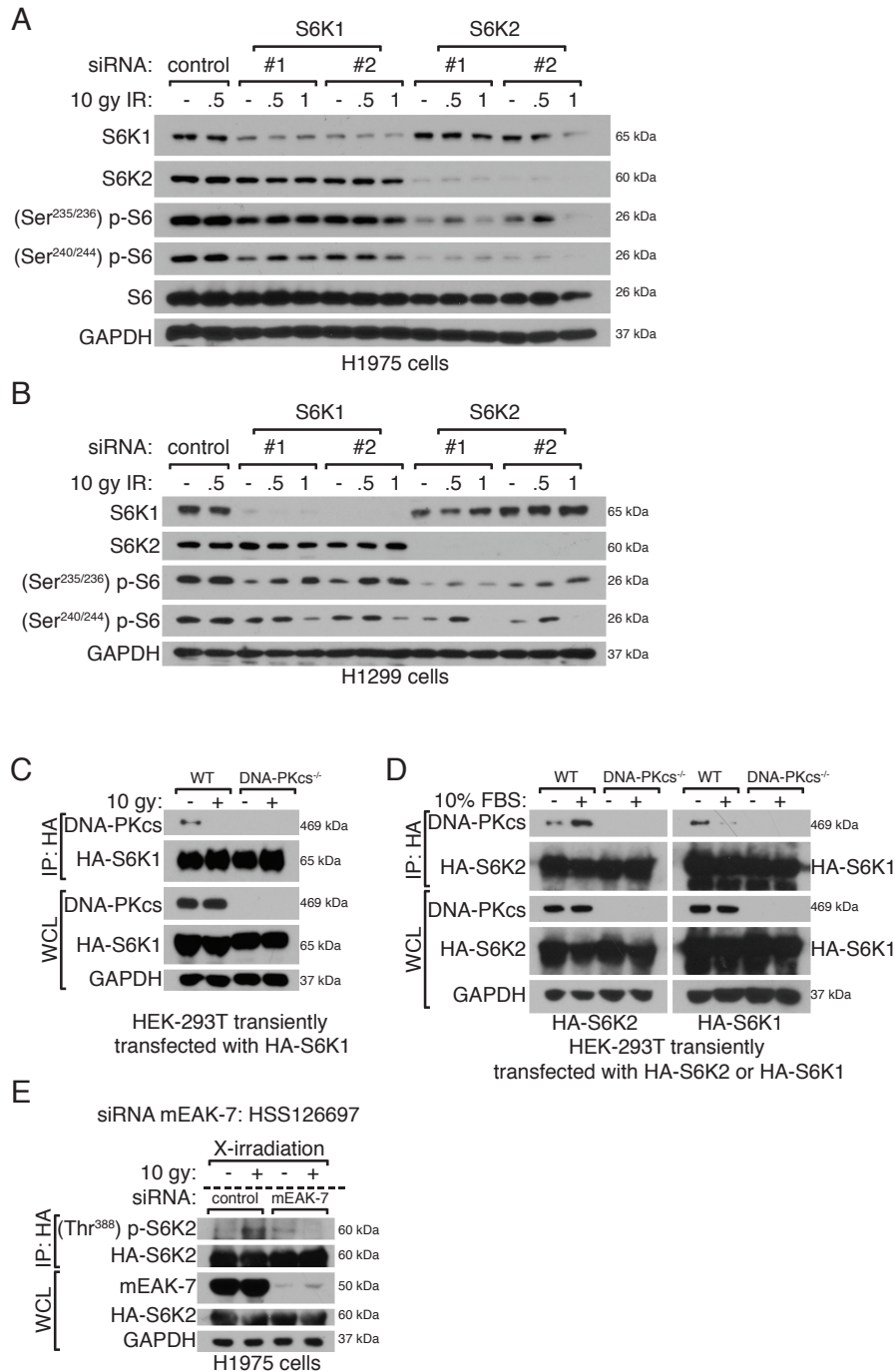
339 10 days. Quantification of colony formation and analysis via student's t-test (n=6) of (A),
340 * $P < 0.01$. (B) H1975 cells were treated with control or mEAK-7 siRNA (ID: HSS126697)
341 for 48 hours, and 500 cells were seeded into 60 mm TCPs and grown for 10 days.
342 Quantification of colony formation and analysis via student's t-test (n=6) of (B), * $P < 0.01$,
343 ** $P < 0.001$. (C) H1975 cells were treated with control or mEAK-7 siRNA, subjected to no
344 treatment, 2 gy, or 6 gy of X-ray irradiation, and 5,000 cells were seeded into 60 mm
345 ultra-low attachment plates and grown for 10 days. Quantification of spheroid formation
346 and analysis via student's t-test (n=6), * $P < 0.01$, ** $P < 0.001$. (D) H1299 cells were
347 treated with control or mEAK-7 siRNA (ID: HSS126697), and 2,500 cells were seeded
348 into 60 mm ultra-low attachment plates and grown for 10 days. Quantification of
349 spheroid formation and analysis via student's t-test (n=6) of (D), * $P < 0.01$, ** $P < 0.001$,
350 *** $P < 0.0001$, ‡ $P < 0.00001$, § $P < 0.000001$. (E) H1975 cells were treated with control or
351 mEAK-7 siRNA (ID: HSS126697), and 5,000 cells were seeded into 60 mm ultra-low
352 attachment plates and grown for 10 days. Quantification of spheroid formation and
353 analysis via student's t-test (n=6) of (E), * $P < 0.01$, ** $P < 0.001$, *** $P < 0.0001$, ‡ $P < 0.00001$,
354 § $P < 0.000001$. (F) H1299 cells were treated with control or mEAK-7 siRNA and X-ray
355 irradiated at 20 gy for 30 minutes, 1 hour, or 2 hours and analyzed for Noxa expression
356 by DNA damage.

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362 **Figure S4, related to Figure 5 and Figure 6. DNA damage mediated S6K1/2**
 363 **signaling, and DNA-PKcs binding to S6K1, and second mEAK-7 siRNA effect on**
 364 **DNA damage or nutrient induced S6K2 activation. (A)** H1975 cells were treated with
 365 control, 2 unique S6K1, or 2 unique S6K2 siRNAs, then subjected to no treatment, 10

366 gy of X-ray irradiation for 30 minutes or 1 hour. Immunoblot analysis on mTOR
367 signaling. **(B)** H1299 cells were treated with control, 2 unique S6K1, or 2 unique S6K2
368 siRNAs, then subjected to no treatment, 10 gy of X-ray irradiation for 30 minutes or 1
369 hour. Immunoblot analysis on mTOR signaling. **(C)** HEK-293T DNA-PKcs^{+/+} or HEK-
370 293T DNA-PKcs^{-/-} cells were transiently transfected with or without pRK7-HA-S6K1-WT,
371 then untreated or treated with 10 gy of X-ray irradiation for 1 hour. HA-S6K1 was
372 immunoprecipitated to check DNA-PKcs interaction. This experiment was completed at
373 least 3 times. **(D)** HEK-293T DNA-PKcs^{+/+} or HEK-293T DNA-PKcs^{-/-} cells were
374 transiently transfected with pcDNA3-HA-S6K2 or pRK7-HA-S6K1-WT for 48 hours. Next,
375 cells were starved in DMEM^{-AAs} for 1 hour and reintroduced with 10% FBS in DMEM^{AAs}
376 for 30 minutes. Cells were collected in CHAPS lysis buffer and immunoprecipitated with
377 HA antibody. **(E)** H1975 cells were transiently transfected with pcDNA3-HA-S6K2 and
378 control or mEAK-7 siRNA (ID: HSS126697) for 48 hours. Next, cells were untreated or
379 treated with 10 gy of X-ray irradiation for 30 minutes, followed by IP of HA-S6K2, and
380 probed for activated S6K2 signaling.

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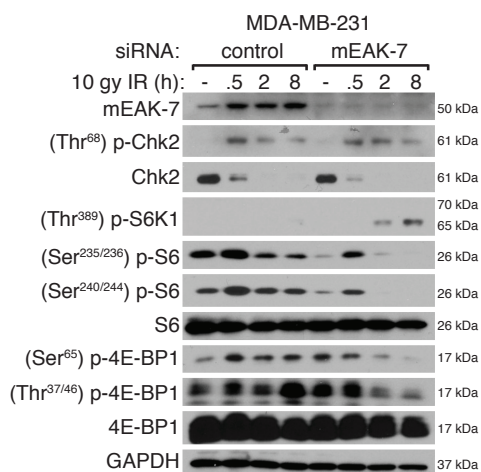
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389 **Figure S5, related to Figure 6. mEAK-7 is required for X-ray irradiation-mediated**
 390 **mTOR signaling in MDA-MB-231 cells.** MDA-MB-231 cells were treated with control
 391 or mEAK-7 siRNA for 48 hours, X-irradiated at 10 gy for 30 minutes, 2 hours, and 8
 392 hours and processed for mTOR signaling. This experiment was completed at least 3
 393 times.

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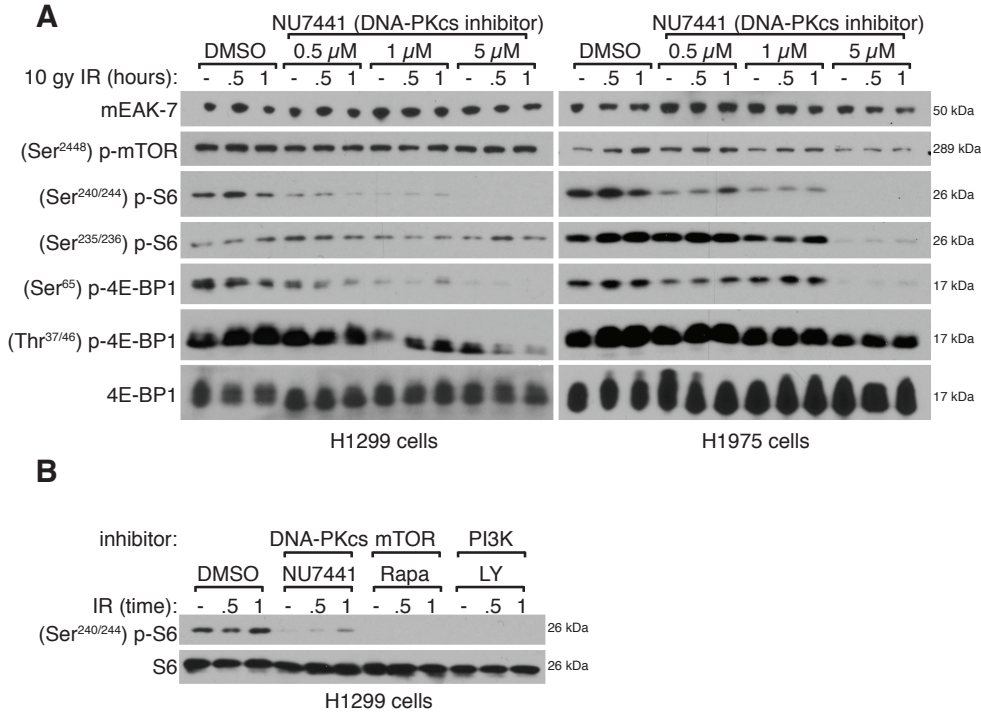
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Figure S6, related to Figure 6. Dose-dependent analysis of NU7441 on IR-

mediated mTOR signaling and inhibition of DNA-PKcs, mTOR, and PI3K

significantly decreased IR-mediated mTOR signaling in H1299 cells. (A) H1299

and H1975 cells were treated with DMSO or 0.5 μ M, 1 μ M, 5 μ M NU7441 for 2 hours

before treated with X-ray irradiation at 10 gy for 30 minutes and 1 hour. Immunoblot

analysis on mTOR signaling. All experiments were repeated at least 3 times. 4E-BP1

was utilized as a loading control. (B) H1299 cells were treated with inhibitors of DNA-

PKcs (5 μ M NU7441, IC₅₀ = 14 nM), mTOR (100 nM rapamycin, IC₅₀ = 1 nM), and

PI3K (50 μ M LY249002, IC₅₀ = 2.3 μ M) for 1 hour before treated with X-ray irradiation

at 10 gy for 30 minutes and 1 hour. Immunoblot analysis on mTOR signaling. We

observed that inhibition of DNA-PKCS, mTOR, or PI3K significantly decreased IR-

416 mediated mTOR signaling. All experiments were repeated at least 3 times. S6 was
417 utilized as a loading control.

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437 **Table S1. Immunoprecipitation-mass spectrometry analysis of HA-mEAK-7.**

438 Extended full list of proteins from IP-MS experiment for Figure 5A.

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458 **Table S2: Detailed patient information from US Biomax TMAs.** Detailed patient
459 information regarding TMAs analyzed for Figure 2A-C, Figure 2D, and Figure S2.

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