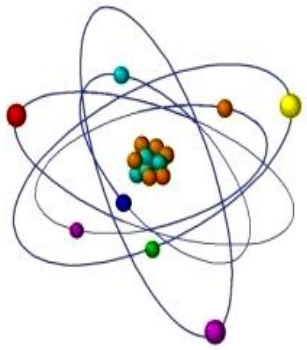
COMPARATIVE ANALYSIS OF RADIATION-INDUCED GENETIC ALTERATIONS AND CANCER-ASSOCIATED MOLECULAR SIGNATURES



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ABSTRACT: *Ionizing radiation is a potent environmental carcinogen capable of inducing complex DNA damage and long-term genomic instability. While radiation-associated mutational signatures have been well characterized at the genomic level, less is known about how radiation-induced damage intersects with transcriptional regulation across diverse cancer types. Advances in sequencing technologies now enable integrated, multi-layered analyses of radiation-exposed tissues and tumors at the genomic, transcriptomic, and proteomic levels. Such integrative approaches allow not only the identification of structural and sequence-level alterations but also the functional consequences of these changes in terms of gene expression and protein activity. By comparing irradiated tissues, tumor samples, and matched normal controls, it becomes possible to identify shared and distinct molecular signatures that reflect both exposure history and disease state. In this study, we performed a comparative transcriptomic analysis to investigate whether ionizing radiation induces gene expression alterations that overlap with transcriptional changes characteristic of diverse cancer forms. By analyzing four malignancies obtained from Gene Expression Omnibus (GEO) databases, and comparing them with irradiation-responsive genes identified in our previous bioinformatic mouse model investigations, we examined not only disease-specific dysregulation but also non-specific, systemic genetic consequences of radiation exposure. By progressively narrowing the gene spectrum using multilevel filtering, first by expression magnitude, then by Differentially Express Genes (DEG) validation against healthy tissue, and finally by cross-dataset intersections, we identified a narrowed set of genes that are altered both by radiation and across several cancer types. Our findings demonstrate extensive overlap between radiation-responsive genes and genes dysregulated in multiple cancers, suggesting that conserved transcriptional stress responses may contribute to tumorigenesis. This integrative approach provides insight into shared molecular pathways linking radiation exposure and cancer development and supports the identification of candidate biomarkers relevant to radiation-associated malignancies.*

K**eywords**: Irradiation, Cancer, Gene Spectrum, Differentially Express Genes

INTRODUCTION

Ionizing radiation is a well-established carcinogen capable of inducing a wide spectrum of DNA damage, including base lesions, single and double strand breaks (DSBs) [1, 2]. Although cells possess highly conserved DNA damage response (DDR) and repair mechanisms, incorrect repair of radiation-induced lesions can result in permanent genomic alterations that lead to malignant transformation [3,4,5]. Understanding how radiation-associated genetic damage differs, or overlaps with spontaneous oncogenic processes remains a central challenge in radiation biology, cancer genomics, and clinical oncology [6].

In recent years, comparative analysis of mutational landscapes often referred to as mutational or genomic signatures has emerged as a powerful approach for distinguishing between distinct etiological sources of DNA damage [7, 8, 9]. Unlike spontaneous cancers, which typically arise through gradual accumulation of replication errors and endogenous DNA damage, radiation-induced tumors display characteristic structural features in the genome [1, 10]. These include an increased frequency of small deletions (typically 1-100 base pairs), large chromosomal rearrangements such as inversions and translocations, and balanced inversions that arise from mis-rejoining of radiation-induced DSBs. Importantly, these structural alterations tend to be distributed relatively uniformly across the genome and show limited dependence on chromatin state or replication timing, distinguishing them from patterns observed in non-irradiated tumors [1,11,12]. The identification of such radiation-specific genomic features has important implications for both basic research and clinical practice. From a mechanistic perspective, this allows a deeper understanding of how ionizing radiation disrupts genomic integrity and overwhelms cellular repair systems [3, 5]. Clinically, the ability to distinguish radiation-induced malignancies from spontaneous tumors is critical for the diagnosis and management of secondary cancers, particularly in patients who have previously undergone radiotherapy. In such cases, recognition of a radiation-associated etiology may directly influence therapeutic decisions, including avoiding further radiation and choosing alternative treatment strategies, such as surgery or systemic therapy [13, 14].

Large-scale sequencing studies of radiation-associated tumors have demonstrated that ionizing radiation does not introduce entirely novel classes of mutations, but rather alters the relative contribution of specific mutation types and structural variants. Secondary malignancies frequently exhibit enrichment of small deletions and balanced inversions across multiple tumor types, supporting their use as potential biomarkers of prior radiation exposure [1, 10]. At the same time, many radiation-induced alterations converge on canonical cancer-related pathways, including cell cycle regulation, DNA replication, checkpoint control, and apoptosis [3, 15]. This convergence complicates etiological attribution but highlights shared molecular vulnerabilities relevant to both radiation biology and oncology [16].

Despite substantial progress in characterizing radiation-associated mutational signatures at the genomic level, less is known about how radiation-induced damage intersects with transcriptional regulation and protein-level responses across different cancer types. Growing evidence suggests that genes involved in DNA damage repair, replication stress response, chromatin remodeling, and cell cycle control play dual roles in both the radiation response and tumor progression [17, 18, 19, 20]. These genes may not be unique drivers of radiation-induced

cancer but rather key nodes in conserved molecular networks that are repeatedly activated under conditions of genomic stress [19, 21].

Furthermore, genes associated with DNA damage susceptibility and aging share common biological features, including participation in damage accumulation, dependence on DNA repair efficiency, and contribution to cellular processes such as senescence, apoptosis, or malignant transformation [22, 23, 24]. They are genetically programmed but are also highly sensitive to external stressors such as ionizing radiation and environmental toxins. This overlap suggests that radiation exposure may accelerate pre-existing molecular trajectories associated with aging and cancer rather than initiate entirely distinct pathways [23, 24, 25].

Advances in sequencing technologies now enable integrated, multi-layered analyses of radiation-exposed tissues and tumors at the genomic, transcriptomic, and proteomic levels [26, 27,28]. Such integrative approaches allow not only the identification of structural and sequence-level alterations but also the functional consequences of these changes in terms of gene expression and protein activity. By comparing irradiated tissues, tumor samples, and matched normal controls, it becomes possible to identify shared and distinct molecular signatures that reflect both exposure history and disease state [27, 29].

In this context, the present study aims to systematically compare molecular alterations induced by ionizing radiation with those observed in cancerous tissues using an integrated analytical framework. By combining transcriptomic profiling, protein analysis, and bioinformatic approaches, we investigate whether radiation-induced gene expression changes overlap with transcriptional alterations characteristic of diverse malignancies. Analyzing multiple GEO datasets representing different cancer types and comparing them with irradiation-responsive genes identified in our previous bioinformatic mouse model studies, we tried to identify conserved genes and pathways at the intersection of radiation response and tumorigenesis. This approach enables the differentiation of universal stress-related transcriptional responses from malignancy-specific oncogenic mechanisms and provides insight into how external radiation exposure intersects with endogenous drivers of cancer development.

MATERIALS AND METHODS

Overview of the Bioinformatic Analysis Strategy

To investigate shared molecular mechanisms between ionizing-radiation responses and diverse cancer forms, we conducted a comparative multi-dataset transcriptomic analysis using publicly available datasets from the NCBI Gene Expression Omnibus (GEO). Our goal was to identify genes dysregulated both after irradiation (based on our previously published mouse tissue bioinformatic approach) and in different malignancies. Such shared genes may represent radiation-induced stress responses, oncogenic factors, or immunomodulatory regulators important for tumor iniciation or progression.

Differentially expressed genes (DEGs) from irradiated mouse tissues were used as the reference radiation-response signature [30]. We compared this radiation-response signature against the Differentially Expressed Genes obtained by comparing healthy (normal) samples against cancerous samples within each GEO dataset. All datasets were obtained directly from

GEO for downstream analysis. Five datasets representing four cancer forms were included: breast cancer, lung cancer, prostate cancer, and pancreatic carcinoma. Specifically, we focused on genes whose expression changes were driven by the disease form and identified the narrow subset of overlapping genes that were common across multiple cancer types within the previously defined group of genes shared between irradiation and cancer.

Datasets Used in the Study

1. Breast Cancer Dataset - GSE62598 (GPL7202)

This dataset captures granulocytic immune infiltrates essential for breast cancer metastasis to the liver. Expression profiling was performed on *Mus musculus* 4T1 breast cancer subpopulations with different organotropic properties using the GPL7202 microarray platform. This dataset provides a robust comparison between breast cancer associated expression signatures and our radiation-induced DEGs.

2. Lung Adenocarcinoma, c-Myc Transgenic Model - GSE10954 (GPL1261)

This murine dataset characterizes transcriptional changes driven by c-Myc overexpression in alveolar epithelial cells, resulting in bronchiolo-alveolar carcinoma (BAC) and papillary adenocarcinoma (PLAC). Sixteen transgenic and sixteen non-transgenic female mice were used, pooled into four replicates per group. Expression profiling was done using the Affymetrix Mouse Genome 430 2.0 Array (GPL1261). This model provides a controlled framework for comparing oncogene-driven lung tumorigenesis with radiation responses.

3. Human Lung Cancer Sample - GSM494567 (GPL570)

This sample represents a primary stage IB lung carcinoma surgically resected from a 48-year-old female patient. RNA was hybridized onto the GPL570 Affymetrix Human Genome U133 Plus 2.0 platform. It serves as a real-world human lung cancer reference complementing the c-Myc mouse model.

4. Prostate Cancer Dataset - GSE55945 (GPL570), Sample GSM1348935

This RNA sample originates from malignant prostate tissue lacking the TMPRSS2:ERG fusion. RNA extraction, Bioanalyzer QC, biotin-UTP labeling, and hybridization were performed using standard Affymetrix U133 Plus 2.0 workflows. This dataset represents a prostate cancer transcriptional profile appropriate for cross-pathology comparisons.

5. Pancreatic, Gastric, and Hepatocellular Carcinoma Dataset - GSE49515

This human dataset includes peripheral blood mononuclear cell (PBMC) transcriptomes from healthy donors and patients with pancreatic carcinoma, gastric carcinoma, or hepatocellular carcinoma. Hybridization was done using Affymetrix gene arrays. The dataset facilitates evaluation of systemic cancer-associated expression changes relative to irradiation responses.

Dataset Selection Rationale

These five GEO datasets were strategically selected to encompass a broad spectrum of malignancies across both human and murine systems. This design enables robust comparisons between normal and tumor states and strengthens the identification of conserved biological pathways shared between radiation exposure and cancer development etiology.

Raw data handling and metadata parsing were performed using Bioconductor in R, while GEOparse, pandas and numpy were used in Python coding for numerical preprocessing, alignment, and dataset integration [31, 32, 33, 34].

Gene Selection and Comparison Strategy

All datasets were aligned using standardized GENE_SYMBOL identifiers. Normalized expression matrices provided by the original GEO submissions were used for analysis. Each cancer dataset was independently compared against the irradiation-derived DEG signature from mouse tissues.

To focus on the most biologically relevant signals, we selected from each cancer dataset the top 15 upregulated and top 15 downregulated genes, ranked by $\log_2$ fold-change relative to irradiation-responsive genes. These filtered gene sets were then compared across datasets to identify:

1. shared radiation - cancer genes,
2. cancer-specific expression patterns
3. multi-disease overlap genes.

Final Integration and Visualization

Analysis of the Total Gene Set

The initial analytical layer involved a broad comparison of all malignant disease datasets against irradiation-induced DEGs. While early analyses focused on genes exhibiting the strongest absolute expression changes, a refined approach was later implemented using DEGs calculation derived from healthy versus cancer comparisons via Bioconductor pipelines in R [31].

Gene filtering was further guided by multiple visualization strategies, including heatmaps, and intersection analyses.

A disease - gene association heatmap (Fig.1) was generated where: rows represent genes, columns represent cancer datasets, where colors indicate upregulation or downregulation. This heatmap visualizes cross-cancer convergence of transcriptional responses.

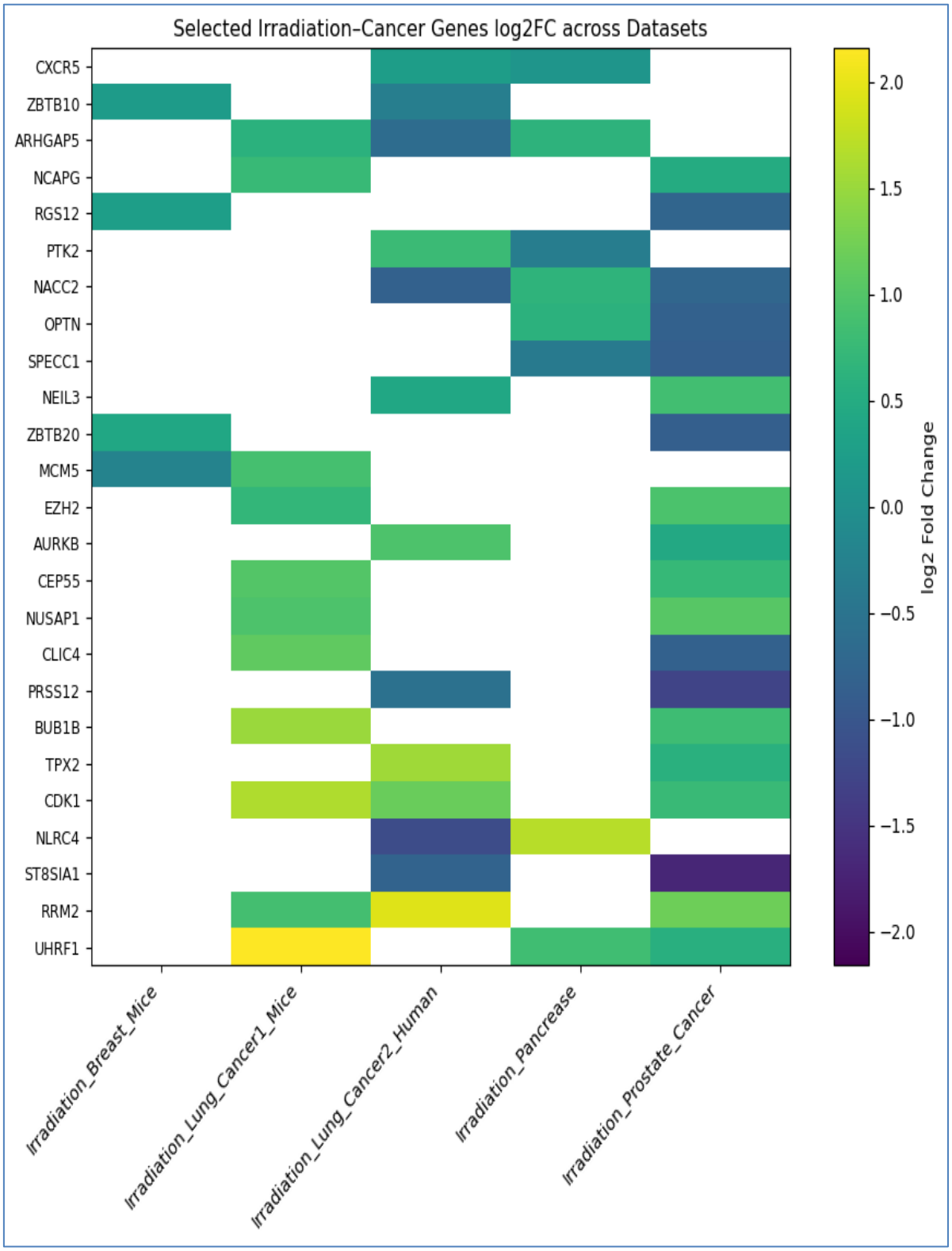

Figure 1. Heatmap illustrating irradiation-connected DEG patterns across cancer datasets.
Rows correspond to individual genes, while columns correspond to different cancer datasets (Breast, Lung1, Lung2, Prostate, Pancreas).

Colors represent log_2 fold-change values relative to irradiation-derived DEGs:

- yellow - upregulated genes
- Blue - downregulated genes
- White - gene absent or not significantly regulated

This plot highlights clusters of genes exhibiting conserved upregulation or downregulation across multiple cancers, suggesting shared pathways.

To quantify gene sharing and visualize complex multidimensional intersections, we constructed UpSet plots (Fig. 2)

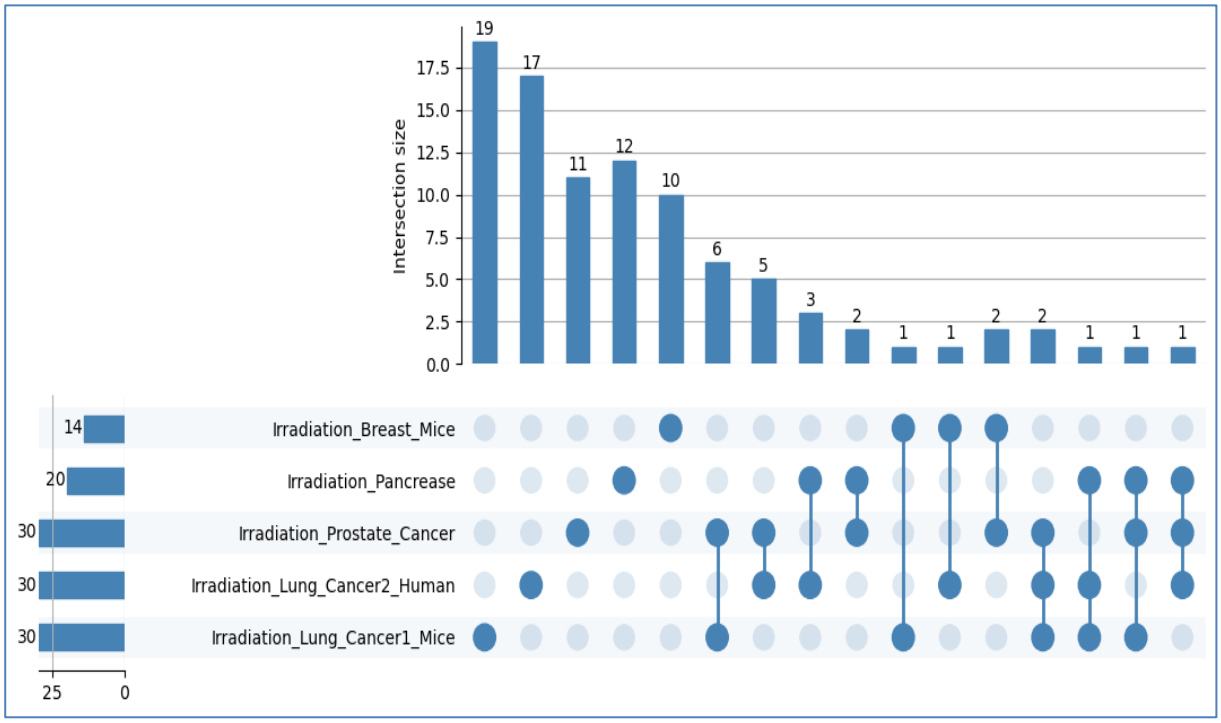

Figure 2. UpSet plot showing intersections of irradiation–cancer gene sets illustrating the size and composition of shared gene sets across irradiation and cancer datasets

Bars indicate the number of genes shared among specific combinations of datasets, while the dot-matrix below identifies the contributing dataset groups.
This visualization enables detection of complex overlaps that cannot be captured by traditional Venn diagrams. Highly overlapping gene groups highlight potential radiation-associated signatures common to several cancer types.

These plots demonstrate number of genes which are shared across datasets and how many cancers share the same genes.

Intersections in initial data are represented in table (Tab.1)

Table 1. Gene intersections derived from the comparison of irradiation DEGs with filtered cancer-associated gene sets (top 15 upregulated and top 15 downregulated genes per dataset)

Comparison Type	N	Genes
Irradiation_Breast_Mice	14	ANLN, BARD1, BSPRY, DUT, E2F2, GEM, HIST1H2BK, HIST1H2BM, MCM5, MYBL2, RGS12, ST3GAL5, ZBTB10, ZBTB20
Irradiation_Lung_Cancer1_Mice	30	ARHGAP5, AURKA, BRCA1, BUB1B, CCNA2, CCR2, CDCA5, CDCA8, CDK1, CEP55, CKAP2, CKAP2L, CLIC4, DOCK5, ECT2, ESCO2, EZH2, FGL2, FIGNL1, HELLS, ISG20, MCM5, NCAPG, NUSAP1, POLE, PRC1, RRM2, TCF19, TOP2A, UHRF1
Irradiation_Lung_Cancer2_Human	30	ARHGAP5, AURKB, CCNF, CD55, CDK1, CLSPN, CXCR5, ESPL1, HIST1H2BB, HIST1H3B, KCNA2, KIF14, MCM10, MPO, NACC2, NCAPG2, NEIL3, NLRC4, PRSS12, PTK2, RAB6B, RRM2, SLC6A19, SNORA21, SNORD8, SPAG5, ST8SIA1, TANC2, TPX2, ZBTB10
Irradiation_Prostate_Cancer	30	ALAD, ARHGAP23, AURKB, BIRC5, BUB1B, CDCA3, CDK1, CEP55, CLIC4, CRIP2, EZH2, F2R, FNIP2, LMNB1, NACC2, NCAPG, NEIL3, NUSAP1, OPTN, PRSS12, RGS12, RRM2, SETBP1, SPECC1, SSX2IP, ST8SIA1, TPX2, UBE2C, UHRF1, ZBTB20
Irradiation_Pancreas	20	ARHGAP5, BHLHE40, CASP3, CCNE2, CNTLN, CXCR5, FHL2, GGT1, HIST1H1D, ITGAX, NACC2, NLRC4, NMRAL1, OPTN, PTK2, RNF32, SPECC1, SYCE2, UHRF1, ZEB2
Irradiation_Breast_Mice ∩ Irradiation_Lung_Cancer1_Mice	1	MCM5
Irradiation_Breast_Mice ∩ Irradiation_Lung_Cancer2_Human	1	ZBTB10
Irradiation_Breast_Mice ∩ Irradiation_Prostate_Cancer	2	RGS12, ZBTB20
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Lung_Cancer2_Human	3	ARHGAP5, CDK1, RRM2
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Prostate_Cancer	9	BUB1B, CDK1, CEP55, CLIC4, EZH2, NCAPG, NUSAP1, RRM2, UHRF1
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Pancreas	2	ARHGAP5, UHRF1
Irradiation_Lung_Cancer2_Human ∩ Irradiation_Prostate_Cancer	8	AURKB, CDK1, NACC2, NEIL3, PRSS12, RRM2, ST8SIA1, TPX2
Irradiation_Lung_Cancer2_Human ∩ Irradiation_Pancreas	5	ARHGAP5, CXCR5, NACC2, NLRC4, PTK2
Irradiation_Prostate_Cancer ∩ Irradiation_Pancreas	4	NACC2, OPTN, SPECC1, UHRF1
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Lung_Cancer2_Human ∩ Irradiation_Prostate_Cancer	2	CDK1, RRM2
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Lung_Cancer2_Human ∩ Irradiation_Pancreas	1	ARHGAP5
Irradiation_Lung_Cancer1_Mice ∩ Irradiation_Prostate_Cancer ∩ Irradiation_Pancreas	1	UHRF1
Irradiation_Lung_Cancer2_Human ∩ Irradiation_Prostate_Cancer ∩ Irradiation_Pancreas	1	NACC2

Each row of this table (Tab.1) represents a pairwise or multi-dataset intersection, listing: the datasets included, the number of shared genes (N), and the corresponding gene names. Large intersections reveal strong cross-disease convergence, particularly among lung (mouse and human), prostate, and pancreatic cancer datasets.

RESULTS

Intersection Analysis of Irradiation-Associated Genes Across Cancer Datasets

Our analysis demonstrates that several genes, including CDK1, RRM2, ARHGAP5, UHRF1, NACC2 appear across multiple cancer datasets, indicating common transcriptional perturbations between irradiated tissues and diverse malignancies.

The heatmap analysis (Fig. 1) reveals conserved expression patterns across cancers. Upregulated clusters of radiation-associated genes are shared predominantly among lung, prostate, and pancreatic cancers, while downregulated clusters extend across breast, lung, prostate, and pancreatic datasets. These findings support shared mechanisms involving cell-cycle progression, DNA repair, chromatin remodeling, and immune regulation.

UpSet analysis and intersection data (Fig.2, Table 1) identify numerous shared genes, with the largest overlaps occurring among lung (mouse and human), prostate, and pancreatic cancers. The most frequently shared genes, such as CDK1, RRM2, ARHGAP5, UHRF1, and NACC2 form functional groups associated with mitotic control, replication stress, and genome stability.

Due to filtering and selection of only the top 15 upregulated and top 15 downregulated genes per dataset based on $\log_2$ fold-change relative to irradiated mouse tissues, we obtained a focused gene set enriched for the most robust and biologically meaningful overlaps.

To characterize the degree of overlap between irradiation-responsive genes and cancer-associated transcriptional profiles, we organized shared genes according to the number of cancer datasets in which they co-occurred. This approach effectively illustrates the spectrum of cross-disease overlap, ranging from simple pairwise shared genes to complex multi-cancer expression signatures.

Genes Shared Between Two Cancer Datasets

These genes were identified exclusively in pairwise intersections and did not appear in any three-dataset overlap.

- MCM5 - Breast (mouse) ∩ Lung (mouse)
- ZBTB10 - Breast (mouse) ∩ Lung (human)
- RGS12, ZBTB20 - Breast (mouse) ∩ Prostate
- BUB1B, CEP55, CLIC4, EZH2, NCAPG, NUSAP1 - Lung (mouse) ∩ Prostate
- AURKB, NEIL3, PRSS12, ST8SIA1, TPX2 - Lung (human) ∩ Prostate
- CXCR5, NLRC4, PTK2 - Lung (human) ∩ Pancreatic
- OPTN, SPECC1 - Prostate ∩ Pancreatic

These pairwise overlaps suggest cancer-type–specific convergence with irradiation responses.

Genes Shared Between Three Cancer Datasets

Genes in this category were detected in three-dataset intersections, representing a stronger and more conserved multi-disease signal.

- CDK1, RRM2 - Lung (mouse) ∩ Lung (human) ∩ Prostate
- ARHGAP5 - Lung (mouse) ∩ Lung (human) ∩ Pancreatic
- UHRF1 - Lung (mouse) ∩ Prostate ∩ Pancreatic
- NACC2 - Lung (human) ∩ Prostate ∩ Pancreatic

These genes form a core multi-cancer irradiation-associated signature, linking radiation response with key oncogenic processes across distinct malignancies.

Summary of Cross-Dataset Convergence

1. Pairwise-only genes: 18
2. Three-dataset shared genes: 5
3. Maximum overlap observed: Three cancer types
4. Most recurrent multi-cancer genes: CDK1, RRM2, ARHGAP5, UHRF1, NACC2

The analysis of radiation-induced DEGs and cancer transcriptomic datasets (Tab.1) revealed a limited set of genes (CDK1, RRM2, ARHGAP5, UHRF1, NACC2) that appear across multiple disease intersections. They are present in intersections of three or more cancer datasets, including lung (mouse and human) and prostate tissues, highlighting their conserved roles in cell cycle regulation and replication stress [20, 35, 36] (Gollapalli et al., 2024; Zhang et al., 2009; Koppenhafer et al., 2020). Similarly, UHRF1 was identified as shared among lung, prostate, and pancreatic cancer intersections, emphasizing its key role in DNA double-strand break repair pathway choice and chromatin maintenance [21, 37] (Mistry et al., 2010; Zhang et al., 2016).

Heatmap analysis (Fig. 1) confirmed these observations: CDK1 and RRM2 form clusters of consistent upregulation across multiple cancer types, whereas UHRF1 shows conserved increased expression in lung, prostate, and pancreatic tissues. ARHGAP5 and NACC2, found in two- or three-dataset intersections, participate in more specialized oncogenic processes: ARHGAP5 through regulation by the lncRNA ARHGAP5-AS1 and m6A RNA modification, and NACC2 through interactions with the HDM2/TP53/RB axis and LINE-1 retrotransposition [38, 39] (Zhu et al., 2019; Bojang et al., 2025). These data indicate that, in addition to classical DNA damage response components (DDR) components, it is critical to consider a broader network context including proteins involved in replication stress, cell cycle control, epigenetic regulation, and chemoresistance.

According to this we can say that the identified proteins are not only well-established participants in radiation- and cancer-associated processes (CDK1, RRM2, UHRF1, ARHGAP5, NACC2) but also represent components of pathways that should be studied together with other proteins involved in similar signaling pathways and cellular processes. This

approach enables the identification of systemic interactions and potential therapeutic targets within complex networks of DNA damage response and tumor stress signaling.

CONCLUSION

In this study, we performed a comparative transcriptomic analysis to investigate whether ionizing radiation induces gene expression alterations that overlap with transcriptional changes, which characterize diverse cancer forms. Analyzing five GEO datasets representing several malignancies and comparing them with irradiation-responsive genes identified in our previous bioinformatic mice model investigations, we were able to examine not only common disease-specific dysregulations, but rather the non-specific, systemic genetic consequences of radiation exposure.

Our results demonstrate that a substantial proportion of radiation-responsive genes are also dysregulated across multiple cancers. By progressively narrowing the gene spectrum using multilevel filtering - first by expression magnitude, then by DEG validation against healthy tissue, and finally by cross-dataset intersections - we identified narrowed set of genes that are altered both by radiation and across several cancer types. These genes likely represent critical nodes at the intersection of exogenous (radiation-related) and endogenous (tumor-driven) factors. When comparing the total number of DEGs induced by irradiation (approximately 300 genes) with the DEGs observed in tumor samples, we found that many irradiation-induced DEGs are embedded within the cancer DEG profiles. This overlap suggests that genes most severely affected by radiation may contribute to the transcriptional landscape of tumorigenesis.

Importantly, this approach allows us to begin distinguishing which components of the cancer-associated gene expression signature may reflect universal stress responses triggered by non-specific external influences such as radiation, and which components more likely arise from endogenous oncogenic mechanisms specific to each malignancy.

In other words, by identifying genes affected simultaneously by irradiation and by multiple cancers, we gain a unique opportunity to estimate the potential contribution of external versus internal factors to cancer induction and development.

Our bioinformatic analysis, which utilized a combination of heatmaps and UpSet intersection analysis, yielded clear evidence of link between the effects of ionizing radiation and cancer.

We found an extensive overlap between genes that respond to radiation exposure and genes that show altered expression in various cancer types. More importantly, we identified group of multi-datasets shared genesin, including CDK1, RRM2, ARHGAP5, UHRF1, and NACC2, that appeared across several different malignancies after rigorous Differentially Expressed Gene (DEG) validation. Crucially, our data provides evidence that several of these shared genes are active participants in the canonical pathways already known to be affected by radiation [21, 40] (Huang RX et al,.2020, Mistry et al., 2010).

Collectively, these findings support the powerful hypothesis that recurrent, conserved transcriptional responses to ionizing radiation may represent early, intrinsic mechanisms that promote tumor development.

Overall, this work highlights a core subset of genes, like CDK1, RRM2, ARHGAP5, UHRF1, and NACC2, that likely play dual roles in both radiation response and tumorigenesis. These specific genes provide a strong basis for future mechanistic studies, serving as potential biomarkers for radiation-associated cancer risk and as prime candidates for deep investigations exploring how external, radiation-caused stress intersects with internal oncogenic processes.

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