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# Pan-Cancer Exploration of rDNA Copy Number and Its Clinical and Immunological Significance

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## Abstract

Cancer remains one of the leading causes of death worldwide, and uncovering its underlying mechanisms continues to be a central focus of biomedical research. A representative trait of cancer cells is their unlimited proliferative capacity, which is tightly linked to ribosome biogenesis. This study aimed to investigate the role and mechanism of ribosomal DNA copy number (rDNA CN), which serves as the foundation for ribosome metabolism. I developed a computational pipeline to estimate rDNA CN from whole-genome sequencing (WGS) data and applied it to seven TCGA cancer cohorts to perform a pan-cancer analysis. The analytical framework involved statistical assessments and survival modeling, including Kaplan–Meier and Cox proportional hazards models, to examine the association between rDNA CN and clinical outcomes. Additionally, RNA-seq data from the TCGA cohorts were utilized for immunological profiling and transcriptomic analysis. Notably, a higher 45S rDNA copy number was associated with improved survival outcome in bladder urothelial carcinoma (BLCA) and pancreatic adenocarcinoma (PAAD), although such associations were not found in all other cancer types. Results from immunological and transcriptomic analyses further suggest that the functional impact of rDNA CN is tumor-specific, yet broadly associated with immunological characteristics.



***Keywords:*** Ribosomal DNA (rDNA), Copy number, Pan-cancer, Survival analysis

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# Abbreviations

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|---|---|
| **TCGA** | The Cancer Genome Atlas |
| **BLCA** | Bladder Urothelial Carcinoma |
| **COAD** | Colon Adenocarcinoma |
| **GBM** | Glioblastoma Multiforme |
| **LUAD** | Lung Adenocarcinoma |
| **LUSC** | Lung Squamous Cell Carcinoma |
| **PAAD** | Pancreatic Adenocarcinoma |
| **PRAD** | Prostate Adenocarcinoma |
| **rDNA** | Ribosomal DNA |
| **rRNA** | Ribosomal RNA |
| **RP** | Ribosomal Protein |
| **CNV** | Copy Number Variation |
| **OS** | Overall Survival |
| **PFI** | Progression-Free Interval |
| **GO** | Gene Ontology |
| **KEGG** | Kyoto Encyclopedia of Genes and Genomes |
| **WGS** | Whole Genome Sequencing |
| **RNA-seq** | RNA Sequencing |
| **DEG** | Differentially Expressed Gene |
| **TME** | Tumor Microenvironment |
| **TCR** | T Cell Receptor |
| **IGH** | Immunoglobulin Heavy Chain |
| **TIL** | Tumor-Infiltrating Lymphocyte |
| **CoxPH** | Cox Proportional Hazards Model |
| **HR** | Hazard Ratio |
| **CI** | Confidence Interval |