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these processes is the accurate detection of rare DNA and RNA mutations. which result as a consequence of infidelity. Until recently, this has not been possible, as the high error rates of available methods has limited their ability accurately detect rare mutations among a preponderance of wildtype molecules. The solution to this problem, as the Loeb lab and others have

found, is to perform single molecule sequencing of individually barcoded DNA and RNA molecules. In the present work, I present to the cause, three projects which apply the applied Duplex use of barcoding individual DNA and RNA molecules in order to enable develop cancer highly accurate and sensitive analyses of DNA replication and RNA transcription fidelity. (i) The addition to question of why CS

patients don 't get cancer despite being repair-deficient insights into has puzzled scientists for decades. While many have speculated as we have Sequencing to definitively answer this question: CS patients fail to because they do not accumulate quickly than re pair-proficient individuals. In finally solving this long-

standing mystery, we provide novel the mutagenic consequences of UV treatment in CS cells, at an unparalleled sensitivity. (ii) The question of why GBM patients do so poorly and always recur has long plaqued doctors and scientists. Here, we expand on the mutations more excellent clonal mutation work of our predecessors, revealing that the substantial inter- and intratumoral clonal heterogeneity is further compounded by GBM patients considerable subclonal heterogeneity. We show that subclonal mutations are highly heterogenous within individual GBM tumors, between GBM tumors from different patients, as well as between primary and recurrent tumors from the same patient. Our findings of high subclonal

heterogeneity in GBM tumors suggest that do so poorly because their tumors already contain a reservoir of mutations that potentially enable them to adapt to any treatment currently available. This underlies the importance of expanding subclonal mutation studies of GBMs to better antibiotics. understand makeup. (iii) The question of difficult to what, if any,

contribution RNA mutations have to health and disease has been one that has remained unanswered for more than 50 years. RNA mutations have long been hypothesized to play roles in human health and disease, as well as in several other processes, including RNA virus evolution and bacterial resistance to Unfortunately, their mutational until now, it has been very study the

hypothesis that increased transcriptional mutagenesis, resulting in RNA mutations, high level of contributes to or drives these processes because there have not been the tools available to do so. I have. therefore. developed a method to accurately sequence RNAs. Here, I demonstrate that Accurate RNA Consensus Sequencing (ARC-seq) has inherent adaptability to enable

stringency, which eliminates a damageinduced artifacts. Lalso show that RNA polymerase mutants induce increased transcriptional mutagenesis in vivo, with different mutants producing varying RNA mutation spectrums. Finally, I demonstrate the utility of ARC-seq to address questions on the biological

importance of transcriptional mutagenesis in vivo by using ARC-seq to show that oxidative stress induces high levels of transcriptional mutagenesis in both mRNA and rRNA. Thus, ARC-seg will enable studies on how perturbing a cell's environment or machinery affects the fidelity of transcription and to what extent RNA mutations contribute to aging, cancer,

eration, as well as the evolution and acquired resistance of viruses and bacteria. Together the three projects encompassed in this thesis demonstrate the power of combining the use of barcoding individual DNA and RNA molecules in order to enable highly accurate and sensitive analyses of DNA replication and RNA transcription fidelity.

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discusses the determination of adenosine- and aminoacyl adenosineterminated sRNA chains by ionexclusion chromatography. One paper notes that the problems involved in preparing acetylaminoacyl-tRNA are similar to those found in peptidyltRNA synthesis, in particular, to the lability of the ester bond between the amino acid and the tRNA. Another paper explains a new method that will attach fluorescent dyes to cytidine residues in tRNA; it also notes the possible use of Nhydroxysuccinimide esters of dansylglycine and Nmethylanthranilic acid in the described method. One paper

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