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Complete RNA-seq analysis of cancer transcriptomes from FFPE samples

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We have developed a new protocol that enables sequencing of the complete transcriptome from formalin-fixed, paraffin-embedded (FFPE) samples. The method uses a DSN (Duplex-Specific Nuclease) normalization process to remove ribosomal RNA and other abundant transcripts, which allows full-length RNA-seq libraries to be created from even the most highly degraded samples. We have used this protocol to study various sub-types of breast cancer and compare our results from FFPE samples with RNA derived from fresh/frozen tissues of the same tumors. We observe very good concordance of the gene expression changes when comparing fresh RNA and FFPE RNA. Since this method does not use a poly-A selection procedure, we are able to sequence all of the RNA in the tumor including many interesting non-coding RNAs that are usually missed in other gene expression assays. We will show data analyzing the gene expression changes of mRNA and ncRNA, and also characterize SNPs and mutations, alternative splicing and fusion transcripts in these cancers.

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