xGen™ Highlights in Oncology Research

Introduction

Oncology research demands flexibility across diverse sample types, sequencing strategies, and analytical approaches. This curated collection of recent publications showcases how researchers are leveraging Integrated DNA Technologies (IDT) xGen solutions across applications including **cfDNA, FFPE, cell lines**, and **tissue samples**. The tables that follow summarize each study and highlight a wide breadth of workflows—from **targeted panels** to **methylation** to **whole exome** sequencing. Together, these studies illustrate how xGen technologies support high-quality data generation and enable deeper insights into cancer biology. These and numerous other publications demonstrate IDT's commitment to delivering performance you can trust—helping researchers simplify complexity, gain deeper insights, and accelerate the pace of discovery.

xGen cfDNA & FFPE Library Preparation Kit

Featured publication	Experiment snapshot	Research highlights
Investigating the oncogenic role of aberrant EZH2 in hepatoblastoma Glaser K, *Sci Rep*. 2026 Feb 6;16:7563.	**Research area:** Epigenetics in hepatoblastoma **Sample type:** FFPE, cell lines, murine **Integrated DNA Technologies product:** xGen cfDNA & FFPE DNA Library Preparation Kit, GOAL consortium probes	• Classify histopathologic subtypes by EZH2 staining pattern and show that EZH2 is more prevalent in embryonal histology • Variant of unknown significance in both *EZH2* and *SUZ12* • EZH2 promotes hepatoblastoma progression through epigenetic silencing and noncanonical signaling pathways and contributes to hepatoblastoma pathogenesis
A Universal Duplex Sequencing Approach for Accurate Detection of Somatic Mutations Nandi SP, *bioRxiv* [Preprint]. 2025 Sep 16:2025.09.14.676103.	**Research area:** Somatic mutation detection **Sample type:** Sperm, cell lines, tissue samples **Integrated DNA Technologies product:** xGen cfDNA & FFPE DNA Kit, xGen Exome Hybridization Panel, xGen Pan-Cancer Hybridization Panel, UDI primers	• Describes creation of UDSeq for evaluation of somatic mutations by using duplex sequencing to help enable confident identification of rare somatic mutations • Use sperm as a test tissue due to haploid genome, and evaluated mutations present in sperm from men of various ages • UDSeq captures mutational signatures from heterogeneous populations without clonal expansion, reproduces exposure-specific patterns in cell lines and rodent models, and enables cross-species profiling

xGen Methyl-Seq DNA Library Prep Kit

Featured publication	Experiment snapshot	Research highlights
DNA methylation memory of pancreatic acinar-ductal metaplasia transition state altering Kras-downstream PI3K and Rho GTPase signaling in the absence of Kras mutation Lo EKW, *Genome Med.* 2025 Mar 28;17(1):32.	**Research area:** Epigenetic memory in pancreatic cancer **Sample type:** Fresh frozen tissue from transgenic mice **Integrated DNA Technologies product:** xGen Methyl-seq DNA library prep kit	• Generated a mouse model to mimic the acinar to ductal metaplasia (ADP) transitional step that often occurs during oncogenesis • Targeted overexpression of KLF4 to acinar cells is sufficient to reproduce the physiological characteristics of ADM • AP-1 family transcription factors were found to be positive regulators of ADM, as their motifs were enriched at regions hypomethylated in ADM lesions relative to normal acini • Motifs of pancreatic development transcription factors were enriched at regions hypermethylated in ADM lesions • Showed that cells have differential methylation before and after the ADP transitional step, indicating an epigenetic memory
Direct genetic transformation bypasses tumor-associated DNA methylation alterations Hertzel S, *Genome Biol.* 2025 Jul 17;26(1):212. doi: 10.1186/s13059-025-03650-2.	**Research area:** Methylation landscape in tumor vs healthy human cells **Sample type:** Fresh metastasis samples + gDNA (engineered human and mouse models) **Integrated DNA Technologies product:** xGen Methyl-seq DNA library prep kit	• In vitro models do not recapitulate methylation behavior observed in tumors, showing limitations of existing models of human tumors • Hypermethylation effects can be detected in a broad range of reference tissues • Neither in vitro models nor mouse models recapitulated the CpG pattern seen in cancer tissues • Introduction of tumor-associated genetic alterations in vitro does not trigger robust CGI hypermethylation in melanocytes

Accelerating the pace of genomics

These results underscore how Integrated DNA Technologies (IDT) brings together trusted genomic expertise and high-quality xGen solutions to help researchers see more from every sample. By turning complex liquid biopsy questions into clearer answers, we enable teams to work faster, with greater confidence—accelerating discoveries that can shape the future of cancer research. Grounded in science, driven by discovery—Integrated DNA Technologies turns deep expertise into breakthroughs that accelerate what's possible.

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