When we think about the causes of cancer, gene mutations usually come to mind. But mutations are not the only culprits in cancer. Scientists now know that gene expression—whether a gene turns on or stays silent—is directed by chemicals that latch onto genes. These chemical alterations are referred to as “epigenetic” changes because—unlike mutations—they don’t alter the gene’s DNA structure. Instead, the epigenetic “marks” on genes control whether a gene is turned on or not.

One common epigenetic change occurs when bulky chemical units called methyl groups (chemical formula \( \text{CH}_3 \)) latch onto genes. This is called methylation, and it generally prevents a gene from being turned on.

“Methylation is a normal way of regulating genes in the cell,” says Amit Verma, M.B.B.S., above left, associate professor of medicine and of developmental and molecular biology. “But it sometimes occurs inappropriately, turning off genes that suppress cell growth and division. When that happens, cancer can result.”

To study methylation, Dr. Verma needed a technique for scanning genes, looking for methyl groups—which is why he turned to John Greally, M.B., B.Ch., Ph.D., associate professor of genetics, for HELP.

HELP (which stands for Hpa II tiny fragment Enrichment by Ligation-mediated PCR) is a technique developed by Dr. Greally that allows investigators to evaluate