The complete epigenomes of the most frequent tumors mapped

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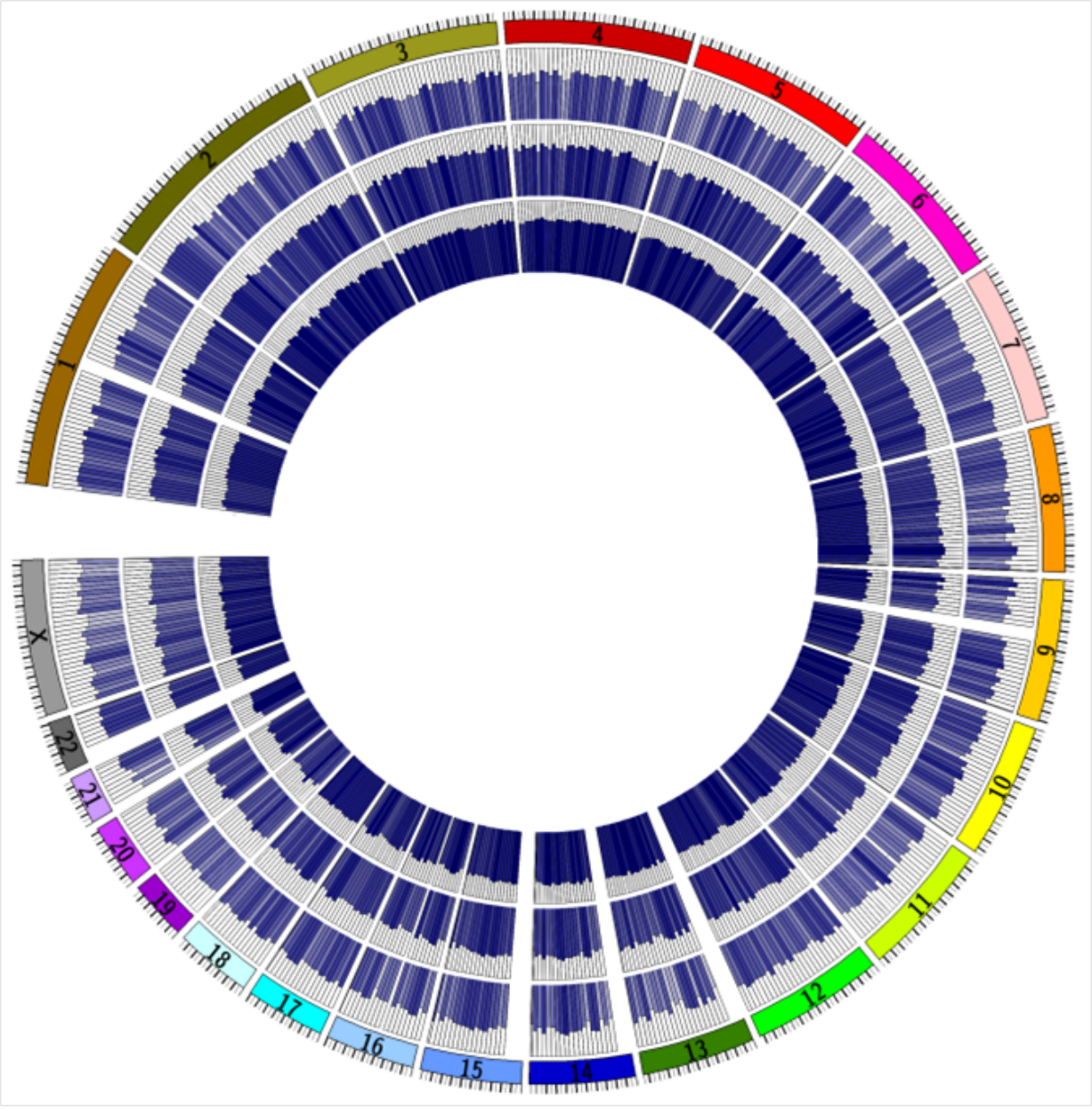

Example of three complete colon cancer epigenomes of a patient. The innermost concentric circle represents the normal colon tissue, the intermediate the primary colon tumor and the outermost themetastasis derived from that colon tumor. As the tumor progresses the representation changes from dark blue to light blue, indicating the loss of the correct epigenetic signals. In the periphery, the 23 human chromosomes are represented with different colors. Credit: IDIBELL

A research team from the Bellvitge Biomedical Research Institute (IDIBELL) has managed to characterize the complete epigenomes of the most frequent tumors, including those of colon, lung and breast cancer. Their work, published in *Oncogene*, was led by Dr. Manel Esteller, Director of the Epigenetics and Cancer Biology Program at IDIBELL, ICREA Researcher and Professor of Genetics at the University of Barcelona, and represents a big step in the study of origin and progression of these tumors.

"Our analysis has allowed us to get a first unbiased look at all the tumor cell methylomes in solid tumors," says group leader Dr. Manel Esteller. "We have not only found that many anti-cancer genes specifically slow down their activity. in the cancer-affected organs, but we have also shown that there are other alterations in distant chromosomal regions that affect these organs, since in the three-dimensional world of the cells these sequences are in very close relative positions."

Tumor inhibitory genes are known to lose their protective function if a certain chemical modification ("epi-genetic", that is, over the gene) is added. The main modification is usually a stop signal called DNA methylation. The human genome has 28,000 million candidate points to be regulated by this modification, but the most used techniques only allow researchers to study 1 million points. The IDIBELL study

overcomes this barrier.

At the same time, the research shows that sometimes there are long DNA fragments in which all neighboring genes undergo alterations of their chemical signals, as if they were blocks simultaneously altered in an epigenetic way.

"This is just the very beginning", says Dr. Esteller. "All the data obtained in this study are now publicly accessible and will allow new bioinformatic analyses that will surely provide us with more clues as to the origin and progression of these tumors."

More information: E Vidal et al, A DNA methylation map of human cancer at single base-pair resolution, *Oncogene* (2017). DOI: 10.1038/onc.2017.176

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