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Preview

A holistic view of the malignant organism we call glioblastoma

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Refers to

Glioblastoma evolution and heterogeneity from a 3D whole-tumor perspective

Cell, Volume 187, Issue 2, 18 January 2024, Pages 446-463.e16 Radhika Mathur, Qixuan Wang, Patrick G. Schupp, Ana Nikolic, Stephanie Hilz, Chibo Hong, Nadia R. Grishanina, Darwin Kwok, Nicholas O. Stevers, Qiushi Jin, Mark W. Youngblood, Lena Ann Stasiak, Ye Hou, Juan Wang, Takafumi N. Yamaguchi, Marisa Lafontaine, Anny Shai, Ivan V. Smirnov, David A. Solomon, Susan M. Chang, Shawn L. Hervey-Jumper, Mitchel S. Berger, Janine M. Lupo, Hideho Okada, Joanna J. Phillips, Paul C. Boutros, Marco Gallo, Michael C. Oldham, Feng Yue, Joseph F. Costello



Tumors are not simply a chaotic mass of mutated cells but can follow complex organizational principles, including in space. In this issue of Cell, Mathur and colleagues reconstruct a 3D genomic, epigenomic, and transcriptomic spatial cartograph of glioblastoma, offering a "whole-tumor" perspective with patterns of clonal expansion that are embedded in neurodevelopmental hierarchy.

Section snippets

Main text

Tumors are nurtured by a complex ecosystem of various malignant and non-malignant cells. Our understanding of tumor evolution and its origin rests upon two foundational theories, one being the stochastic model, which paints malignancies as a disorganized patchwork of diverse genetic clones (Figure 1A), and the other being the cancer stem cell model, which predicts that a malignancy is hierarchically organized in a manner analogous to the normal tissue (Figures 1B and 1C). Regardless, this...

Acknowledgments

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Declaration of interests

The authors	declare no	competing	interests

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Nat. Commun. (2020)

There are more references available in the full text version of this article.

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