

Cell Research



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Volume 30 Number 9 September 2020

Deep WGS of 10588 individuals by The ChinaMAP Consortium
ERCC6L2 promotes orientation-specific joining of DNA ends
A pan-cancer blueprint of the tumor microenvironment
Reconstructing cell spatial organization from scRNA-seq data



ISSN 1001-0602



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Center for Excellence in Molecular Cell Science
Chinese Academy of Sciences

SPRINGER NATURE

9 771001060301

Cell Research

(Founded in 1990)

Online submission via:
<http://www.nature.com/cr>
<http://www.cell-research.com>

Cell Research is published monthly by Nature Publishing Group (NPG) in partnership with Center for Excellence in Molecular Cell Science (CEMCS), Chinese Academy of Sciences (CAS) since 2006.

Sponsored by:
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Affiliated with:
The Chinese Society for Cell Biology since August 2007



Granted by:
Publishing Foundation of Chinese Academy of Sciences, National Natural Science Foundation of China, and China Association for Science and Technology



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Volume 30 Number 9 September 2020

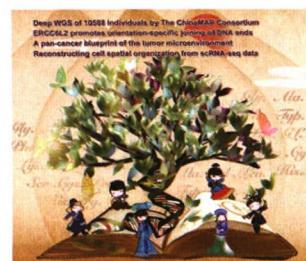
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Cover: ChinaMAP, The China Metabolic Analytics Project analyzed deep whole genome sequences and metabolic traits of 10,588 individuals across 8 ethnic populations and 27 provinces in China. See page 717-731 by Yanan Cao et al. for details.

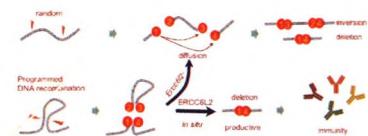
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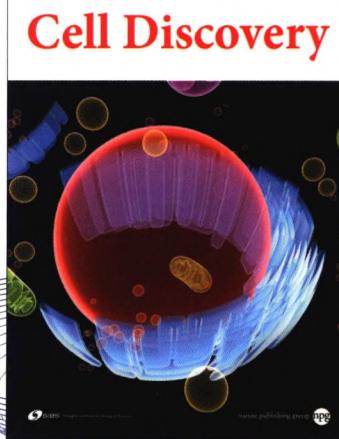
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