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Masahiro Okada, Satoru Yamasaki, Hiroshi Nakazato, Yuhya Hirahara, Takuya Ishibashi, Masami Kawamura, Kanako Shimizu, and Shin-ichiro Fujii
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IFNα-induced TRIM14 transcription suppresses antitumor immunity by recruiting USP14 to inhibit autophagic degradation of PD-L1, indicating that targeting this axis could be an effective immunotherapeutic approach for treating cancer.

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RUVBL1/2 inhibition is a therapeutic strategy to abrogate YTHDF1-driven oncogenic translation and overcome m^{6}A dysregulation in colorectal cancer.

2873 **PRKDC Induces Chemoresistance in Osteosarcoma by Recruiting GDE2 to Stabilize GNAS and Activate AKT**
Wenchao Zhang, Wei Li, Chi Yin, Chengyao Feng, Binfeng Liu, Haodong Xu, Xin Jin, Chao Tu, and Zhihong Li
Targeting PRKDC suppresses AKT activation and increases sensitivity to doxorubicin in osteosarcoma, which provides a therapeutic strategy for overcoming chemoresistance.

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2888 **Comprehensive Proteogenomic Profiling Reveals the Molecular Characteristics of Colorectal Cancer at Distinct Stages of Progression**
Lingling Li, Dongxian Jiang, Hui Liu, Chunmei Guo, Qiao Zhang, Xuedong Li, Xiaojian Chen, Zheqi Chen, Jinwen Feng, Subei Tan, Wen Huang, Jie Huang, Chen Xu, Chen-Ying Liu, Wei Yu, Yingyong Hou, and Chen Ding
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Michela Menegollo, Robert B. Bentham, Tiago Henriques, Seow Q. Ng, Ziyu Ren, Clarinde Esculier, Sia Agarwal, Emily T.Y. Tong, Clement Lo, Sanjana Ilangovan, Zorka Szabadkai, Matteo Suman, Neill Patani, Avinash Ghanate, Kevin Bryson, Robert C. Stein, Mariia Yuneva, and Gyorgy Szabadkai
A method for identifying the transcriptomic signatures of metabolic switches underlying divergent routes of cellular transformation stratifies breast cancer into metabolic subtypes, predicting their biology, architecture, and clinical outcome.

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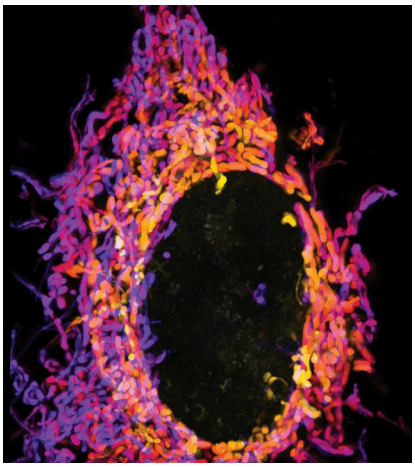

Metabolic adaptation accompanies cellular state conversions during cancer evolution. MCbiclust is a method for identifying interspersed gene sets by massive correlated biclustering that was employed to investigate whether metabolic switches associated with specific metabolic states can be recognized by locating large alternating gene expression patterns. MCbiclust uncovered gene sets with switch-like behavior that could be used to predict mitochondrial content, metabolic activity, and central carbon flux in tumors. High-resolution image analysis of mitochondria across cancer cell populations confirmed the mitochondrial abundance and function predicted by gene expression profiling using MCbiclust. For details, see article by Menegollo and colleagues on page 2911.

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