Selected Publications Citing the Sentieon Software

1. The Gossypium stocksii genome as a novel resource for cotton improvement
Corrinne E. Grover, Daojun Yuan, Mark A. Arick II, Emma R. Miller, Guanjing Hu, Daniel, G. Peterson, Jonathan F. Wendel, and Joshua A. Udall
Iowa State University, Huazhong Agricultural University, Mississippi State University, Chinese Academy of Agricultural Sciences, USDA/Agricultural Research Service
bioRxiv 2021.02.23.432605 (2021). doi:10.1101/2021.02.23.432605

2. A novel variant of CDK19 causes a severe neurodevelopmental disorder with infantile spasms
Shenghai Yang, Weishi Yu, Qian Chen and Xiaodong Wang
Children' s Hospital, Capital Institute of Pediatrics, Cipher Gene Ltd
Cold Spring Harbor Molecular Case Studies (2021). doi:10.1101/mcs.a006082

3. Systematic characterization of mutations altering protein degradation in human cancers
Collin Tokheim, Xiaoqing Wang, Richard T. Timms, Boning Zhang, Elijah L. Mena, Binbin Wang, Cynthia Chen, Jun Ge, Jun Chu, Wubing Zhang, Stephen J. Elledge, Myles Brown, X. Shirley Liu
Dana-Farber Cancer Institute, Harvard T.H. Chan School of Public Health, Howard Hughes Medical Institute, Harvard Medical School, Tongji University, The Harker School, Anhui University of Chinese Medicine
Molecular Cell (2021). doi:10.1016/j.molcel.2021.01.020

4. Biallelic loss-of-function in NRAP is a cause of recessive dilated cardiomyopathy
Juha W. Koskenvuo , Inka Saarinen, Saija Ahonen, Johanna Tommiska, Sini Weckström, Eija H. Seppälä, Sari Tuupanen, Tiia Kangas-Kontio, Jennifer Schleit, Krista Heliö, Julie Hathaway, Anders Gummesson, Pia Dahlberg, Tiina H. Ojala, Ville Vepsäläinen, Ville Kytölä, Mikko Muona, Johanna Sistonen, Pertteli Salmenperä, Massimiliano Gentile, Jussi Paananen, Samuel Myllykangas, Tero-Pekka Alastalo, Tiina Heliö
Blueprint Genetics, Helsinki University Hospital, Sahlgrenska University Hospital, Kuopio University Hospital,
PLoS One 16 (2021). doi:10.1371/journal.pone.0245681

5. Whole genome sequencing of skull-base chordoma reveals genomic alterations associated with recurrence and chordoma-specific survival
Jiwei Bai, Jianxin Shi, Chuzhong Li, Shuai Wang, Tongwu Zhang, Xing Hua, Bin Zhu, Hela Koka, Ho-Hsiang Wu, Lei Song, Difei Wang, Mingyi Wang, Weiyin Zhou, Bari J. Ballew, Bin Zhu, Belynda Hicks, Lisa Mirabello, Dilys M. Parry, Yixuan Zhai, Mingxuan Li, Jiang Du, Junmei Wang, Shuheng Zhang, Qian Liu, Peng Zhao, Songbai Gui, Alisa M. Goldstein, Yazhuo Zhang & Xiaohong R. Yang
Capital Medical University, Beijing Tiantan Hospital, China National Clinical Research Center for Neurological Diseases, National Cancer Institute, Beijing Institute for Brain Disorders, Frederick National Laboratory for Cancer Research
Nature Communications 12 (2021). doi:10.1038/s41467-021-21026-5

6. Whole-Genome Resequencing Reveals Genetic Structure and Introgression in Chinese Pudong White Pigs
Min Huang, Zhongping Wu, Xiaopeng Wang, Desen Li, Shaojuan Liu, Sumei Zheng, Lijuan Yang, Bingbing Liu, Guixin Li, Yongchuang Jiang, Hui Zhang, Hao Chen, Jun Ren
South China Agricultural University, Zhongkai University of Agriculture and Engineering, Jiangxi Science and Technology Normal University
Research Square (2021). doi:10.21203/rs.3.rs-160133/v1

7. Genome-wide SNP data of Izumo and Makurazaki populations support inner-dual structure model for origin of Yamato people
Timothy Jinam, Yosuke Kawai, Yoichiro Kamatani, Shunro Sonoda, Kanro Makisumi, Hideya Sameshima, Katsushi Tokunaga & Naruya Saitou
National Institute of Genetics of Japan, Graduate University for Advanced Studies, National Center for Global Health and Medicine of Japan, University of Tokyo, RIKEN Center for Integrative Medical Sciences, Makurazaki City Medical Association, University of the Ryukyus
Journal of Human Genetics (2021). doi:10.1038/s10038-020-00898-3

8. Comparative evolutionary genetics of deleterious load in sorghum and maize
Roberto Lozano, Elodie Gazave, Jhonathan P. R. dos Santos, Markus G. Stetter, Ravi Valluru, Nonoy Bandillo, Samuel B. Fernandes, Patrick J. Brown, Nadia Shakoor, Todd C. Mockler, Elizabeth A. Cooper, M. Taylor Perkins, Edward S. Buckler, Jeffrey Ross-Ibarra & Michael A. Gore
Cornell University, University of Cologne, University of Illinois at Urbana–Champaign, University of California Davis, Donald Danforth Plant Science Center, University of North Carolina at Charlotte
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9. MAT2A Inhibition Blocks the Growth of MTAP-Deleted Cancer Cells by Reducing PRMT5-Dependent mRNA Splicing and Inducing DNA Damage
Peter Kalev, Marc L. Hyer, Stefan Gross, Zenon Konteatis, Chi-Chao Chen, Mark Fletcher, Max Lein, Elia Aguado-Fraile, Victoria Frank, Amelia Barnett, Everton Mandley, Joshua Goldford, Yue Chen, Katie Sellers, Sebastian Hayes, Kate Lizotte, Phong Quang, Yesim Tuncay, Michelle Clasquin, Rachel Peters, Jaclyn Weier, Eric Simone, Joshua Murtie, Wei Liu, Raj Nagaraja, Lenny Dang, Zhihua Sui, Scott A. Biller, Jeremy Travins, Kevin M. Marks, Katya Marjon
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Cancer Cell 39, 209-224 (2021). doi:10.1016/j.ccell.2020.12.010

10. Network for biomarker immunoprofiling for cancer immunotherapy: Cancer Immune Monitoring and Analysis Centers and Cancer Immunologic Data Commons (CIMAC-CIDC)
Helen X. Chen, Minkyung Song, Holden T Maecker, Sacha Gnjatic, David Patton, J. Jack Lee, Stacey J. Adam, Radim Moravec, X. Shirley Liu, Ethan Cerami, James Lindsay, F. Stephen Hodi, Catherine Wu, Ignacio I. Wistuba, Gheath Al-Atrash, Chantale Bernatchez, Sean C Bendall, Stephen M. Hewitt, Elad Sharon, Howard Streicher, Rebecca A. Enos, Melissa D Bowman, Valerie M Tatard-Leitman, Beatriz Sanchez-Espiridion, Srinika Ranasinghe, Mina Pichavant, Diane M Del Valle, Joyce Yu, Sylvie Janssens, Jenny Peterson-Klaus, Cathy Rowe, Gerold Bongers, Robert R Jenq, Chia-Chi Chang, Jeffrey S. Abrams, Margaret Mooney, James H. Doroshow, Lyndsay N. Harris and Magdalena Thurin
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University of Gothenburg, Clinical Genomics, Umeå University Hospital, University of Uppsala Children's University Hospital, Sahlgrenska University Hospital, Karolinska Institutet
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13. Neoantigen Load as a Prognostic and Predictive Marker for Stage II/III Non-Small Cell Lung Cancer in Chinese Patients
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15. Whole genome sequencing of 10K patients with acute ischaemic stroke or transient ischaemic attack: design, methods and baseline patient characteristics
Si Cheng, Zhe Xu, Yang Liu, Jinxi Lin, Yong Jiang, Yilong Wang, Xia Meng, Anxin Wang, Xinying Huang, Zhimin Wang, Guohua Chen, Songdi Wu, Zhengchang Jia, Yongming Chen, Xuerong Qiu, Jun Wu, Binbin Song, Weizhong Ji, Zhongping An, Wenjun Xue, Lili Zhao, Yu Geng, Hongyan Li, Hao Li, and Yongjun Wang
Beijing Tiantan Hospital, Capital Medical University, China National Clinical Research Center for Neurological Diseases, The First people's Hospital of Taizhou, Wuhan First Hospital, The First People's Hospital of Xi'an, The Second People's Hospital of Jinzhong, WuYuan County People's Hospital, Qiqihar City Rongjian Stroke Prevention and Treatment Institute, Peking University Shenzhen Hospital, Luoyang Central Hospital, Qinghai Provincial People's Hospital, Tianjin Huanhu Hospital, Pingdingshan First People's Hospital, Changzhi People's Hospital, Zhejiang Provincial People's Hospital, Xinjiang Uygur Autonomous Region People's Hospital
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17. Expanding genetic spectrum and discriminatory role of steroid profiling by LC-MS/MS in 11β-hydroxylase deficiency
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18. Clonal Hematopoiesis Before, During, and After Human Spaceflight
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Guangzhou University of Chinese Medicine, Shantou University Medical College, Institute of Botany of Chinese Academy of Sciences, University of Chinese Academy of Sciences, Sun Yat-Sen University, National Orchid Conservation Center of China, and Fujian Agriculture and Forestry University
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Dimitra Aggeli, Yuping Li, Gavin Sherlock
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Sujaya Srinivasan, Natallia Kalinava, Rafael Aldana, Zhipan Li, Sjoerd van Hagen, Sander Y.A. Rodenburg, Megan Wind-Rotolo, Ariella S. Sasson, Hao Tang, Xiaozhong Qian, Stefan Kirov
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