

Recent Publications Featuring Rubicon Genomics Products

ThruPLEX®

Cell-free DNA

Copy number variations in urine cell free DNA as biomarkers in advanced prostate cancer.

Xia Y, Huang CC, Dittmar, R, Du M, Wang Y, Liu, H, Shenoy N, Wang L and Kohli M. *Oncotarget*, 2016 Apr 26. doi: 10.18632/oncotarget.9027.

Evaluation of exome sequencing to estimate tumor burden in plasma.

Klevebring D, Neiman M, Sundling S, Eriksson L, Darai Ramqvist E, Celebioglu F, Czene K, Hall P, Egevad L, Gronberg H, Lindberg J. *PLoS One*. 2014 Aug 18;9(8): e104417.DOI:10.1371/journal.pone.0104417. eCollection 2014.

Chip-seq

Genomic Characterization of Metformin Hepatic Response

Marcelo R. Luizon, Walter L. Eckalbar, Yao Wang, Stacy L. Jones, Robin, P. Smith, Megan Laurance⁵, Lawrence Lin¹, Paul J. Gallins⁶, Amy S. Etheridge, Fred Wright, Yihui Zhou, Cliona Molony, Federico Innocenti, Sook Wah Yee, Kathleen, M. Giacomini, Nadav Ahituv. *PLOS Genetics*. Published: November 30, 2016. <http://dx.doi.org/10.1371/journal.pgen.1006449>.

TRIM24 is an oncogenic transcriptional activator in prostate cancer.

Groner AC, Cato L, de Tribolet-Hardy J, Bernasocchi T, Janouskova H, Melchers D, Houtman R, Cato AC, Tschopp P, Gu L, Corsinotti A, Zhong Q, Fankhauser C, Fritz C, Poyet C, Wagner U, Guo T, Aebersold R, Garraway LA, Wild PJ, Theurillat JP, Brown M. *Cancer Cell*. 2016 May 24. pii: S1535-6108(16)30170-2. doi: 10.1016/j.ccell.2016.04.012.

Loss of Pcgf5 affects global H2A monoubiquitination but not the function of hematopoietic stem and progenitor cells.

Sha Si, Yaeko Nakajima-Takagi, Kazumasa Aoyama, Motohiko Oshima, Atsunori Saraya, Hiroki Sugishita, Manabu Nakayama, Tomoyuki Ishikura, Haruhiko Koseki, Atsushi Iwama. *PLoS One*. 2016 May 2;11(5):e0154561. DOI: 10.1371/journal.pone.0154561. eCollection 2016

Sp7/Osterix is restricted to bone-forming vertebrates where it acts as a Dlx co-factor in osteoblast specification.

Hironori Hojo, Shinsuke Ohba, Xinjun He, Lick Pui Lai, Andrew P. McMahon. *Dev Cell*. 2016 April 26. pii: S1534-5807(16)30197-6. Doi:10.1016/j.devcel.2016.04.002

Differential regulation of mouse and human nephron progenitors by the six family of transcriptional regulators.

O'Brien L, Guo Q, Lee YJ, Tran T, Benazet JD, Whitney PH, Valouev A, McMahon AP. *Development*. 2016 Feb 15;143(4):595-608. DOI: 10.1242/dev.127175

BET inhibitor resistance emerges from leukaemia stem cells.

Fong, C. Y., Gilan, O., Lam, E. Y., Rubin, A. F., Ftouni, S., Tyler, D., Stanley, et al. BET inhibitor resistance emerges from leukaemia stem cells. *Nature*. 2015;525(7570):538-42. DOI: 10.1038/nature14888.

Batf3 maintains autoactivation of Irf8 for commitment of a CD8α(+) conventional DC clonogenic progenitor.

Grajales-Reyes GE, Iwata A, Albring J, Wu X, Tussiwand R, Kc W, Kretzer, N. M., Briseño, C. G., Durai, V., Bagadia, P., Haldar, M., Schönheit, J., Rosenbauer, F., Murphy, T.L. and Murphy, K. M. *Nat Immunol*. 2015;16(7):708-17. DOI: 10.1038/ni.3197.

A microfluidic device for epigenomic profiling using 100 cells.

Cao Z, Chen C, He B, Tan K, Lu C. *Nat Methods*. 2015. DOI: 10.1038/nmeth.3488.

SCML2 establishes the male germline epigenome through regulation of histone H2A ubiquitination.

Hasegawa, K., Sin, H.S., Maezawa, S., Broering, T.J., Katashov, A. V., Alavattam, K.G., Ichijima, Y., Zhang, F., Bacon, W. C., Greis, K. D., Andreassen, P. R., Barski, A. and Namekawa, S. H., *Dev Cell*. 2015;32(5):574-88. DOI: 10.1016/j.devcel.2015.01.014

Epigenomic profiling of young and aged HSCs reveals concerted changes during aging that reinforce self-renewal.

Sun D, Luo M, Jeong M, Rodriguez B, Xia Z, Hannah R, Wang H, Le T, Faull KF, Chen R, Gu H, Bock C, Meissner A, Göttgens B, Darlington GJ, Li W, Goodell MA. *Cell Stem Cell*. 2014 May 1;14(5):673-88. DOI: 10.1016/j.devcel.2015.01.014.



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Other

Characterization of the cytokinin-responsive transcriptome in rice

Tracy Raines, Ivory C. Blakley, Yu-Chang Tsai, Jennifer M. Worthen, José Manuel Franco Zorrilla, Roberto Solano, G. Eric Schaller, Ann E. Loraine and Joseph J. Kieber. BMC Plant Biology. 2016;16:260. DOI: 10.1186/s12870-016-0932-z

Metagenome-assembled genomes uncover a global brackish microbiome.

Hugerth LW, Larsson J, Alneberg J, Lindh MV, Legrand C, Pinhassi J, et al. 2015 bioRxiv (2015) DOI: <http://dx.doi.org/10.1101/018465>.

Whole genome amplification with SurePlex results in better copy number alteration detection using sequencing data compared to the MALBAC method.

Deleye, L., De Coninck, D., Christodoulou, C., Sante, T., Dheedene, A., Heindryckx, B., Van den Abbeel, E., De Sutter, P., Menten, B., Deforce, D. and Van Nieuwerburgh, F. Sci Rep. 2015;5:11711. DOI: 10.1038/srep11711.

Whole genome prediction for preimplantation genetic diagnosis.

Kumar, A., Ryan, A., Kitzman, J. O., Wemmer, N., Snyder, M. W., Sigurjonsson, S., Lee, C., Banjevic, M., Zarutskie, P. W., Lewis, A. P., Shendure, J. and Rabinowitz, M. Genome Med. 2015;7(1):35. DOI: 10.1186/s13073-015-0160-4.

Refined DNase-seq protocol and data analysis reveals intrinsic bias in transcription factor footprint identification.

Housheng Hansen, He Clifford, A Meyer, Sheng'en Shawn Hu, Mei-Wei Chen, Chongzhi Zang, Yin Liu, Prakash K Rao, Teng Fe, Han Xu, Henry Long, X Shirley Liu & Myles Brown. Nat Methods. 2014 Jan;11(1):73-8. DOI: 10.1038/nmeth.2762.

PicoPLEX™

G&T-seq: Parallel sequencing of single-cell genomes and transcriptomes

Iain C Macaulay, et al. Nature Methods 12,519–522(2015). April 2015. DOI: 10.1038/nmeth.3370

icomunity newsletter – reproductive and genetic health issue.

Learn how Illumina technologies are used for preimplantation genetic screening, preimplantation genetic diagnosis, non-invasive prenatal testing, and genetic conditions screening.

Using the CytoSure™ embryo screen array to identify aneuploidies and large structural imbalances in polar bodies 1 and 2.

K.R. Held, S. Knebel, V. Baukloh. 1. Reprogenetics Germany GmbH, 2. MVZ Fertility Center Hamburg GmbH

Validation of copy number variation sequencing for detecting chromosome imbalances in human preimplantation embryos.

Wang L, Cram DS, Shen J, Wang X, Zhang J, Song Z, Xu G, Li N, Fan J, Wang S, Luo Y, Wang J, Yu L, Liu J, Yao Y. Biol Reprod. 2014 Jun 25. pii: biolreprod.114.120576. DOI:10.1095/biolreprod.114.120576.

TransPLEX® C-WTA Kit (for Clinical Use)

A cell type-specific view on the translation of mRNAs from ROS-responsive genes upon paraquat treatment of Arabidopsis thaliana leaves.

Benina, M., Ribeiro, D. M., Gechev, T. S., Mueller-Roeber, B., & Schippers, J. H. M. (2014). DOI: 10.1111/pce.12355

Analysis of double-stranded RNA from microbial communities identifies double-stranded RNA virus-like elements.

Decker, C. J., & Parker, R. (2014). DOI: 10.1016/j.celrep.2014.03.049

A lactose-inducible system for metabolic engineering of clostridium ljungdahlii.

Banerjee, A., Leang, C., Ueki, T., Nevin, K. P., & Lovley, D. R. (2014). DOI: 10.1128/AEM.03666-13. Epub 2014 Feb 7.

Gene expression divergence between malaria vector sibling species Anopheles gambiae and An.

Cassone, B. J., Kamdem, C., Cheng, C., Tan, J. C., Hahn, M. W., Costantini, C., & Besansky, N. J. (2014). Gene expression divergence between malaria vector sibling species Anopheles gambiae and An. coluzzii from rural and urban Yaoundé Cameroon. Molecular Ecology. DOI: 10.1111/mec.12733

Maternal bisphenol a exposure impacts the fetal heart transcriptome.

Chapalamadugu, K. C., Vandervoort, C. a, Settles, M. L., Robison, B. D., & Murdoch, G. K.(2014). Maternal bisphenol a exposure impacts the fetal heart transcriptome. PloS One, 9(2), e89096. DOI: 10.1371/journal.pone.0089096



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