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With the advent of RNAi and CRISPR technologies, we can now systematically interrogate the cell-autonomous dependencies of cancer in cell lines. In parallel, the emergence of epigenomic technologies has led to the identification of regulatory elements critical for cell identity and tumorigenesis, including enhancers that are bound by transcription factors (TFs) and play a key role in sustaining the oncogenic program in many cancers. However, it remains less understood how these enhancers mechanistically drive the disease.

Our computational biology group is interested in mining all relevant public and in-house data to improve our understanding of TFs, their target enhancers, and how they drive cancer. Moreover, we are interested in exploring the proliferative as well as transcriptional response upon knock-out of these enhancer elements. To this end, a particular focus is set on leveraging an additional emerging technology, single cell RNAseq, to profile transcriptomic response upon pooled CRISPR genome editing of TFs and their enhancers.

Selected Publications

Project DRIVE: A compendium of cancer dependencies and synthetic lethal relationships uncovered by large-scale, deep RNAi screening. [2]
McDonald ER 3rd, de Weck A, Schlabach MR, Billy E, Mavrakis KJ, Hoffman GR, Belur D, Castelletti D, Frias E, Gampa K, Golji J, Kao I, Li L, Megel P, Perkins TA, Ramadan N, Ruddy DA, Silver SJ, Sovath S, Stump M, Weber O, Widmer R, Yu J, Yu K, Yue Y, Abramowski D, Ackley E, Barrett R, Berger J, Bernard JL, Billig R, Brachmann SM, Buxton F, Caothien R, Caushi JX, Chung FS, Cortés-Cros M, deBeaumont RS, Delaunay C, Desplat A, Duong W, Dwoske DA, Eldridge RS, Farsidjani A, Feng F, Feng J, Flemming D, Forrester W, Galli GG, Gao Z, Gauter F, Gibaja V, Haas K, Hattenberger M, Hood T, Hurov KE, Jagani Z, Jenal M, Johnson JA, Jones MD, Kapoor A, Korn J, Liu J, Liu Q, Liu S, Liu Y, Loo AT, Macchi KJ, Martin T, McAllister G, Meyer A, Mollé S, Pagliarini RA, Phadke T, Repko B, Schouwey T, Shanahan F, Shen Q, Stamm C, Stephan C, Stucke VM, Tiedt R, Varadarajan M, Venkatesan K, Vitari AC, Wallroth M, Weiler J, Zhang J, Mickanin C, Myer VE, Porter JA, Lai A, Bitter H, Lees E, Keen N, Kauffmann A, Stegmeier F, Hofmann F, Schmelzle T, Sellers WR.
Cell. 2017 July 27; 170(3), 577-592.e10.

Correction of copy number induced false positives in CRISPR screens [3]
de Weck A, Golji J, Jones MD, Korn JM, Billy E, McDonald 3rd ER, Schmelzle T, Bitter H, Kauffmann A.
bioRxiv. 2017 June 23; https://doi.org/10.1101/151985 [3]

Disordered methionine metabolism in MTAP/CDKN2A-deleted cancers leads to dependence on PRMT5. [4]
Mavrakis KJ, McDonald ER 3rd, Schlabach MR, Billy E, Hoffman GR, deWeck A, Ruddy DA, Venkatesan K, Yu J, McAllister G, Stump M, deBeaumont R, Ho S, Yue Y, Liu Y, Yan-Neale Y, Yang G, Lin F, Yin H, Gao H, Kipp DR, Zhao S, McNamara JT, Sprague ER, Zheng B, Lin Y, Cho YS, Gu J, Crawford K, Ciccone D, Vitari AC, Lai A, Capka V, Hurov K, Porter JA, Tallarico J, Mickanin C, Lees E, Pagliarini R, Keen N, Schmelzle T, Hofmann F, Stegmeier F, Sellers WR.
Science. 2016 Mar 11; 351(6278):1208-13.

Click here [5] for additional publications.

Links
[1] https://www.novartis.com/our-science/postdoc-program/research-themes/computational-sciences/antoine-de-weck-phd
[2] https://www.ncbi.nlm.nih.gov/pubmed/28753431
[3] https://doi.org/10.1101/151985

[4] http://www.ncbi.nlm.nih.gov/pubmed/26912361
[5] https://scholar.google.ch/citations?user=gPggEa4AAAAJ