

## Audrey Kauffmann, PhD <sup>[1]</sup>



*Oncology*

*Basel, Switzerland*

Next-generation sequencing technologies have been employed extensively to understand the genomic complexity underlying cancer. In our group, we are developing and applying state-of-the-art algorithms to identify the genetic and genomic alterations driving the pathogenesis of the disease with the goal of developing a deeper understanding of the molecular mechanisms of cancer and its response to therapies.

Recent studies of tumor cellular sub-populations have revealed that many human tumors are composed of multiple mutated clonal sub-populations that appear to evolve in parallel and gain distinct patterns of genetic co-alterations leading to intra-tumoral heterogeneity. The presence of intra-tumoral heterogeneity provides an important genetic reservoir allowing tumors to adapt to changing environments or therapeutic selection pressures. Since the mechanisms that drive or maintain disease progression are poorly understood, investigating such mechanisms will provide insights for how best to target therapeutically the resistant primary tumors or metastases. Our group is interested in developing and evaluating computational methods to systematically characterize intra-tumoral heterogeneity.

## Selected Publications

Maximizing the efficacy of MAPK-targeted treatment in PTEN LOF/ BRAF MUT melanoma through PI3K and IGF1R. [2]

Herkert B, Kauffmann A, Mollé A, Schnell C, Ferrat T, Voshol H, Juengert J, Erasmus H, Marszalek G, Kazic-Legeux M, Billy E, Ruddy DA, Stump M, Guthy DA, Ristov M, Calkins K, Maira SM, Sellers WR, Hofmann F, Hall MN, Brachmann SM.  
*Cancer Research* 2016 Jan 15;76(2) 390-402.

Systematic in vivo screening using patient-derived tumor xenograft models to predict human clinical trial drug response. [3]

Gao H, Korn JM, Ferretti S, Monahan JE, Wang Y, Singh M, Zhang C, Schnell C, Yang G, Zhang Y, Balbin A, Barbe S, Cai H, Casey F, Chatterjee S, Chiang D, Chuai S, Cogan SM, Collins SD, Damassa E, Ebel N, Embry M, Green J, Kauffmann A, Kowal C, Leary R, Lehar J, Liang Y, Loo A, Lorenzana E, McDonald ER, McLaughlin ME, Merkin J, Meyer R, Naylor TL, Patawaran M, Reddy A, Rölli C, Ruddy DA, Salangsang F, Santacrose F, Singh A, Tang Y, Tinetto W, Tobler S, Velasquez R, Venkatesan K, Von Arx F, Wang HQ, Wang Z, Wiesmann M, Wyss D, Xu F, Bitter H, Atagja P, Lees E, Hofmann F, Li E, Keen N, Cozens R, Jensen MR, Pryer N, Williams JA, Sellers WR.  
*Nature Medicine* 2015 Nov;21 (11), 1318-1325.

arrayQualityMetrics - a Bioconductor package for quality assessment of microarray data. [4]

Kauffmann A, Gentleman R, Huber W.  
*Bioinformatics* 2009 Feb 1;25(3):415-6.

Click here [5] for additional publications.

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[3] <http://www.ncbi.nlm.nih.gov/pubmed/26479923%20>

[4] <http://www.ncbi.nlm.nih.gov/pubmed/19106121>

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