Andreas Scherer, J Pharmacogenomics Pharmacoproteomics 2014, 5:5
http://dx.doi.org/10.4172/2153-0645.S1.004

OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference on
Predictive, Preventive and Personalized Medicine & Molecular Diagnostics
November 03-05, 2014 Embassy Suites Las Vegas, USA

How does massively parallel sequencing contribute to biomarker development?

Andreas Scherer
Spheromics, Finland

The development of validated and qualified preclinical and clinical biomarkers as surrogate endpoints of toxicity or disease or as early diagnostic indicators of disease progression is a complex process. The development of microarrays in the 1990's had initially raised hopes for faster and possibly more reproducible generation of data which could be used for biomarker discovery, arguably with more or less success. Genomics and related -omics data from massively parallel sequencing (MPS) technologies have to be tested against even higher expectations and are being put under scrutiny. Comparative analyses of microarray data and MPS data will be reviewed, implications and challenges for biomarker development will be discussed.

Biography

Andreas Scherer received his PhD from the University of Freiburg, Germany, in 1997. After Postdoctoral studies at UT Southwestern, Dallas, TX, he joined Novartis Pharma AG, CH, in 2000. He worked in the Biomarker Development group from 2004 until 2007, when he founded his consultancy company Spheromics. From 2011 until 2013 he was Bioinformatics Manager at the Australian Genome Research Facility. Currently he works as data analyst and medical writer, serving customers worldwide. He is Editorial Board Member of two journals, has published a book on microarray data analysis, contributed to book chapters, and has published in peer-reviewed journals.

Andreas.Scherer@Spheromics.com