Session 2: Biology of breast cancer I: Bridging the gap between high throughput technologies and breast cancer treatment in real life

Chairs: C. Kent Osborne (USA), Beat Thürlimann (Switzerland)

- Interpreting genomics data at a functional level: What are we learning from large molecular screening projects? (Peter Campbell, United Kingdom)
- Deep genomic analysis and treatment decisions based on genomic-driven and pathway-matched therapies (Fabrice André, France)
- Discrepancies between genetic tools and immunohistochemistry: Bad pathology and good signature, and vice-versa (Jorge S. Reis-Filho, USA)
- A bad tumor biomarker is as bad as a bad drug: The gap between genomics data and phenotype to predict response (Giuseppe Viale, Italy)
- Discussion

Webcasts

http://bcc14.oncoletter.ch