

## Predictive and prognostic value of integrated exon-level expression to approach drug-response and resistance to EGFR-targeted treatment in non-small cell lung cancer

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Activating mutations in lung cancer are targeted by a series of molecularly targeted therapies. Patients harboring such mutations can receive significant benefit from these therapies. However a proportion of patients without activating mutations can benefit from these therapies, making it urgent to identify novel biomarkers. In a recent publication, we demonstrated the relevance of new exon-level expression biomarkers which predict patient's outcome independently from patient's mutational status. Our aim is to investigate the genome-wide exon-level expression of a panel of early and late lung cancer patients. In a selected population of late stage non-squamous non-small cell lung cancer, pathways associated the mechanisms of action of the tyrosine kinase inhibitor erlotinib and its associated drug resistance will be investigated and genome-wide exon-level expression intensities will be tested for prediction of response to treatment. In early stage NSCLC patients who have received surgical resection only, we are planning to explore the potential prognostic role of exon-arrays, with a special focus on metastasization / recurrence. For this purpose, the latest whole genome exon array platform from Affymetrix® will be used. Our population of patients will be recruited from the St. Gallen Lung Biopsy Biobank.

<b>type of project</b>	fundamental research
<b>status</b>	ongoing - follow up
<b>start of project</b>	2015
<b>end of project</b>	2016
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