Improved gene annotations for microarray based identifications of reporter metabolites in recurrent breast cancer.

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Breast cancer relapse remains the primary cause of breast cancer related death, highlighting the need for a better understanding of residual cells,
which resist initial therapy and are largely elusive in clinical studies.

Here we present an integrated analysis of gene expression measurements from different experimental conditions and different microarray types and versions to investigate reporter metabolite changes of such residual cells, as well as to compare their gene expression profiles.
To improve accuracy of the gene expression data and to allow for cross platform comparisons between the data it is crucial to incorporate the most recent genome annotations in the analysis.
Although various gene annotation models for microarray data exist, they are restricted to developer provided reference genome and transcriptome annotation, build the model with a fixed aligner and only work for arrays with a specific annotation format. Therefore we implemented a pipeline using tools from next generations sequencing to quickly build project specific gene annotation models, and provided a user-friendly interface for updating input parameters.

We present as well a detailed comparison of the gene expression data analysis for different annotation models, and the corresponding reporter metabolite identification.

1. Kiran R. Patil, Jens Nielsen (2005) Uncovering transcriptional regulation of metabolism by using metabolic network topology, *PNAS vol.102 no. 8*