

New method provides better information on gene expression

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Scientists at Karolinska Institutet and the Royal Institute of Technology (KTH) have devised a new high-resolution method for studying which genes are active in a tissue. The method can be used on all types of tissue and is valuable to both preclinical research and cancer diagnostics. The results are published in the journal *Science*.

Disease changes the expression of RNA molecules and proteins in tissues. Microscopic studies of [tissue](#) samples are routinely carried out in laboratories and hospitals in the interests of furthering knowledge and diagnostics, but to date only the location of a small number of RNA molecules has been possible to establish simultaneously.

A collaboration between professors Jonas Frisé (KI) and Joakim Lundeberg (KTH) at SciLifeLab has resulted in a novel method that allows analysis of the quantity of all RNA molecules and provides spatial information from the microscope.

"By placing tissue sections on a glass slide on which we have placed DNA strands with built in address labels we have been able to label the RNA molecules formed by active genes," says Professor Frisé. "When we analyse the presence of RNA molecules in the sample, the address labels show where in the section the [molecules](#) were and we can get high-resolution information on where different genes are active."

The results are also valuable for more precise diagnostics. Current practice is to take a tissue sample, grind it down and analyse the mix of

cells, but the risk is that a few cancer cells become so diluted by the signals from all the other cells in the sample and are therefore overlooked.

"With our method, we can pick up the tumour signal as it is not diluted," he continues. "Because different parts of the tissue sample have their specific address labels we can identify a small number of tumour cells."

The [method](#) can be used on all types of tissue and diseases. It can also provide information about disease heterogeneity in cancer diagnostics, as is demonstrated in the study for breast cancer.

"It makes it possible to study which [genes](#) are active in tissues with greater resolution and precision than ever before, which is valuable to both basic research and diagnostics," says Professor Frisé.

More information: P. L. Stahl et al. Visualization and analysis of gene expression in tissue sections by spatial transcriptomics, *Science* (2016). [DOI: 10.1126/science.aaf2403](https://doi.org/10.1126/science.aaf2403)

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