

**S001** Analysing gene expression levels in single cells  
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Most of the current methods for measuring gene expression levels produce average values from bulk populations of cells. Such analyses mask the behaviour of individual cells in a heterogeneous population. Methods currently available for the analysis of the RNA content of single cells have a number of drawbacks. Single cell quantitative real time polymerase chain reaction (qRT-PCR) is time consuming, expensive and has the potential to introduce amplification-based bias. Gene expression analysis (mRNA) by fluorescence *in situ* hybridisation (FISH) is also expensive, time-consuming and is not yet quantitative.

We have developed a simple, array-based method for the analysis of gene expression in many single cells. The method allows the analysis of up to 50,000 cells in parallel. In combination with a new scanning instrument, with single molecule resolution, and with software for image analysis, this platform has the potential to provide an absolute count of the number of molecules of specific mRNAs in each cell. The presentation will describe the technical basis of the method and discuss its applications.