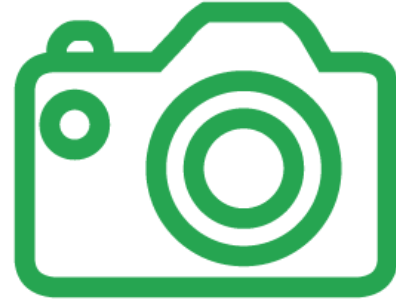
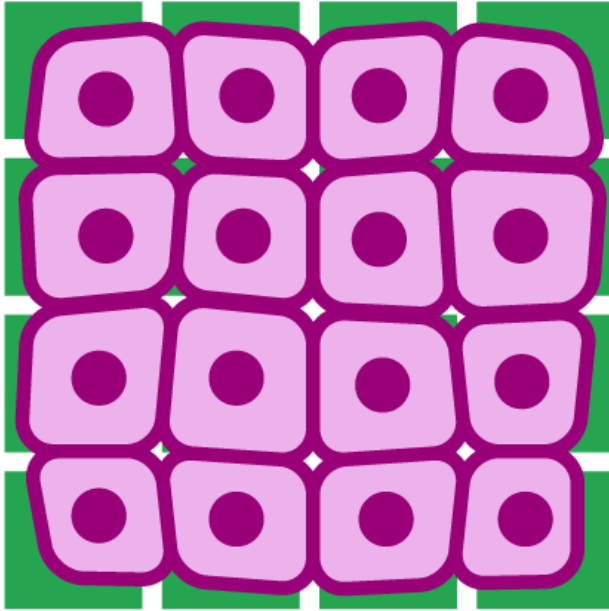


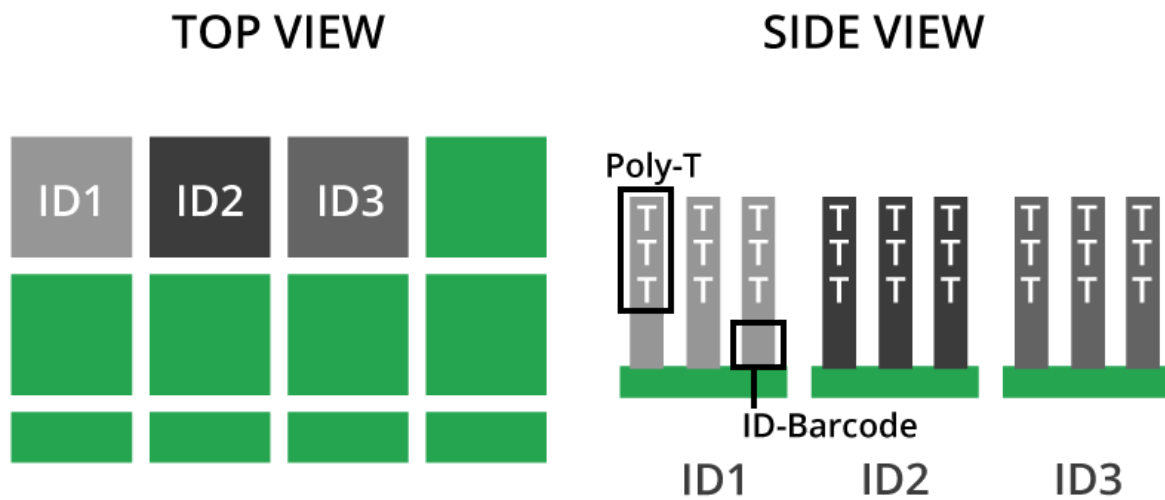


WORKFLOW



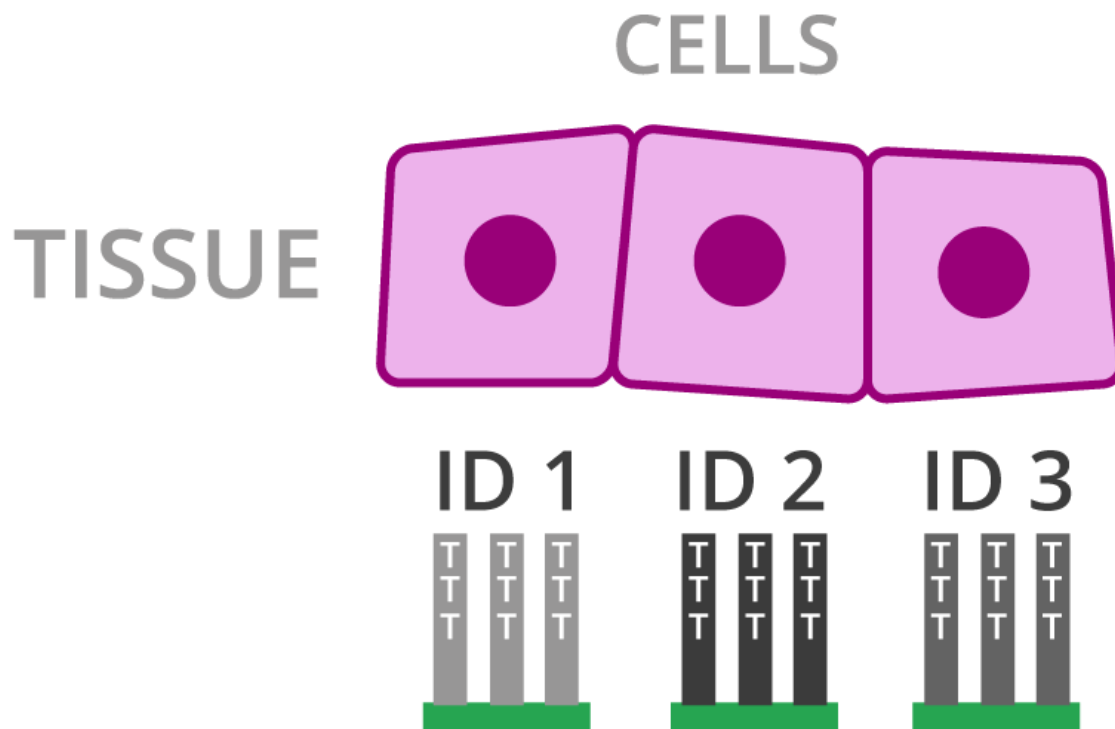
1. Histology

A freshly frozen tissue section is prepared and attached onto our chip. The RNA molecules in each cell contain information about what genes are expressed. The tissue section is imaged in order to retrieve histological information. This allows to see where a cell or a group of cells is located in context of the tissue.



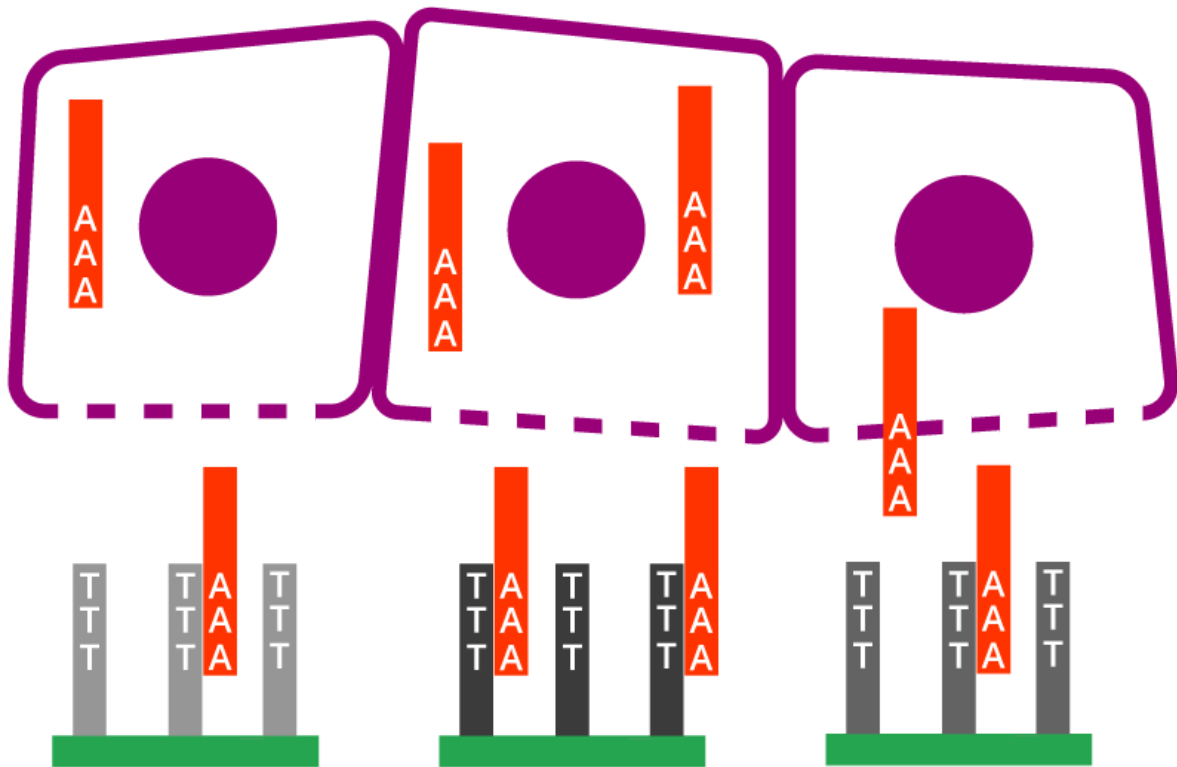
2. The Array

Our chips contain an array of distinguishable capture probes. The Poly-T tails of these capture probes can bind the Poly-A tails of RNA molecules. The arrays are ordered like a chess board where probes with the same ID-Barcode are located in the same square. This allows the determination of where each capture probe, and its bound RNA, originated.



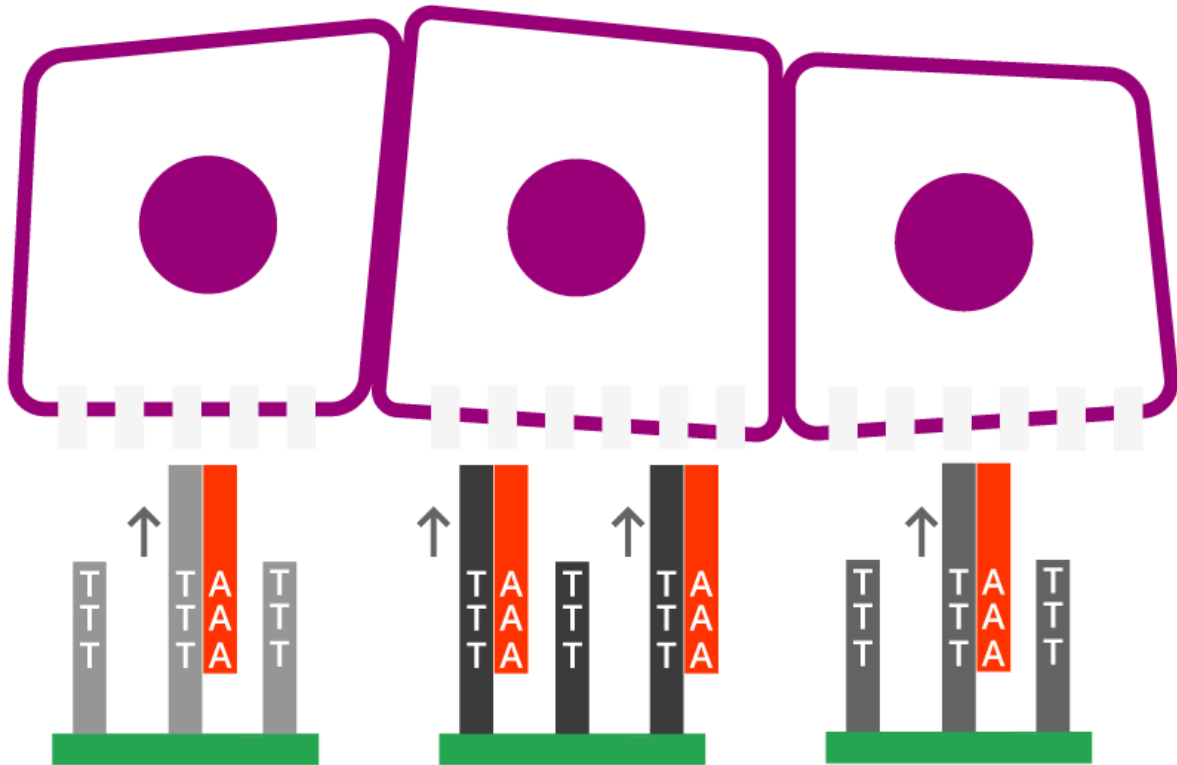
3. Tissue Fixation

The tissue section is fixed. The chip contains a visually detectable frame that is imaged together with the tissue section. This makes it possible to overlay the cell tissue image and the gene expression data in a later step.



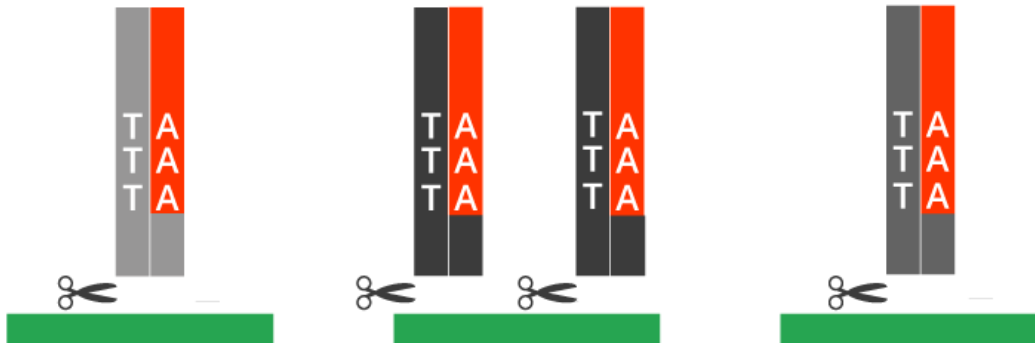
4. Permeabilisation

The tissue is permeabilised with our Permeabilising Reagent which means that small holes in the cell membrane are created. RNA molecules can exit the cells through these and bind to the adjacent capture probes on the chip. Thus the gene expression information is captured on the chip. The following steps are needed to translate the information stored in the captured RNA molecules as data.



5. cDNA Synthesis

cDNA synthesis is performed to create stable double stranded DNA molecules. This is necessary because cDNA-RNA-hybrids are degraded quickly. Furthermore it is a necessary step before preparation of sequence-able libraries.



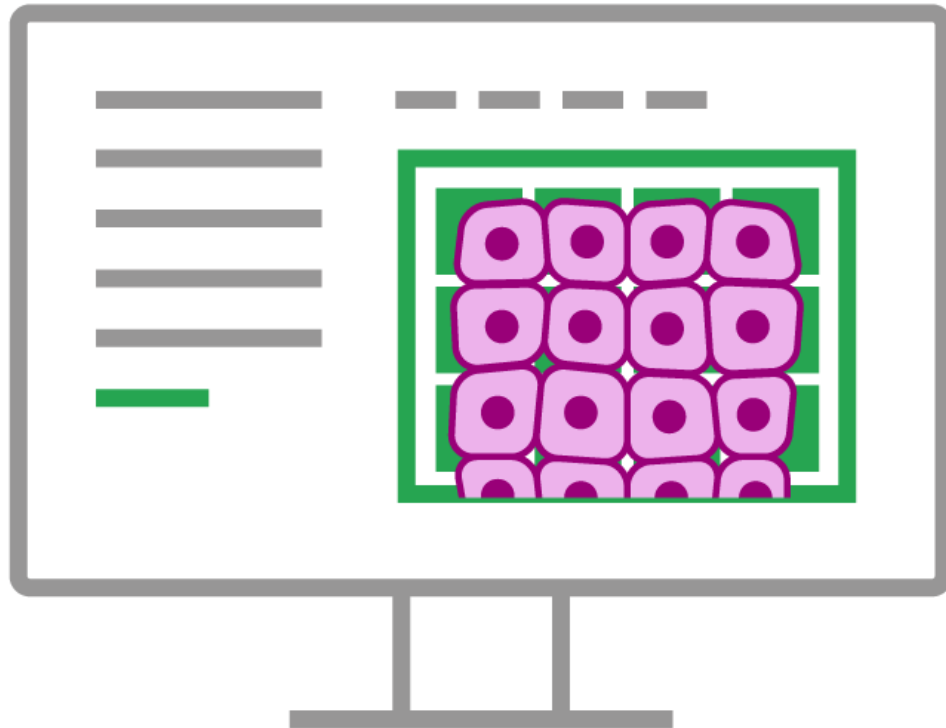
6. Library Preparation

The cDNA-RNA-hybrids are cleaved off the chip. Afterwards library preparation is performed with these. This means the molecules are modified in a way to make it possible to read out the information they code for by using a sequencing instrument.



7. Massively Parallel Sequencing

The created libraries are sequenced. Thereby information on what gene the captured RNA was coding for and where in the tissue the RNA came from is extracted. This data is stored and analyzed in the cloud.



8. Data Visualisation

In the last step all the pieces of information collected earlier are pooled and can be accessed online. This means in practice that you can look at an image of your tissue section and select different areas in the tissue. You can then determine what genes are expressed in these areas and in what quantity. Thereby you can perform extensive novel analyses in only one single experiment.

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