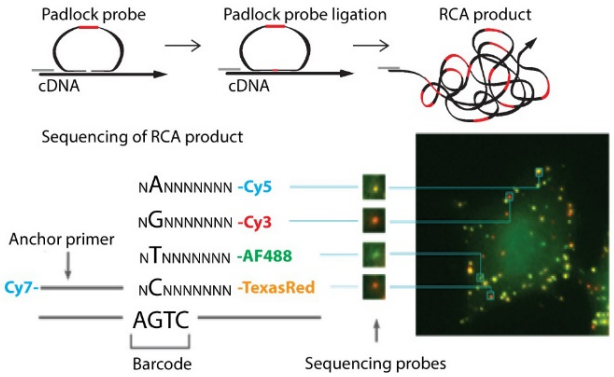
IN SITU SEQ

"*in situ* sequencing"provides **spatially resolved gene expression data** for panels of genes at **subcellular resolution**. The technique has been developed in the lab of Mats Nilsson who has pioneered the field of generating *in situ* gene expression and mutation profiles (Ke, R., et al. 2013 *Nature Methods*, 2013, doi: 10.1038/nmeth.2563.).



***In situ* sequencing using padlock probes**

UNIQUE FEATURES OF IN SITU SEQ

- Preservation of **spatial information** in tissue context
- **Targeted** approach, using padlock probing
- Highly specific amplification tool, offering multiple levels of **molecular specificity**
- **Multiplexing**, up to **few hundred transcripts per sample**
- Sensitivity, tunable
- **High throughput** due to wide-field imaging

In situ sequencing enables localisation and quantification of **more than 100 transcripts** simultaneously with **subcellular resolution in a single tissue section in a single experiment**. (Tiklová K et al. *Nat Commun*.,2019, doi: 10.1038/s41467-019-08453-1.)

SERVICES INCLUDED

- Sample preparation (generating RCA products in the tissues)
- Detecting signals by the barcode-sequencing reaction and imaging
- Mapping coordinates of the gene expression on the tissue section

MAIN APPLICATIONS

The method has been successfully demonstrated for a variety of applications such as mapping of:

- Molecularly defined cell types
- RNA editing
- Mutational heterogeneity
- Splice-variant

across different type of sections including fresh frozen, PFA-fixed and FFPE in various tissues.

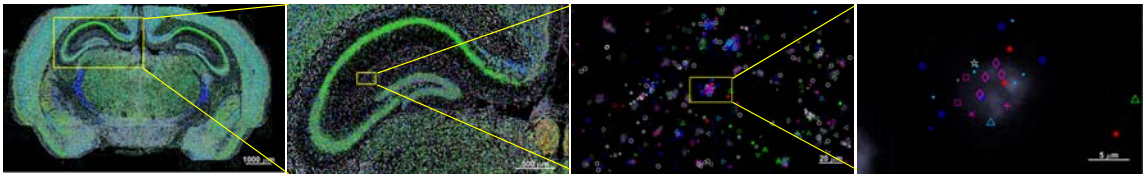


Figure 1: Distribution of 99 genes at different zoom levels in a coronal mouse brain section Qian et al. bioRxiv (2018) doi: 10.1101/431957