

# WP2: Cancer biology and biomarkers in elderly cancer patients

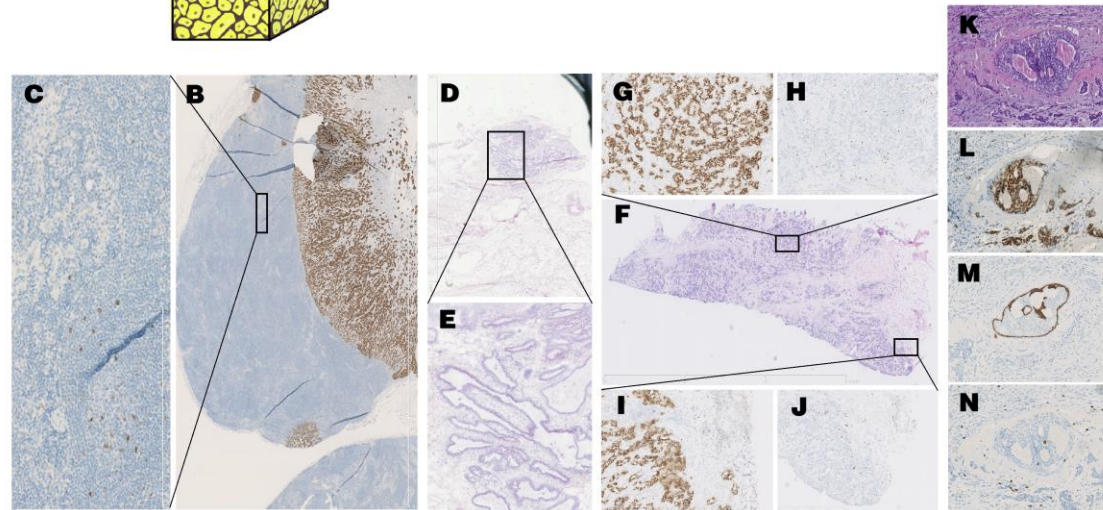
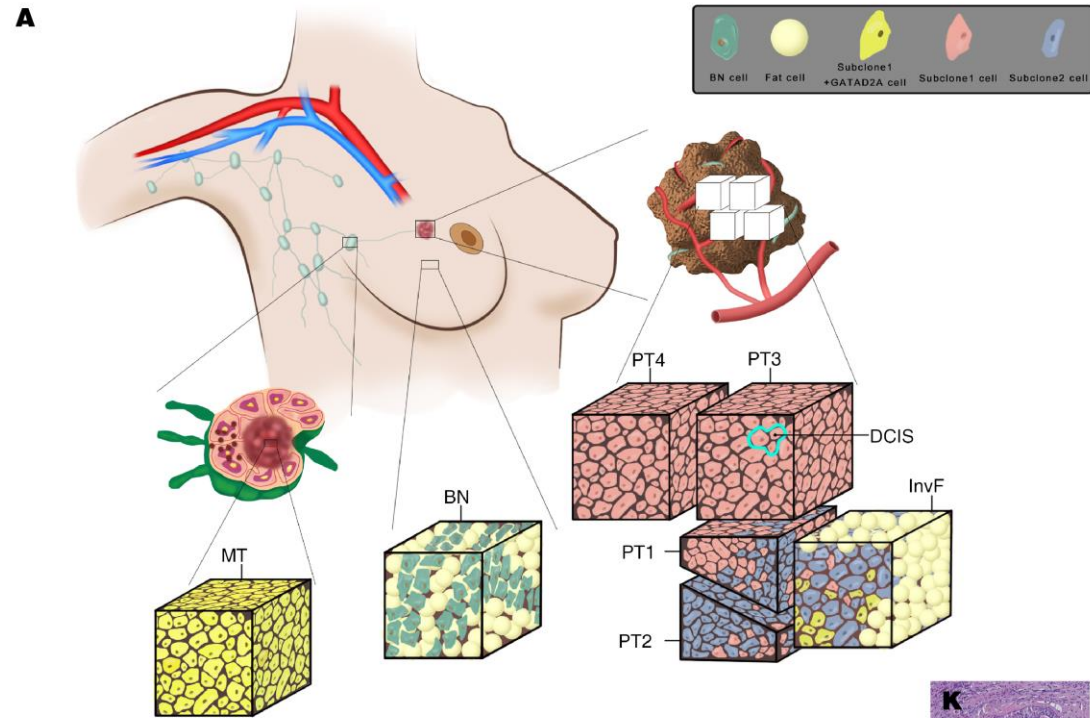
# Tumor heterogeneity and cancer evolution

- Single cancer cells sequencing studies currently use randomly-selected cells, limiting correlations between genomic aberrations, morphology and spatial localization.
- We laser-capture microdissected single cells from morphologically-distinct areas of primary breast cancer and corresponding lymph node metastasis from a 92 year-old breast cancer patient and performed whole-exome or deep-target sequencing of >100 single cells.
- Tumor microheterogeneity

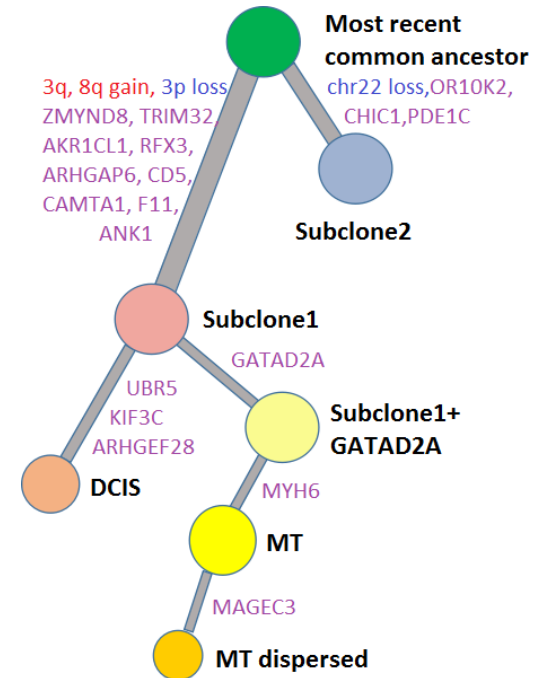
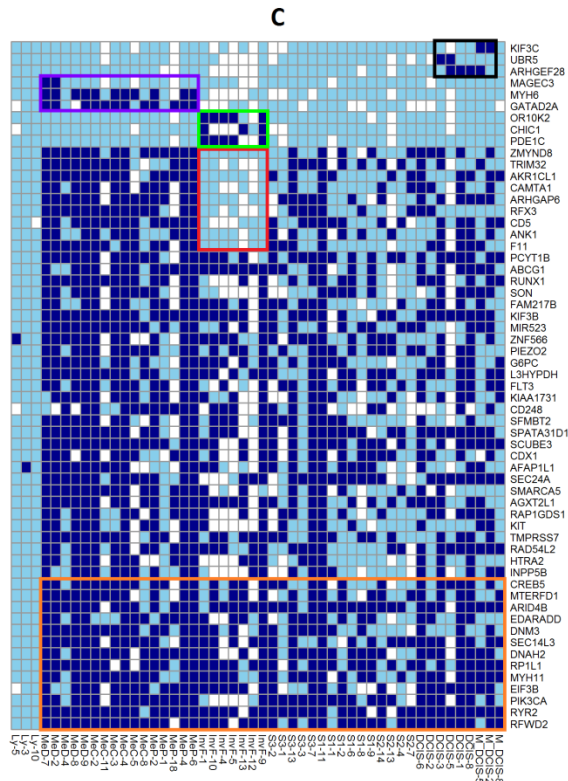
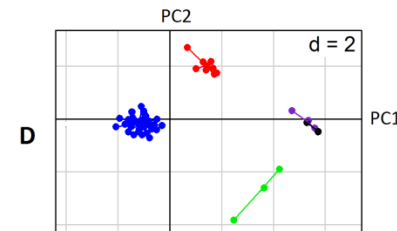
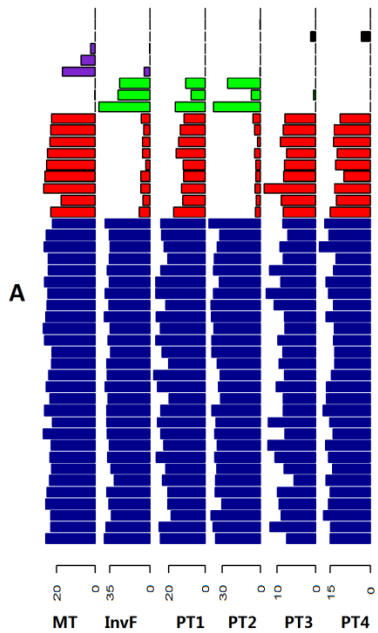


## Sampling:

- ✓ Invasive front (InvF)
- ✓ Three distinct areas within the solid invasive growth (PT1, PT2, PT3)
- ✓ Ductal carcinoma in situ (DCIS)
- ✓ Central and peripheral tumor areas of the sentinel lymph node metastasis (MeC, MeP)
- ✓ Normal lymphocytes from the same lymph node (Ly)
- ✓ Normal breast epithelia cells (BN)

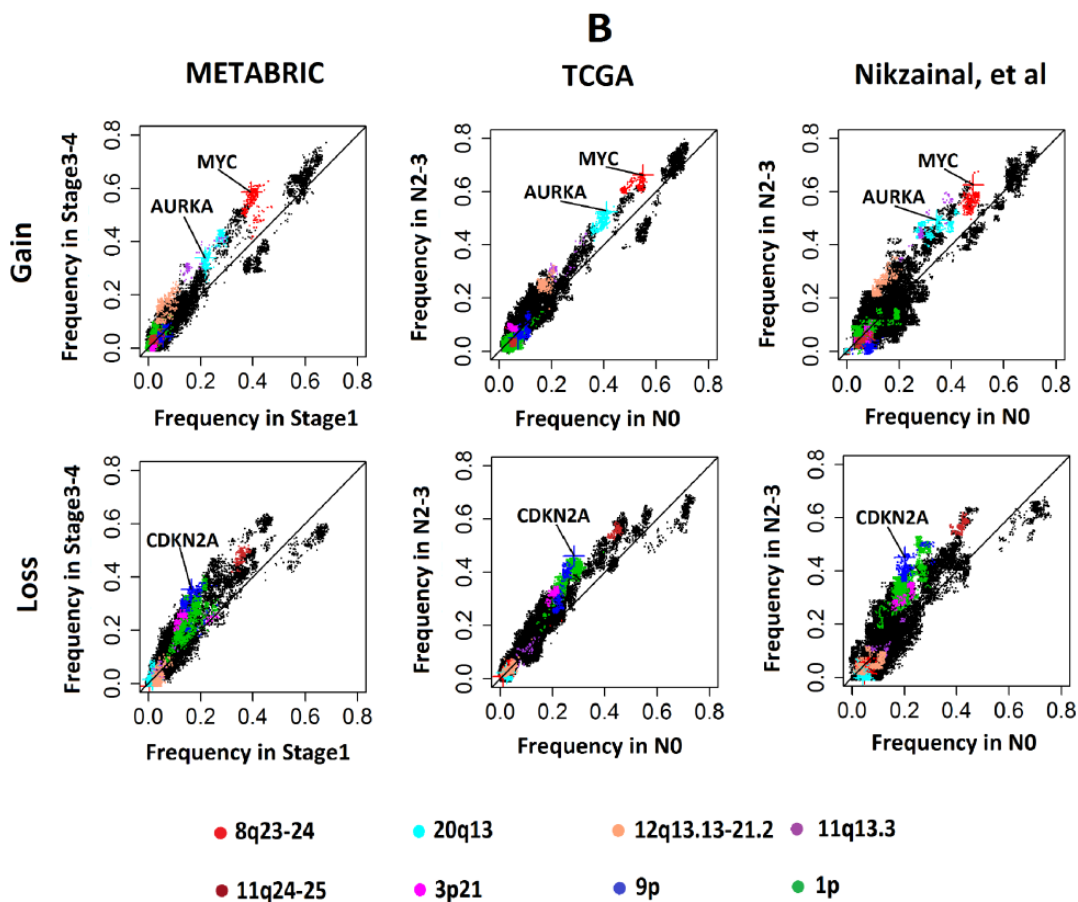


# Single nucleotide variant (SNV) analysis of breast cancer single cells and cell pools identified two dominant subclones and additional spatial location-specific subclones

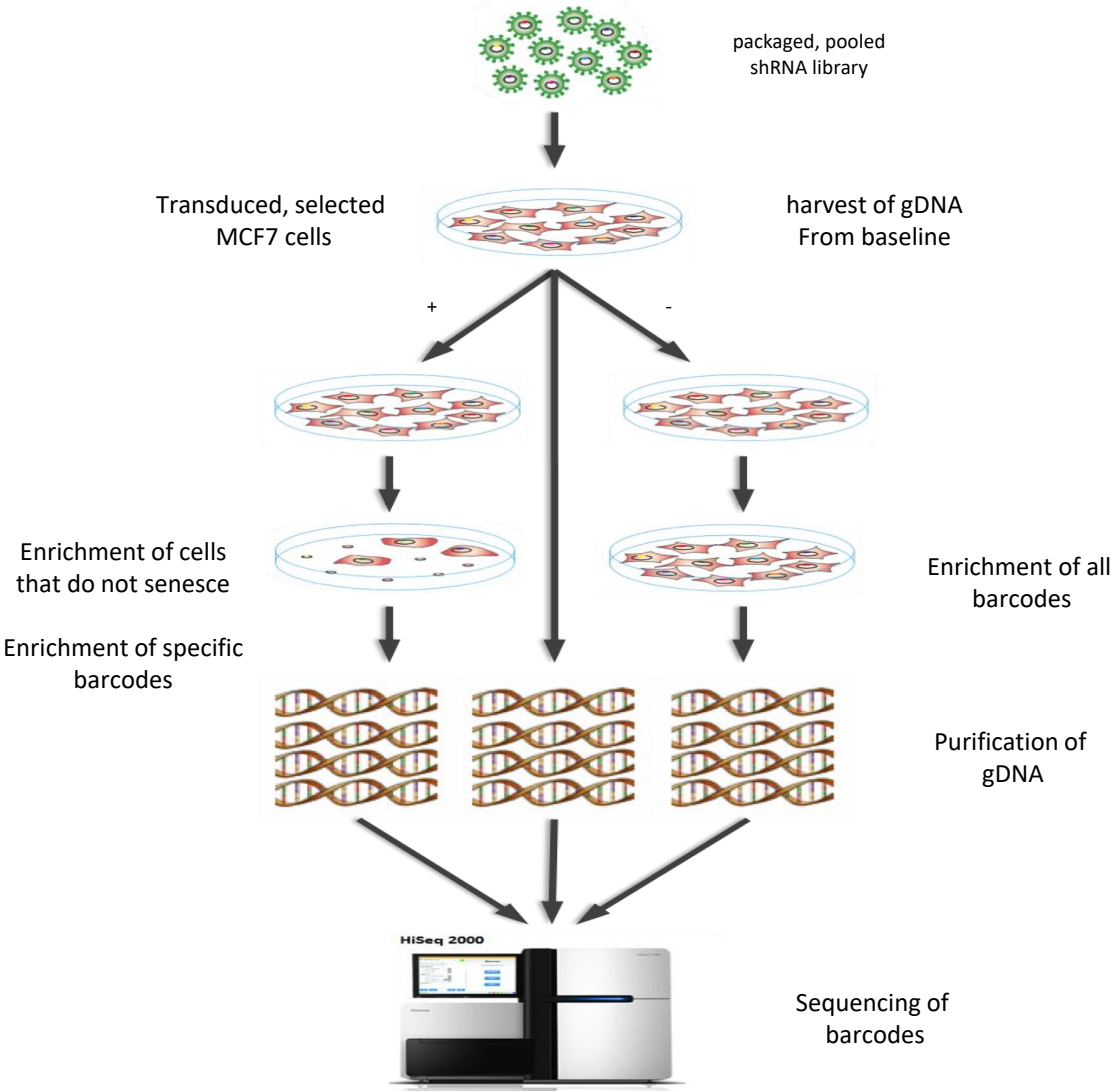


**The evolutionary tree:**  
 primary tumor  
 ↓  
 invasive front  
 ↓  
 lymph node metastasis

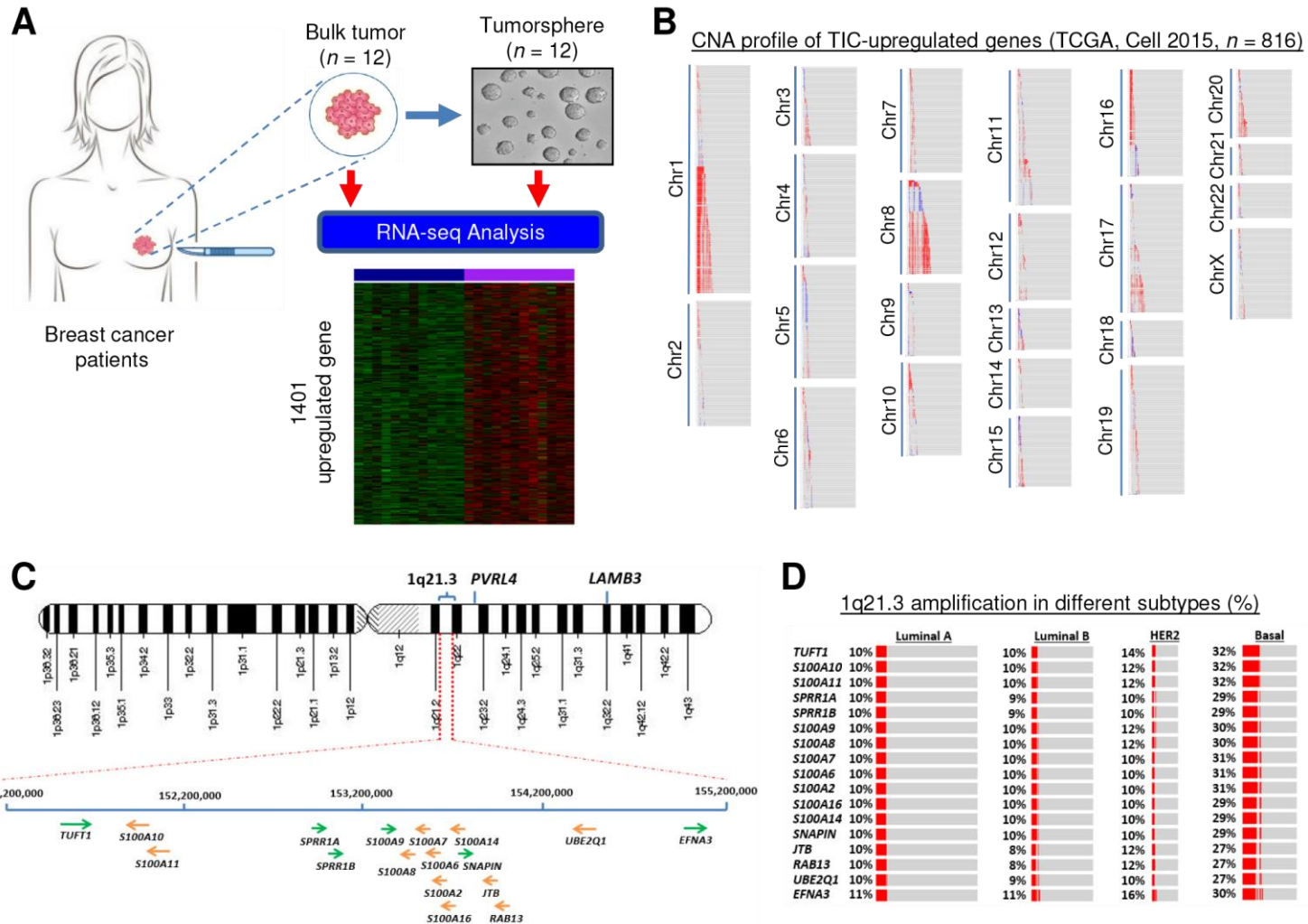
# Whole genome association analysis of frequencies of copy number gains and losses in three big dataset of breast cancers (>2000 patients) demonstrating the correlation between specific copy number alteration and spread to lymph nodes in breast cancer.



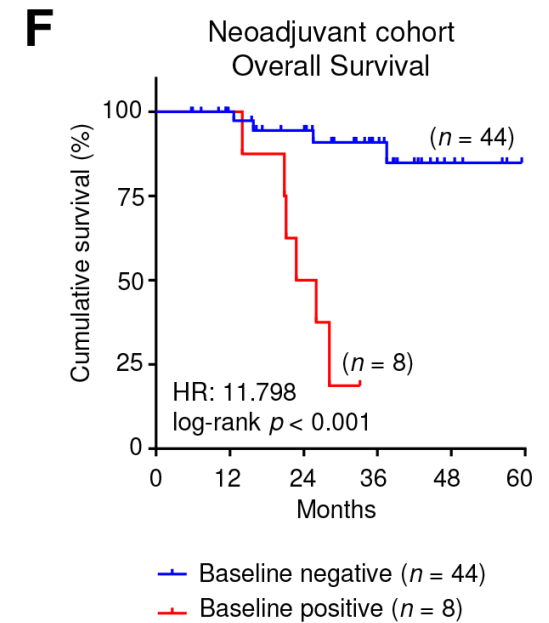
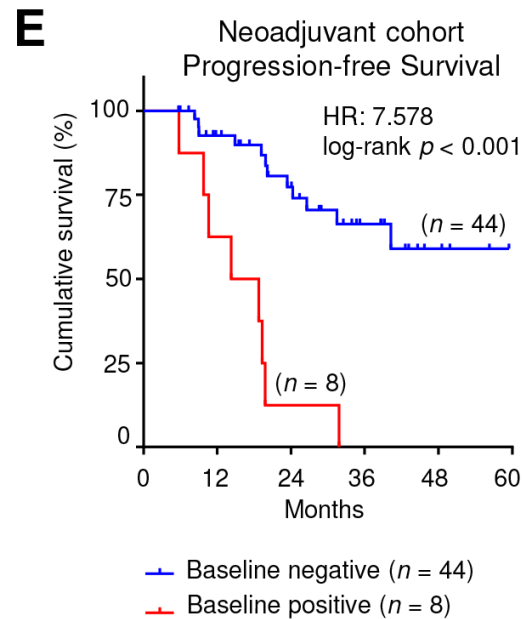
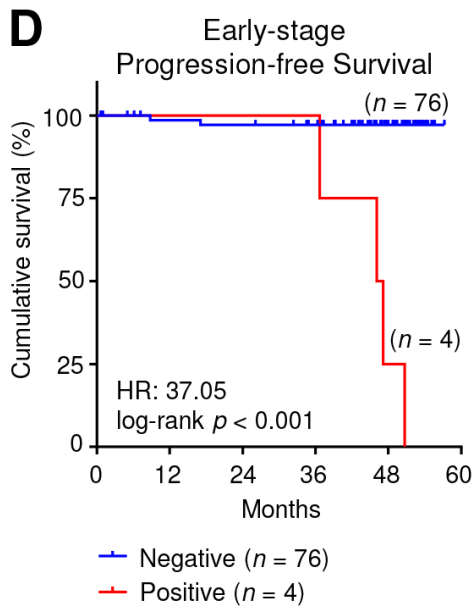
# Genome wide screen to identify genes involved in senescence



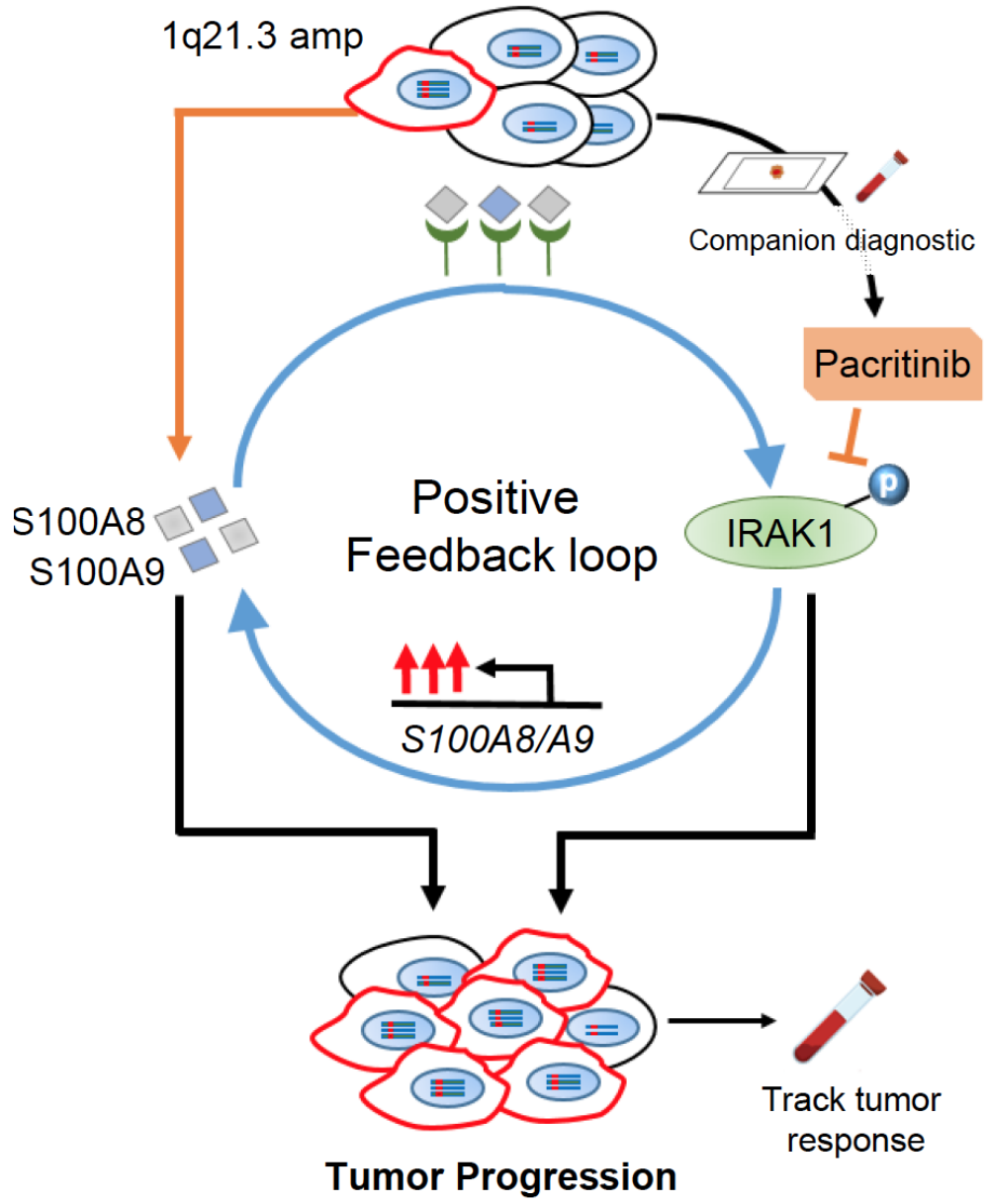
# Genomic interrogation of TICs identifies 1q21.3 amplification in breast cancer



# 1q21.3 amplification of ctDNA in two cohorts identifies patients with high risk of recurrence







# Acknowledgements

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Kræftens Bekæmpelse



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