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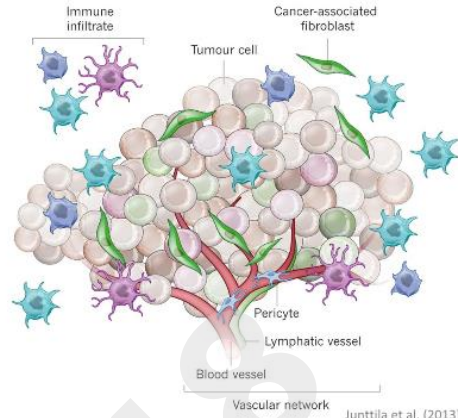
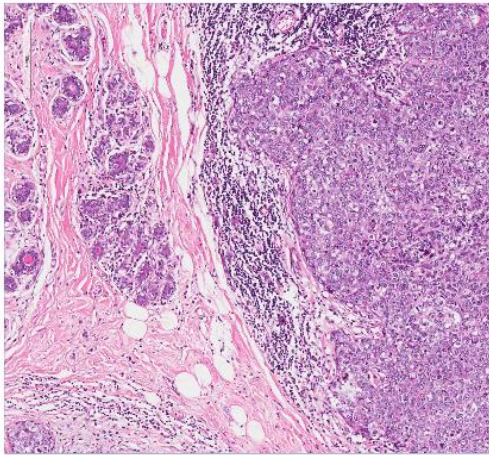
San Antonio Breast Cancer Symposium®, December 4 -8, 2018



# Landscape of the breast tumour microenvironment at single-cell resolution

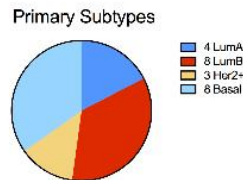
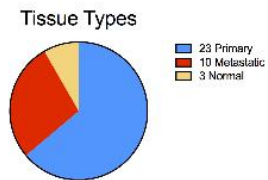
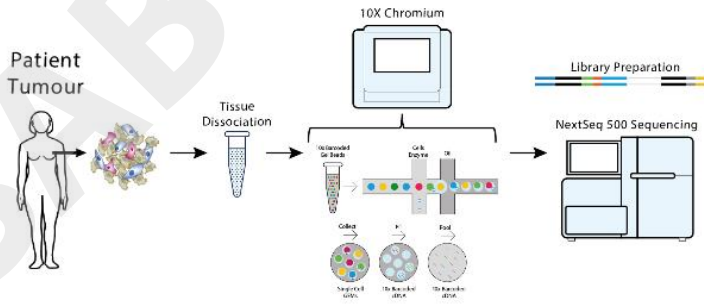
A/Prof Alexander Swarbrick PhD  
Garvan Institute of Medical Research  
Sydney Australia

# Solid cancers are complex cellular 'ecosystems'



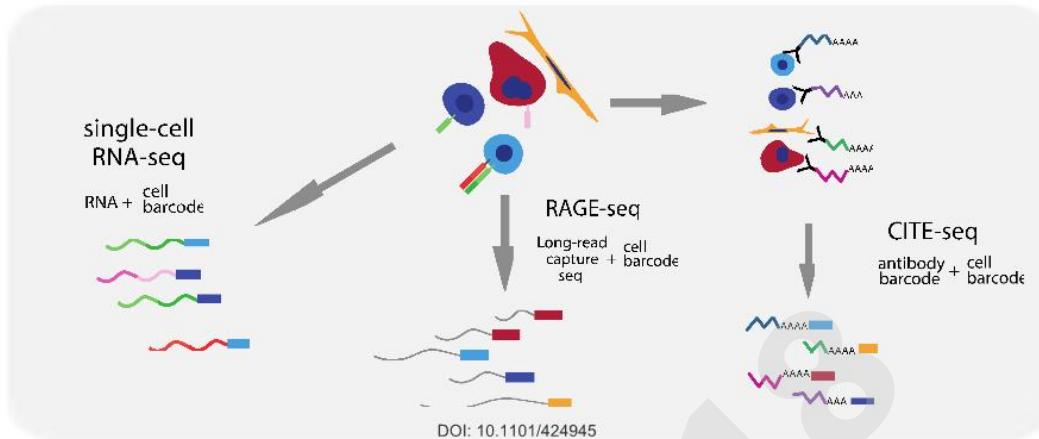
Junttila et al. (2013) *Nature*

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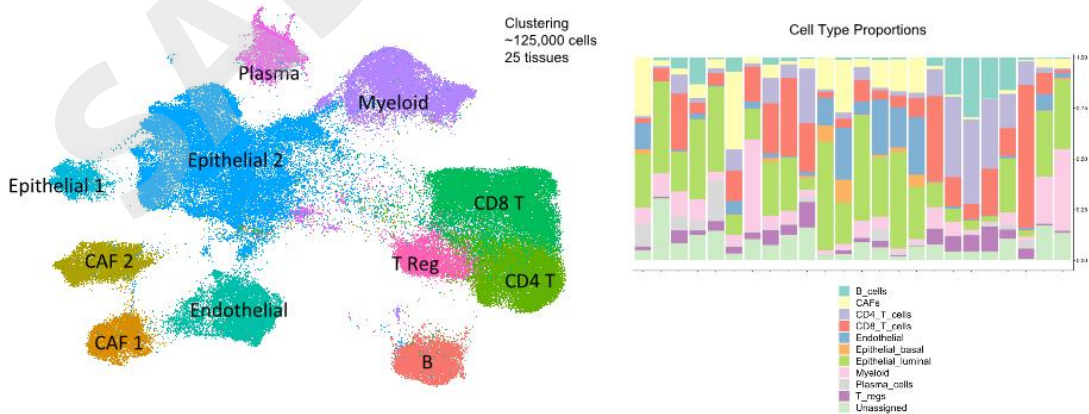
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# Multi-omic single cell analysis



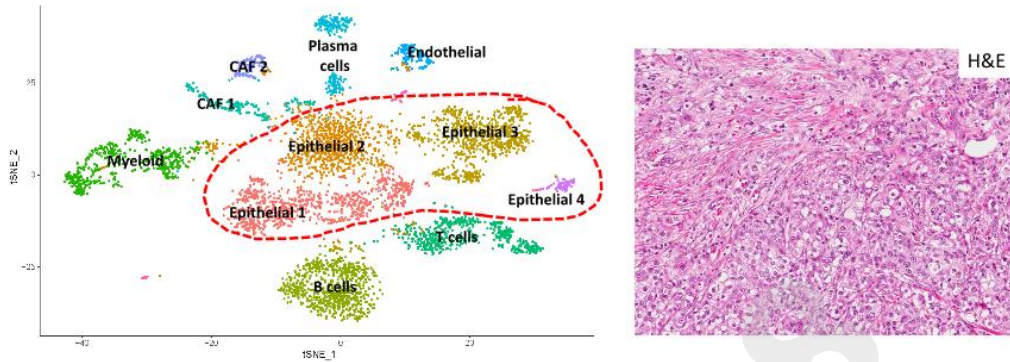
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# A breast cancer cell atlas



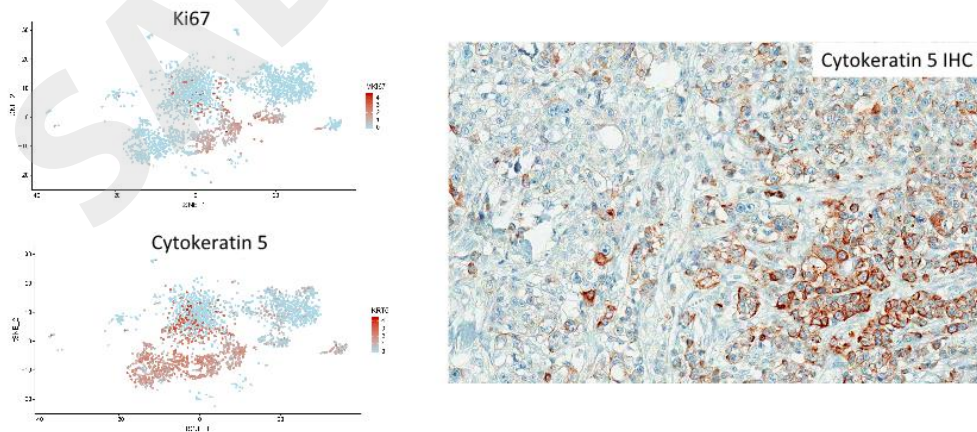
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# Case study: Grade 3 TN IDC



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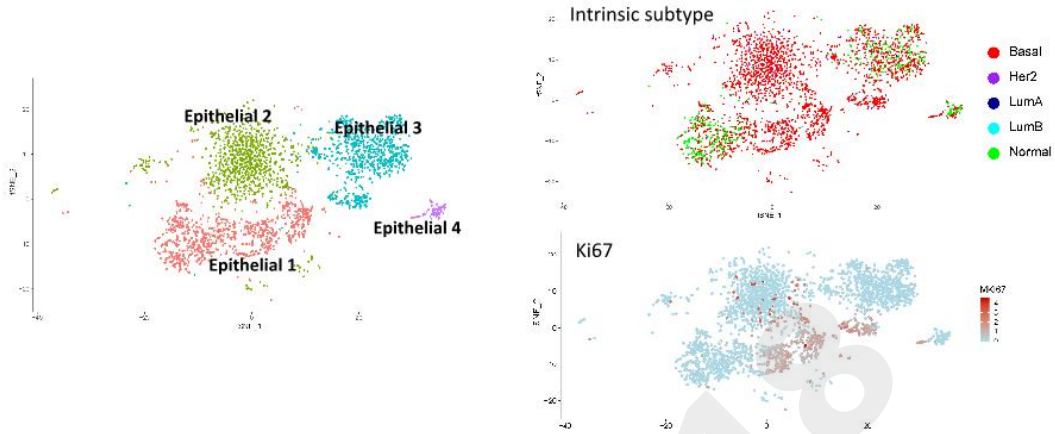
# Epithelial heterogeneity



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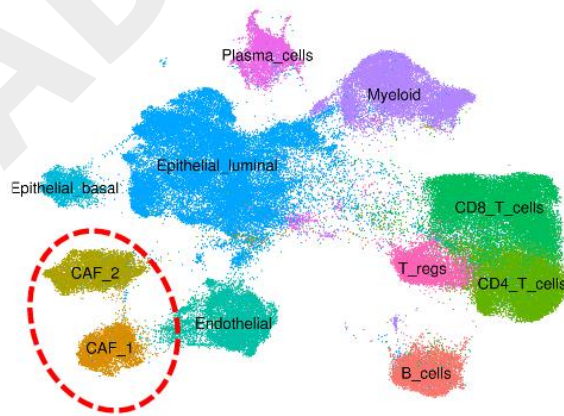


# Intrinsic subtype at cellular resolution



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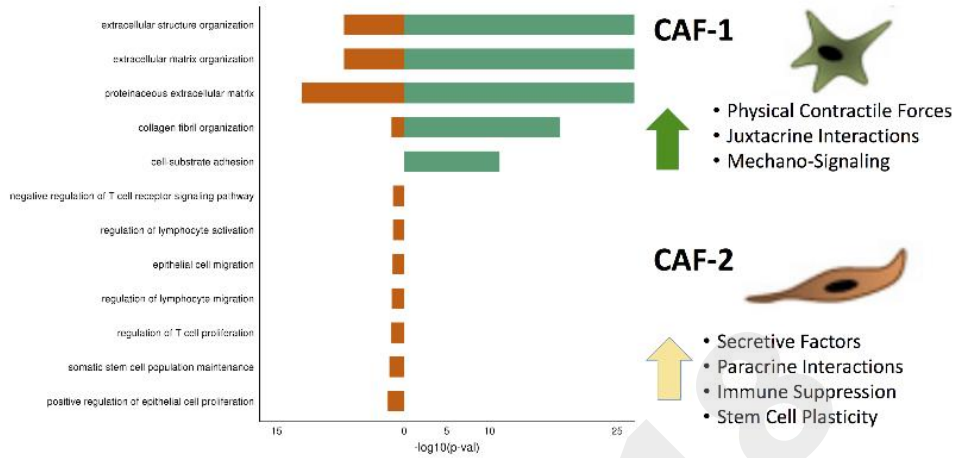
# Fibroblast heterogeneity



Therapeutic targeting of CAFs in mouse and human: Cazet *et al* Nature Communications 2018

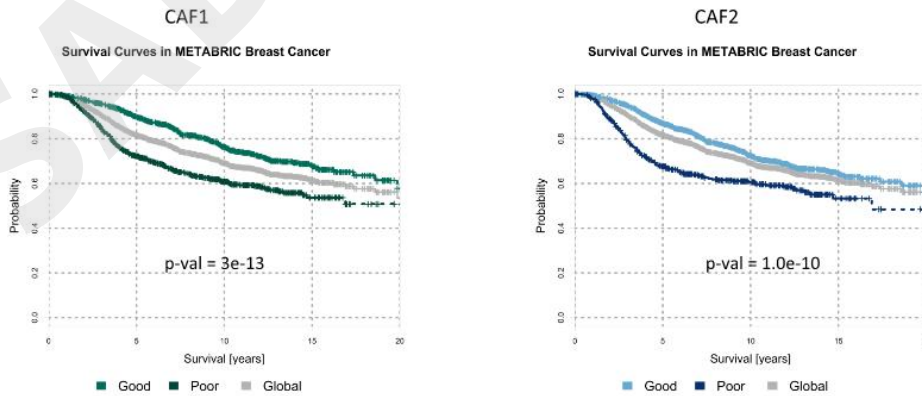
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# Unique classes of cancer-associated fibroblasts



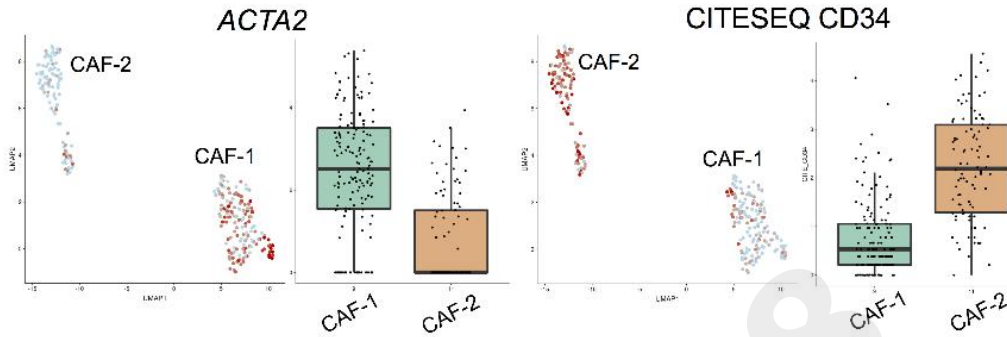
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# CAF signatures are independently prognostic



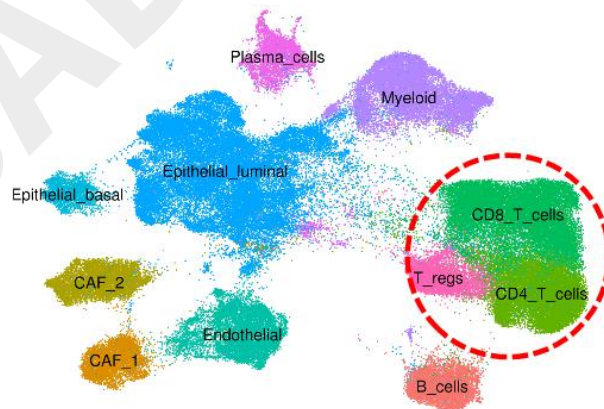
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# New markers for CAF subsets



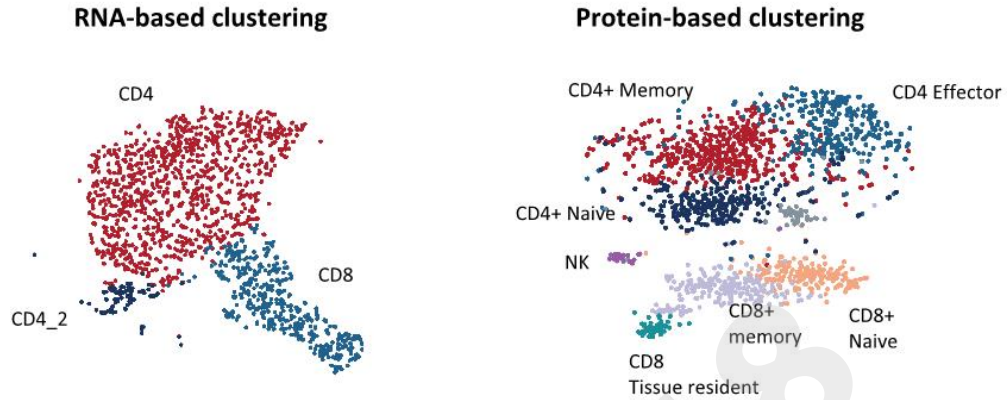
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# The breast cancer immune milieu



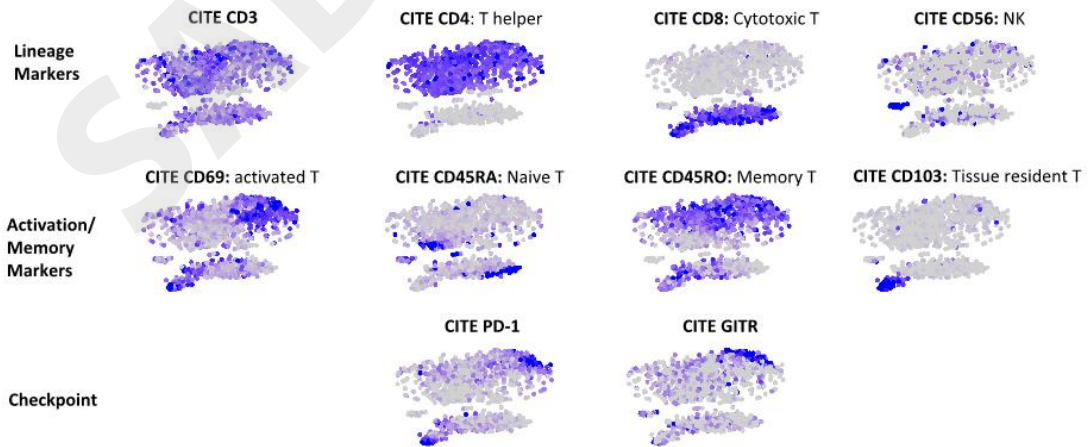
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# CITE-Seq: Improved resolution of T cell subsets



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# CITE-Seq analysis of 98 cell-surface markers



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## Summary and conclusions

- We are building a multi-omic breast cancer cell atlas to drive new discoveries in personalised medicine for breast cancer
- We reveal substantial intra-tumoural neoplastic heterogeneity, including clinically relevant features such as intrinsic subtype
- We have identified and systematically characterised CAF subsets with unique molecular features and clinical associations
- CITE-Seq reveals marked phenotypic heterogeneity of TILs and provides new opportunities for advances in breast cancer immunotherapy

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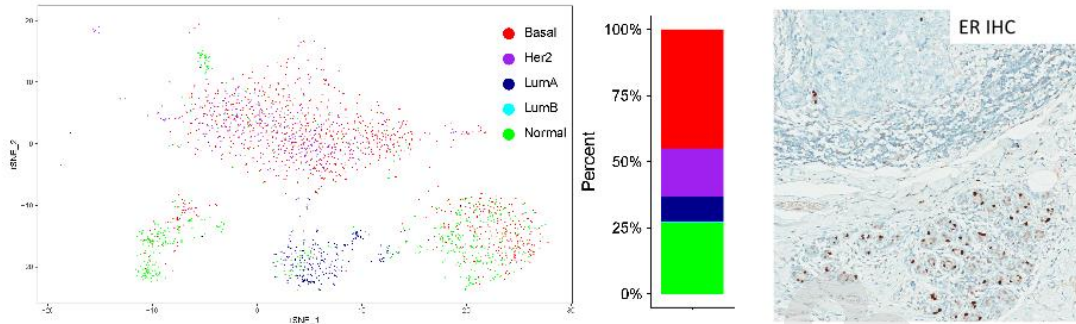
**National  
Breast Cancer  
Foundation**



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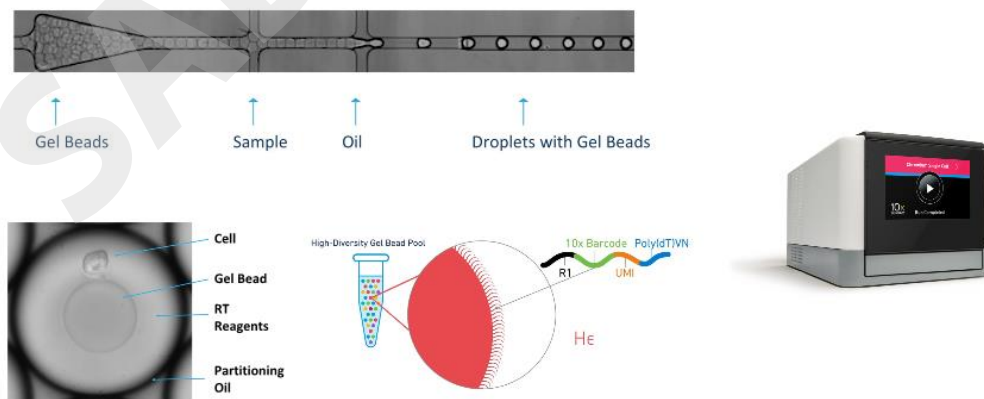


# Identification of benign epithelial cells



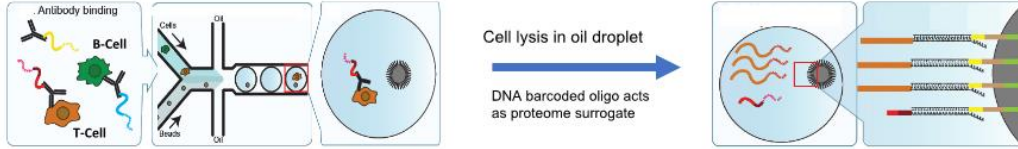
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# Single cell microfluidic technology



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# CITE-Seq: simultaneous protein and transcriptome measurement in single cells



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# High resolution provides greater insights

