



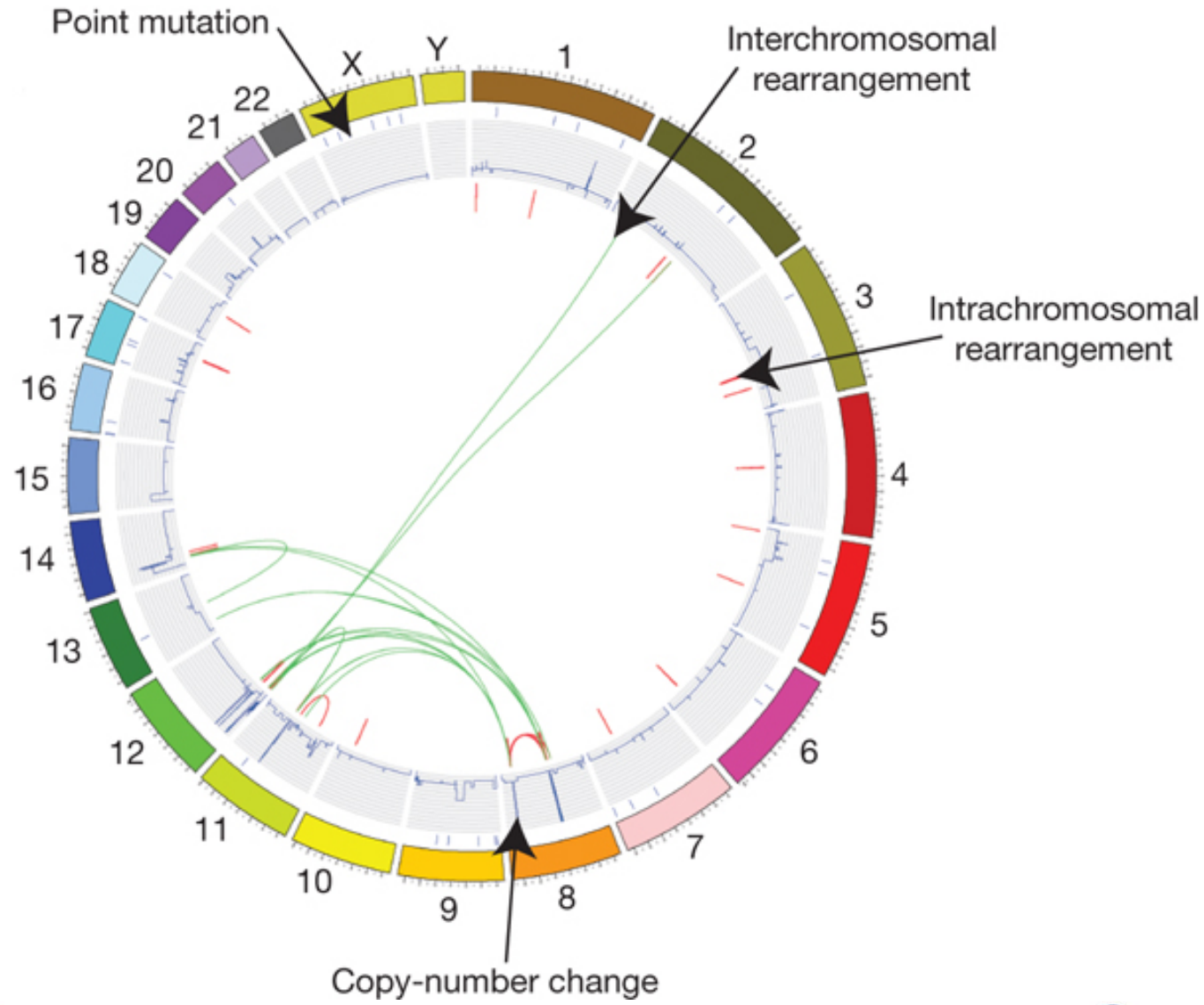
UNIVERSITY OF GOTHENBURG

# **Global analysis of somatic structural alterations and their impact on gene expression in diverse human cancers**

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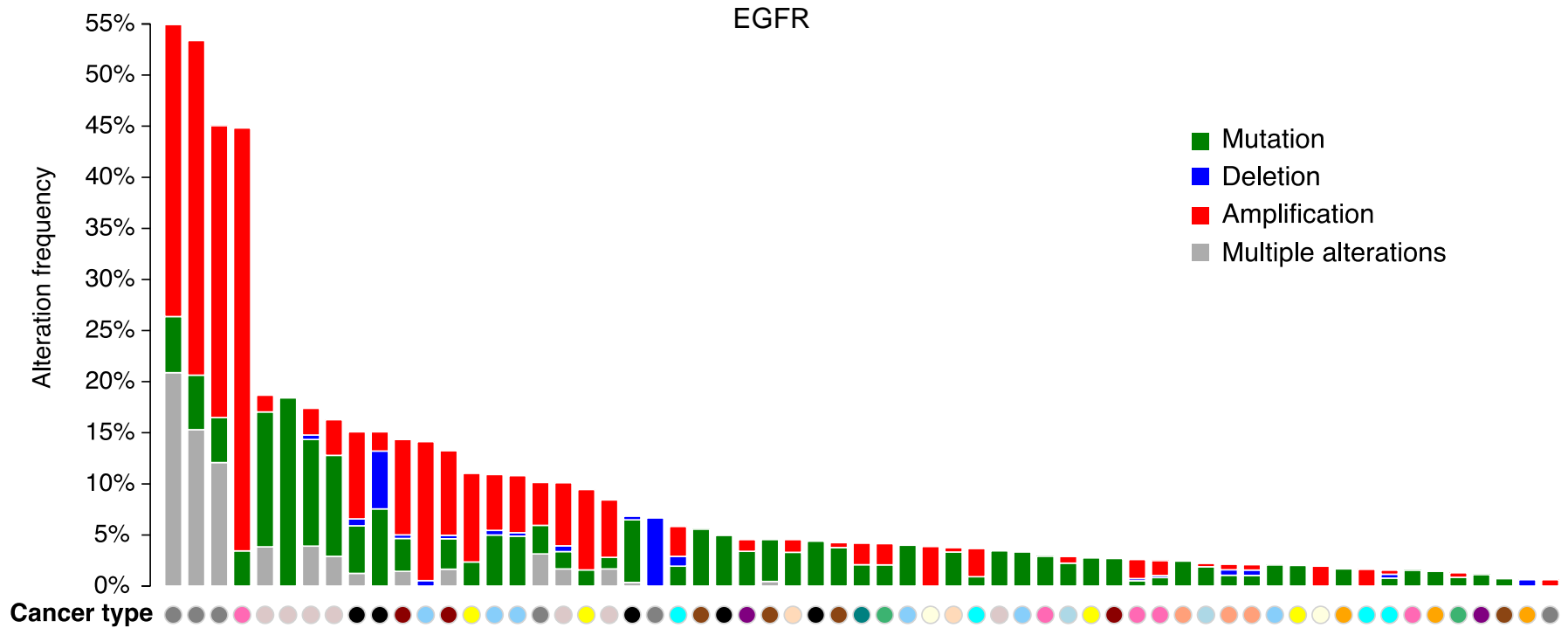
The Sahlgrenska Academy

# Somatic genomic alterations in cancer



Stratton *et al.* Nature 458

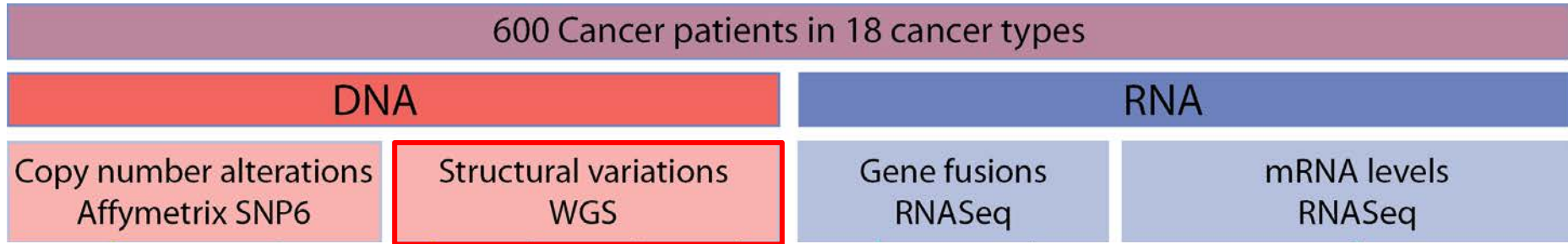
# Mutations and copy number changes are well-explored in pan-cancer studies



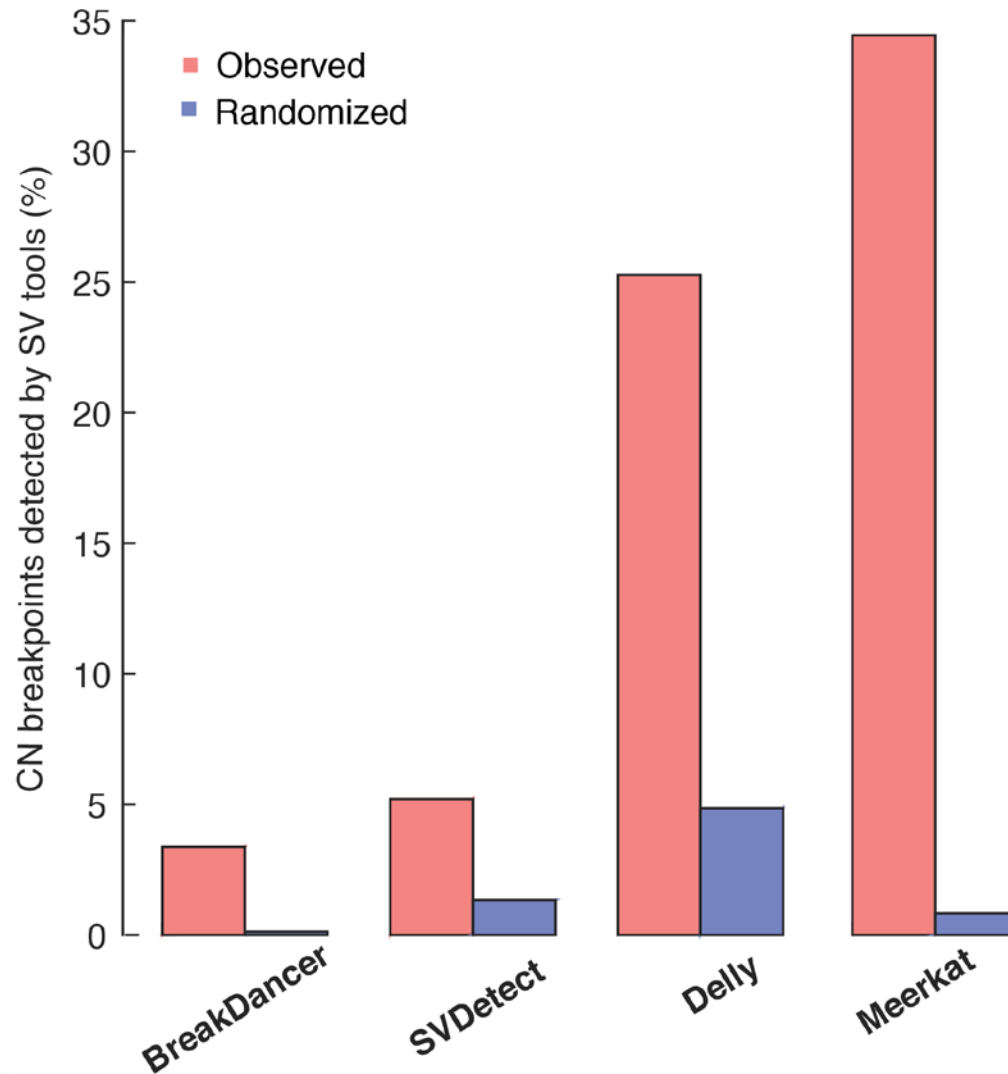
# Structural genomic alterations in cancer

- Not thoroughly explored in pan-cancer studies
- Relation to copy-number changes?
- Overall influence on transcription in tumors?

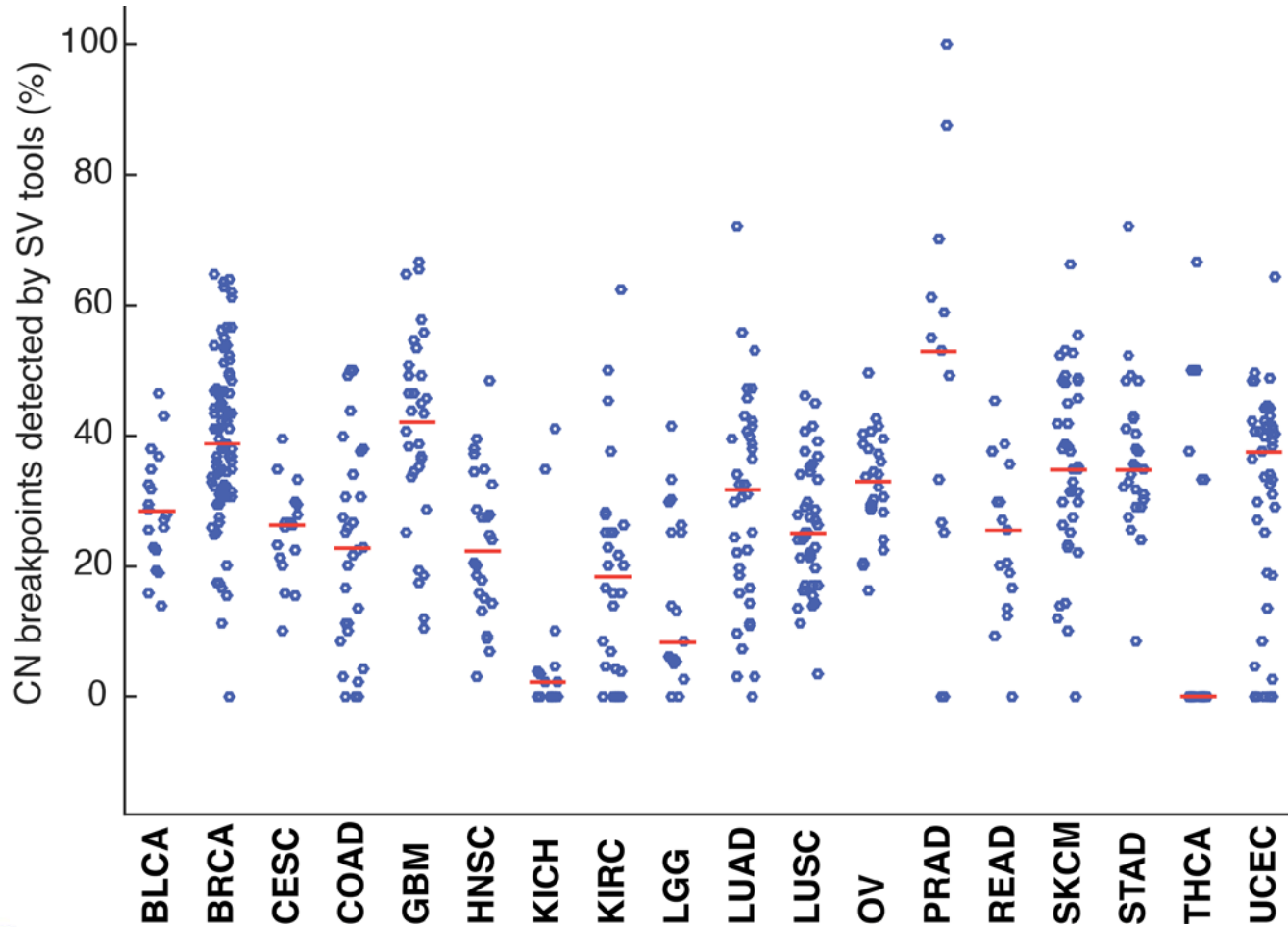
# Integrative analysis of SV, CNA and RNA data across cancers



# Benchmarking WGS-based SV detection methods using copy number data

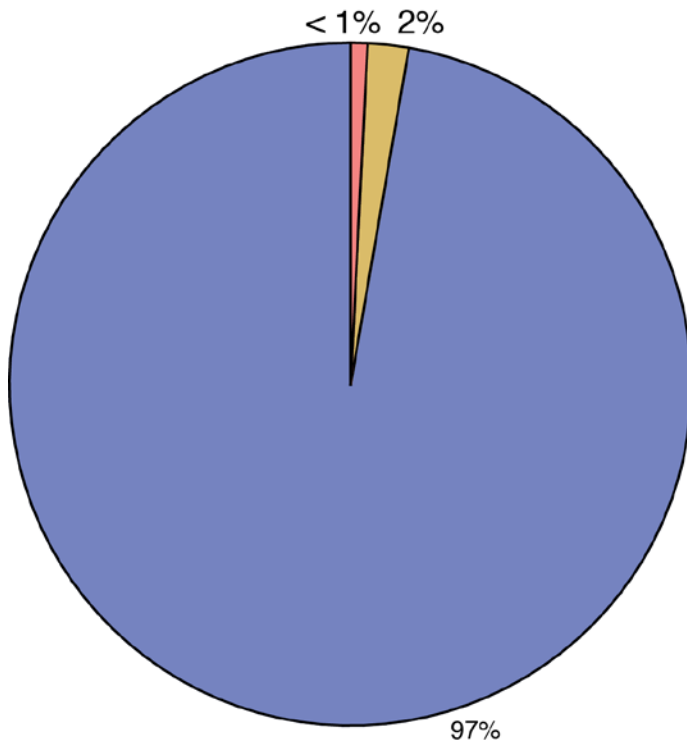


# 35% of SNP6 copy number breakpoints are explained by the WGS-based SV analysis

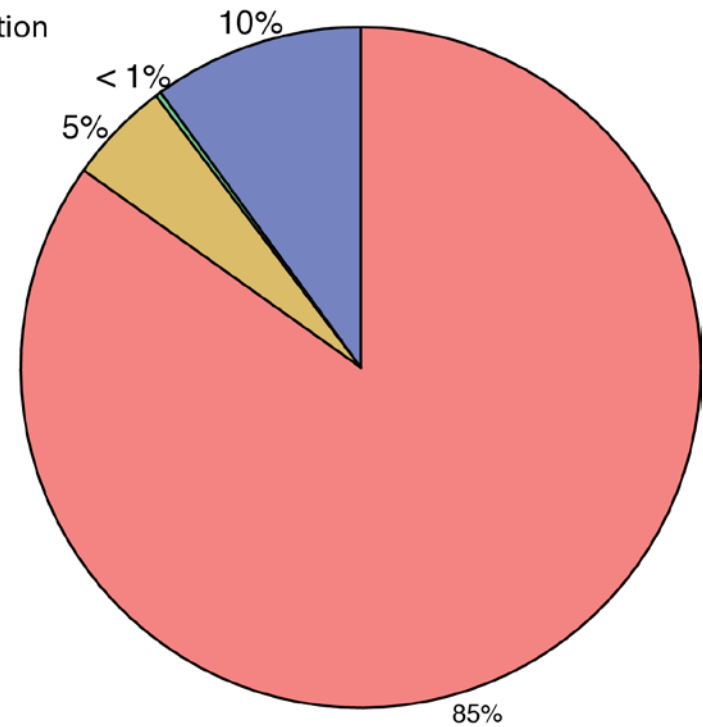


# Most copy number amplifications are tandem duplications

Copy Number deletions



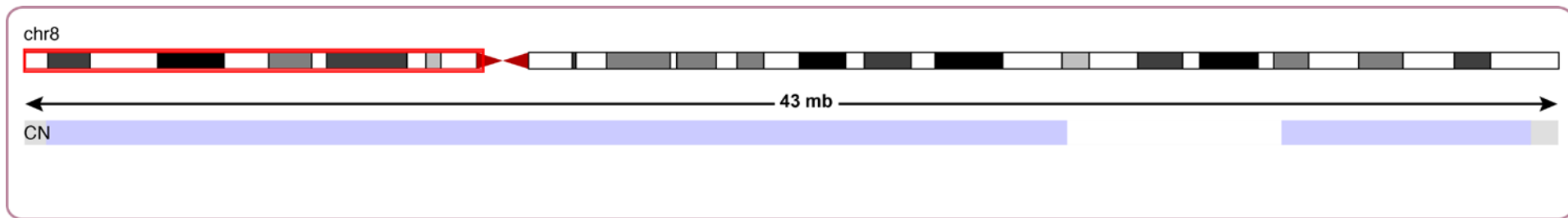
Copy Number amplifications



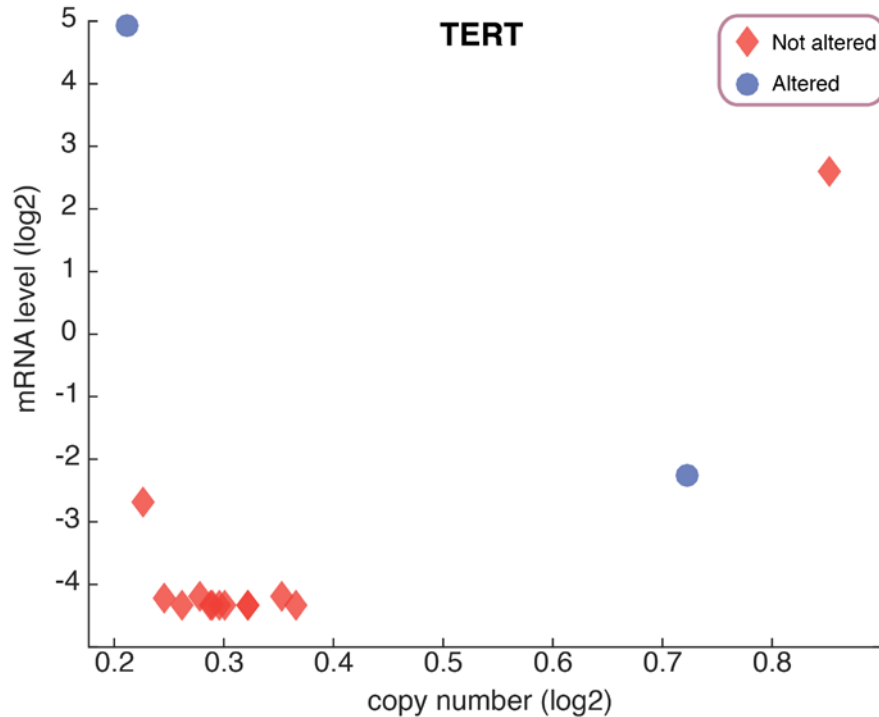
- Tandem Duplication
- Deletions
- Inversions
- Insertions



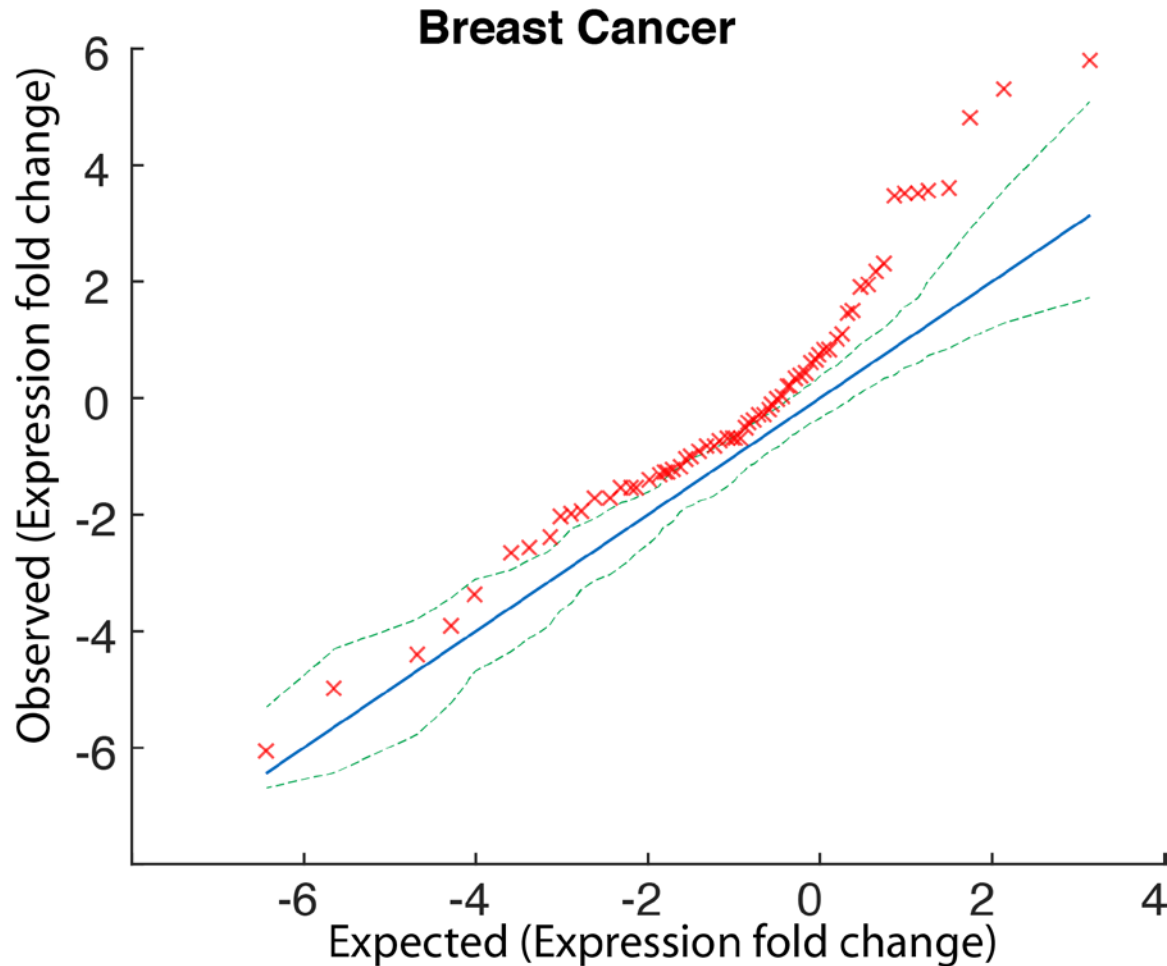
# Some seemingly simple copy-number alterations have a more complex structural basis



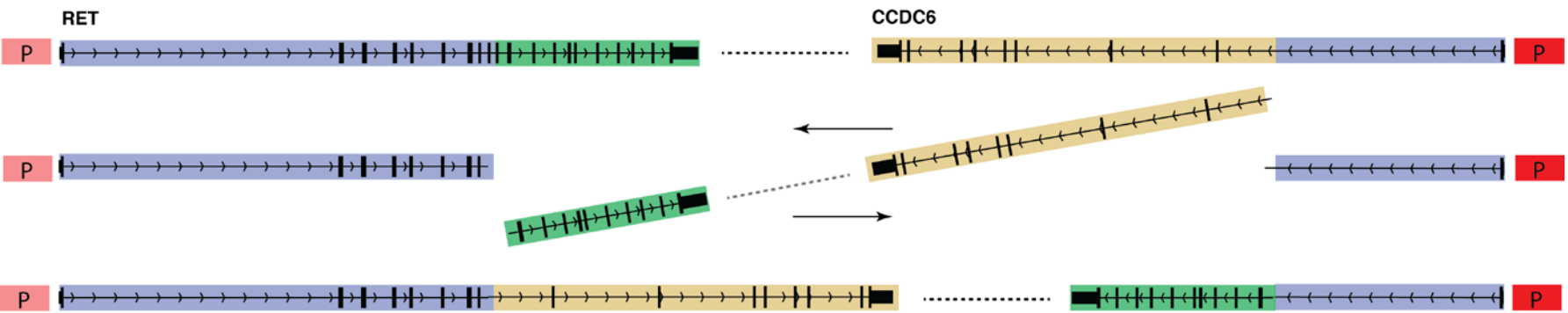
# Structural alteration in regulatory regions change the mRNA level



# Global impact of “promoter hijacking” events on tumors transcriptomes

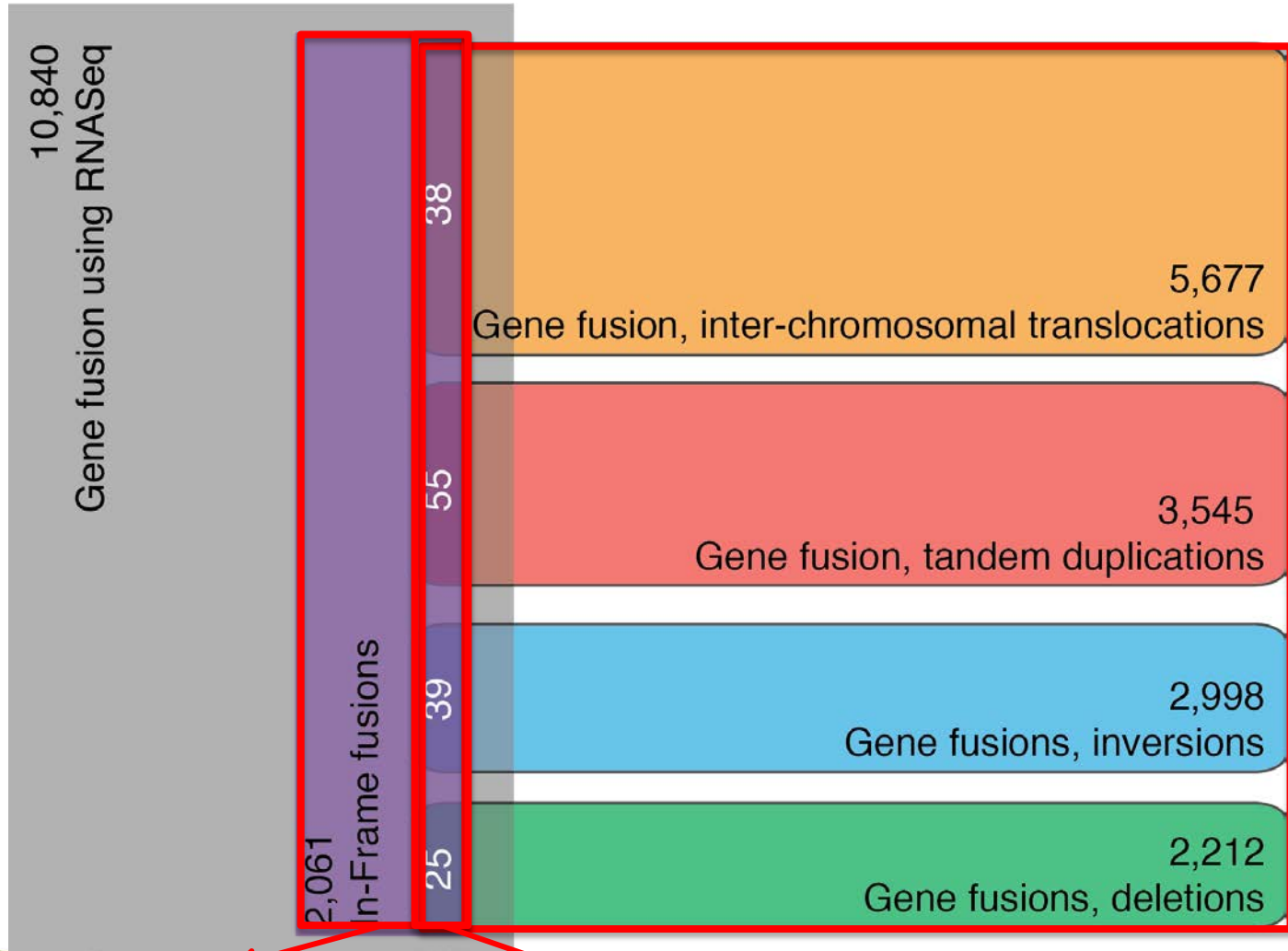


# Example: CCDC6-RET in thyroid carcinoma



# Combined DNA and RNA approach gives more cancer relevant fusions

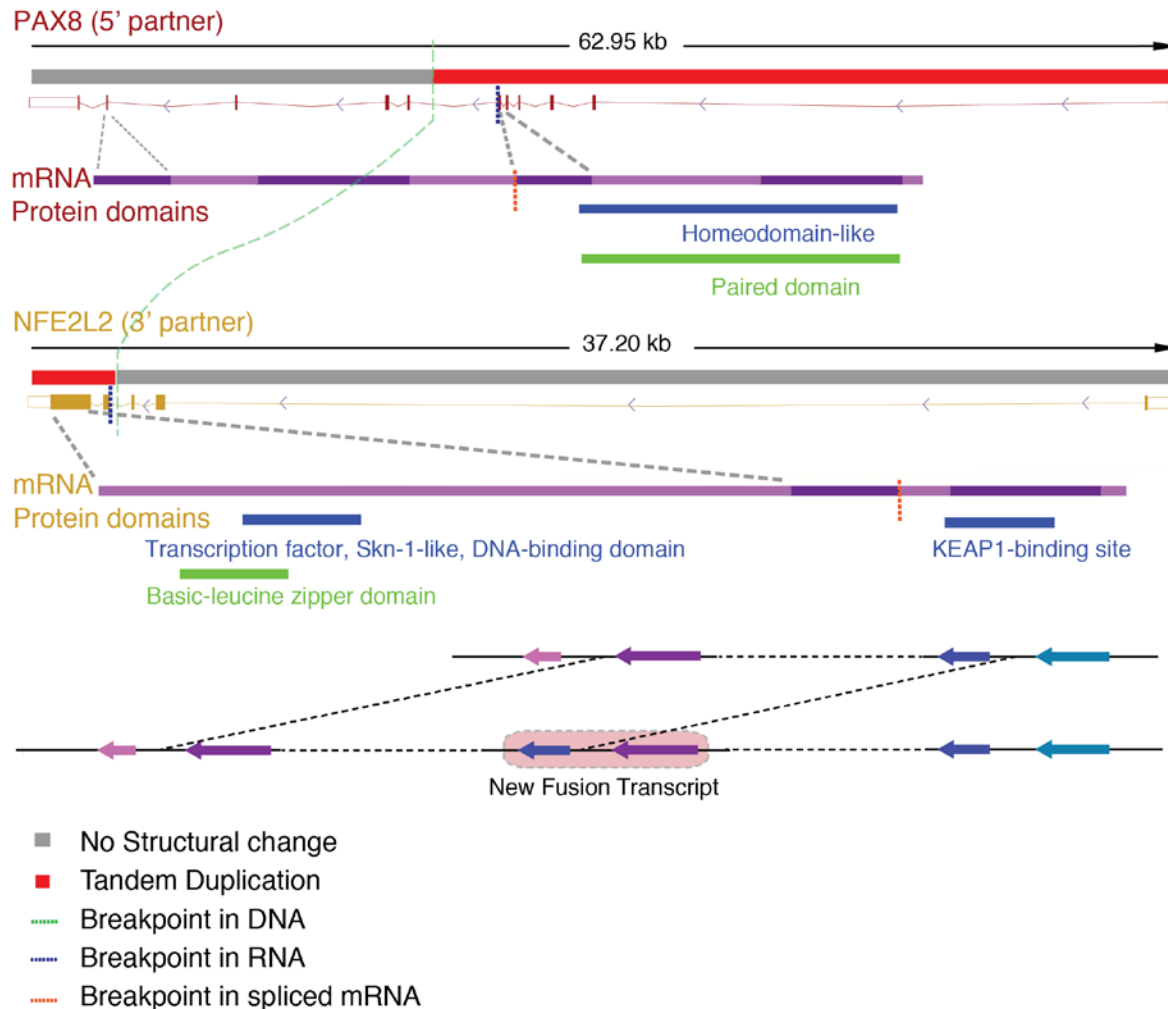
CGC overlap  
8%



CGC overlap  
8%

CGC overlaps  
22%

# Novel fusion transcript in thyroid cancer



# Summary

- Array-based copy-number data is useful to optimize SV detection
- Most copy-number amplifications are due to tandem duplications
- Shuffling regulatory regions such as promoters and enhancers impacts expression levels globally
- detection of fusions can be improved by combining WGS and RNA-seq

# Acknowledgments

## Larsson Lab:

- Erik Larsson
- Arghavan Ashouri
- Johan Fredriksson
- Joakim Karlsson
- Jimmy Van Den Eynden
- Jonas Nilsson
- Santhilal Subhash

## Computational resource:

