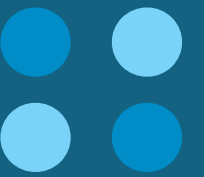


# The molecular diversity of Luminal A breast tumors

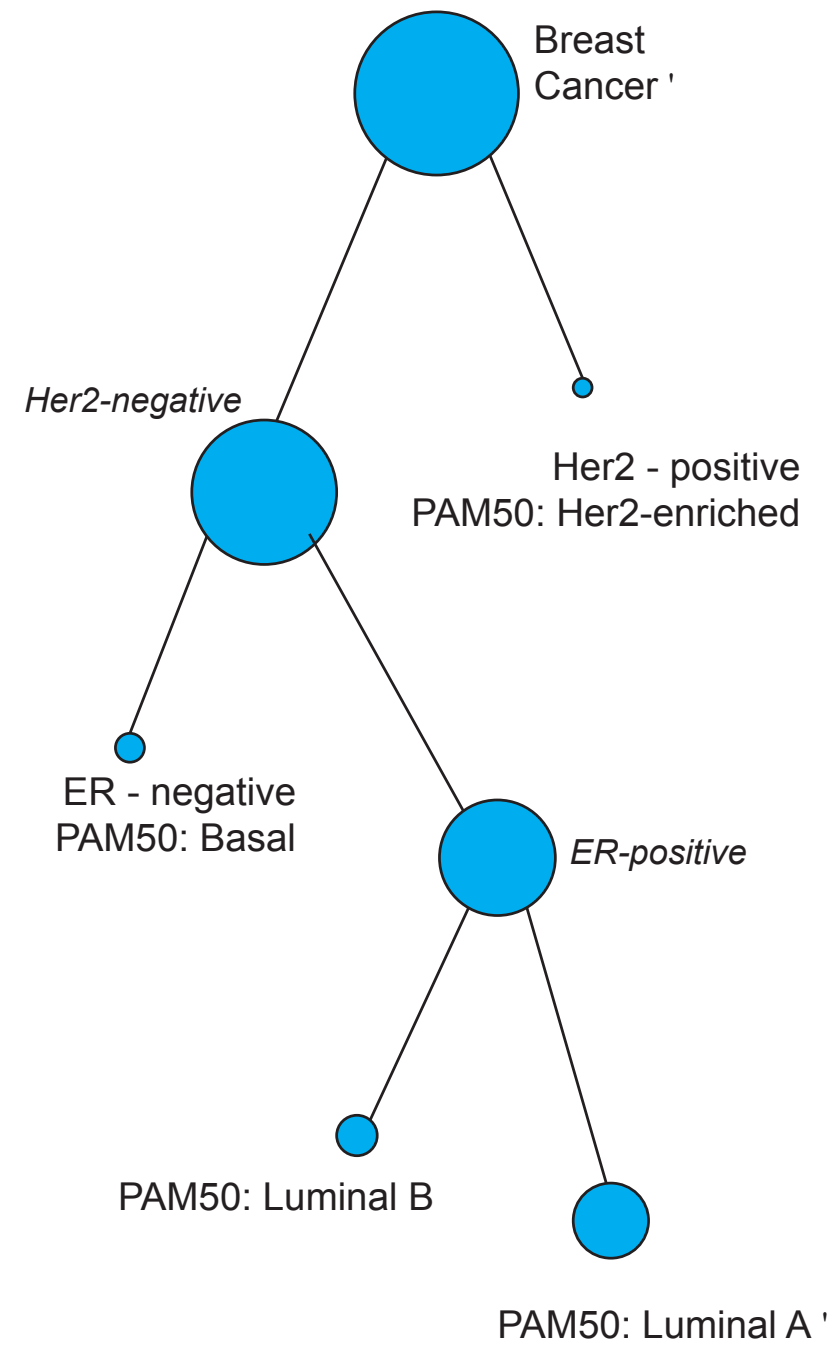
**c B i o**

**Giovanni Ciriello**  
Computational Biology, MSKCC  
*TCGA Annual Symposium*  
Washington DC, 2012

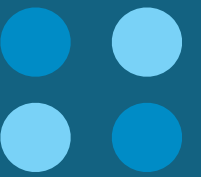
# Breast Cancer Heterogeneity



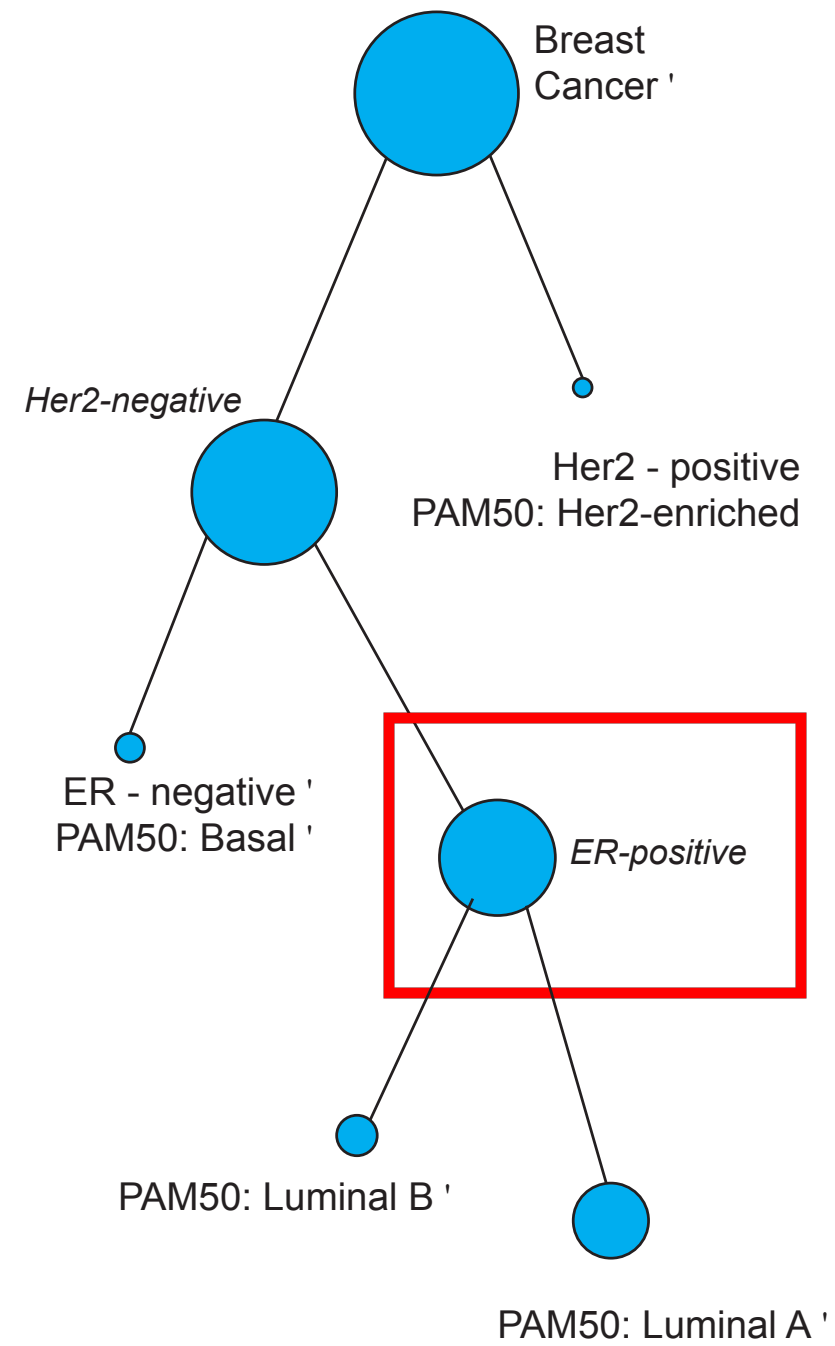
## Breast Cancer Intrinsic Subtypes



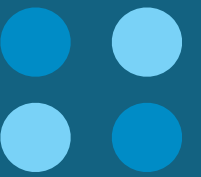
# Breast Cancer Heterogeneity



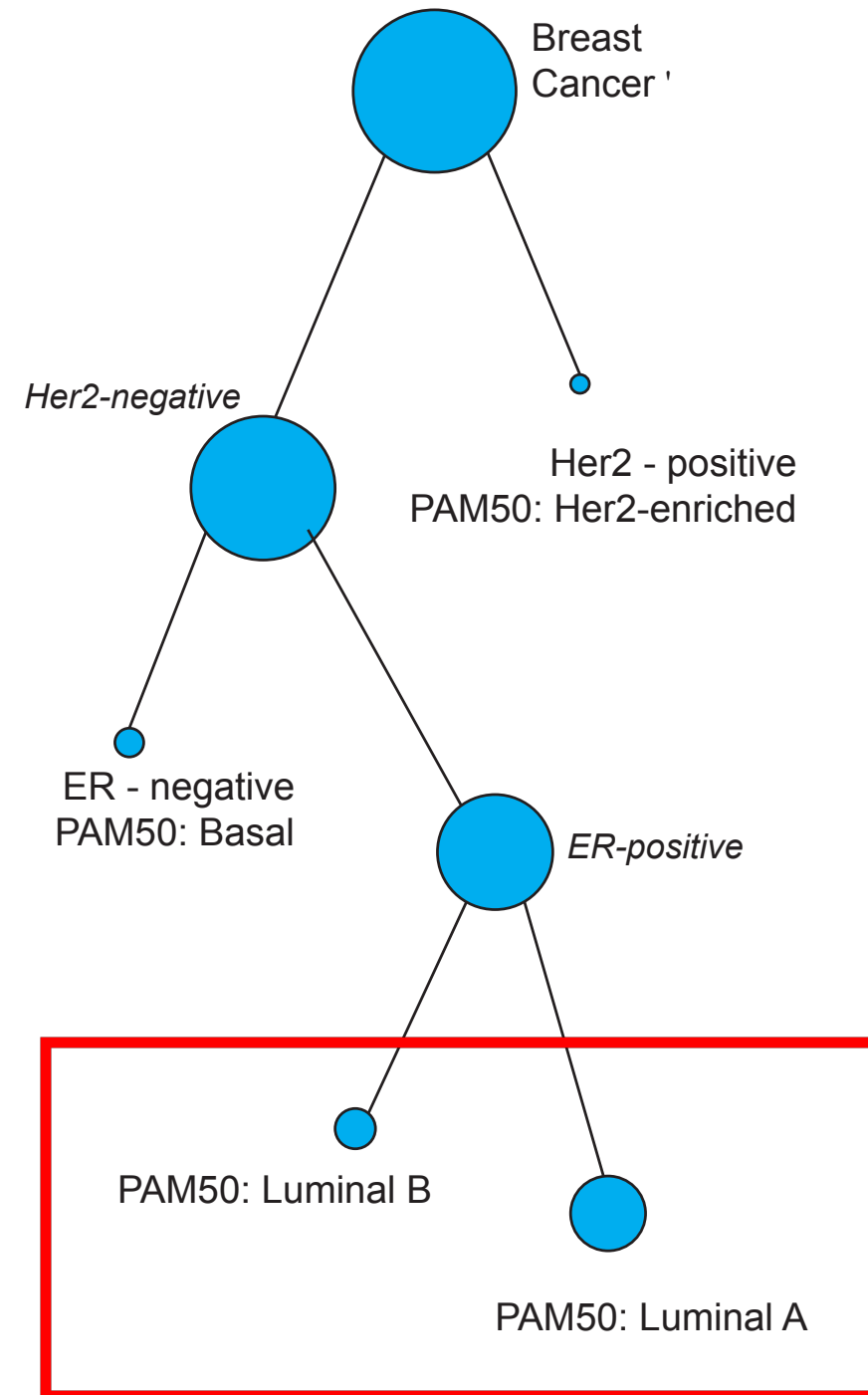
## Breast Cancer Intrinsic Subtypes



# Breast Cancer Heterogeneity

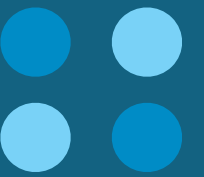


## Breast Cancer Intrinsic Subtypes



**PAM50**  
(Perou et al., 2000)

# Luminal Heterogeneity



## Integrated data from:

TCGA 2012,  
Ellis et al. 2012,  
Banerji et al. 2012  
Curtis et al. 2012  
Russnes et al. 2010

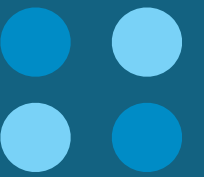


*~ 1500 Luminal tumors*



Copy Number Alterations  
Somatic Mutations  
mRNA expression

# Luminal Molecular Heterogeneity



Integrated data from:

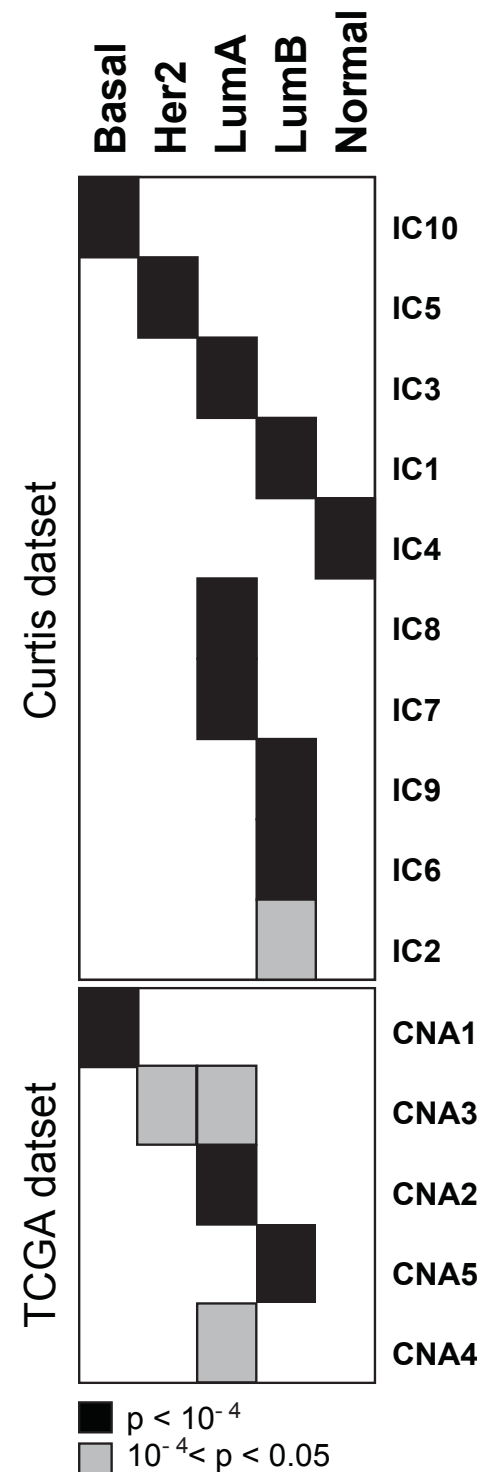
TCGA 2012,  
Ellis et al. 2012,  
Banerji et al. 2012  
Curtis et al. 2012  
Russnes et al. 2010

~ 1500 Luminal tumors

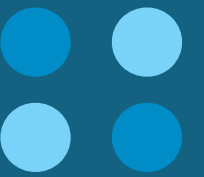
Copy Number Alterations  
Somatic Mutations  
mRNA expression

## PAM50 vs CNA-clusters

(Curtis et al., TCGA)



# Luminal Molecular Heterogeneity



Integrated data from:

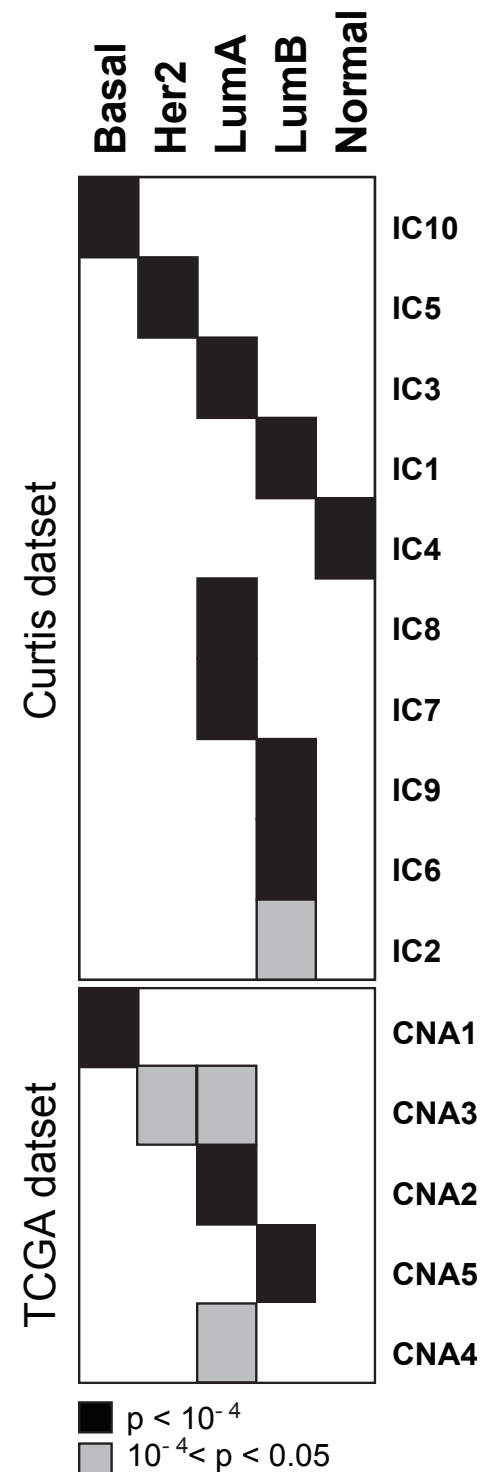
TCGA 2012,  
Ellis et al. 2012,  
Banerji et al. 2012  
Curtis et al. 2012  
Russnes et al. 2010

~ 1500 Luminal tumors

Copy Number Alterations  
Somatic Mutations  
mRNA expression

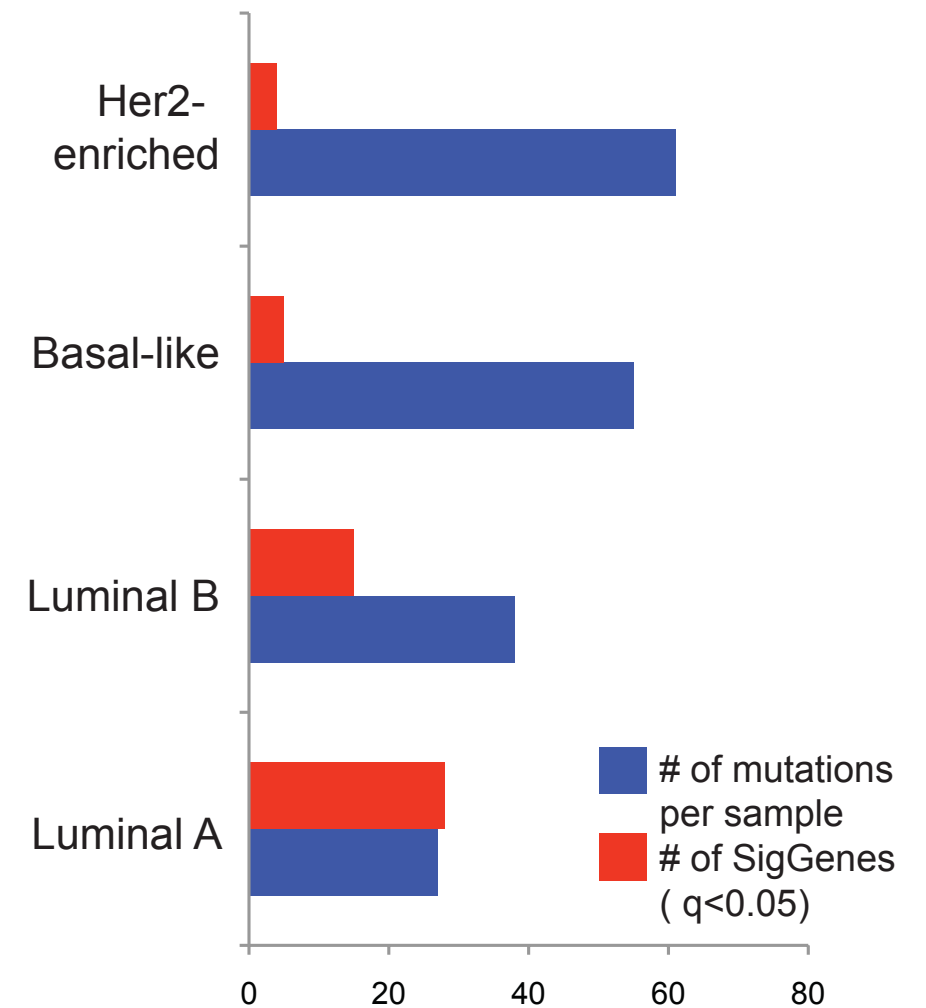
## CNA-clusters

(Curtis et al., TCGA)

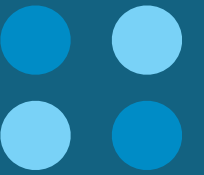


## Somatic Mutations

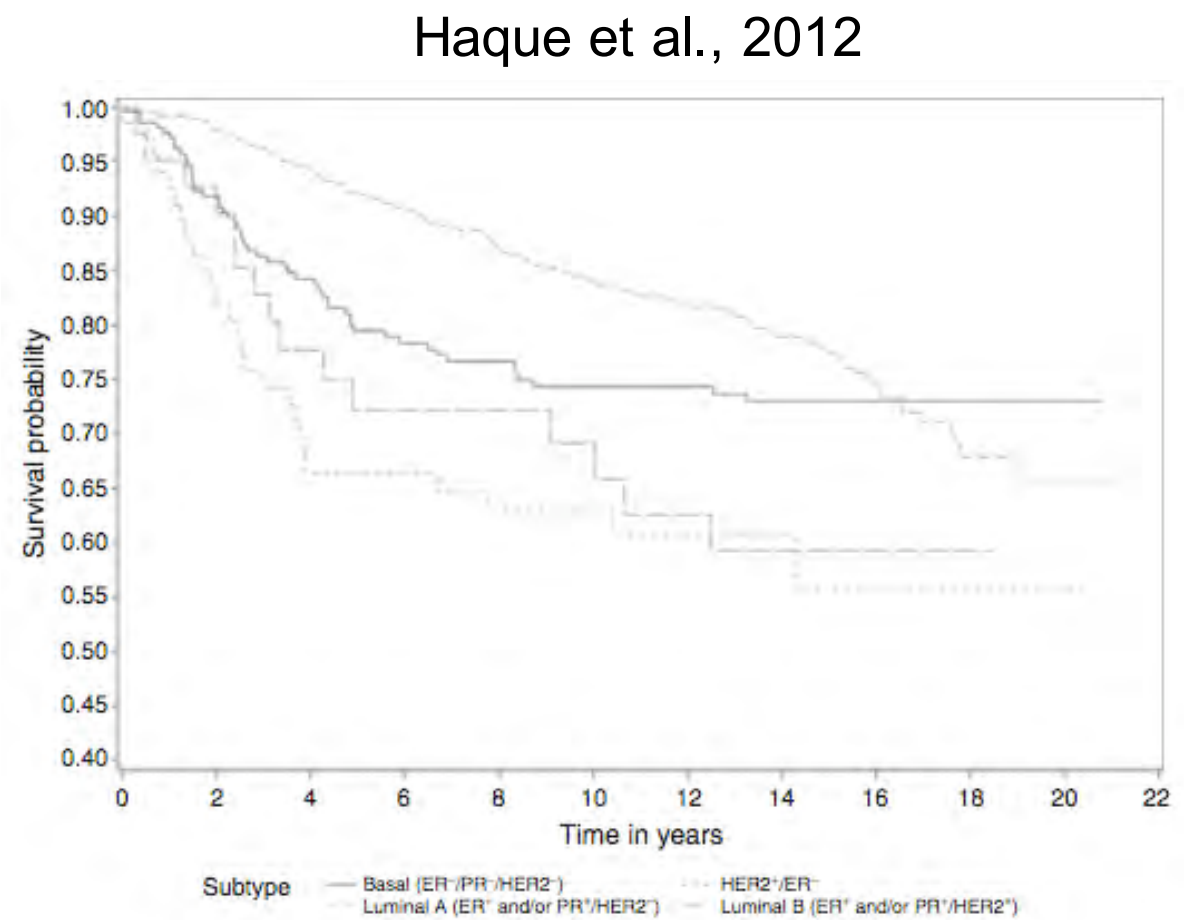
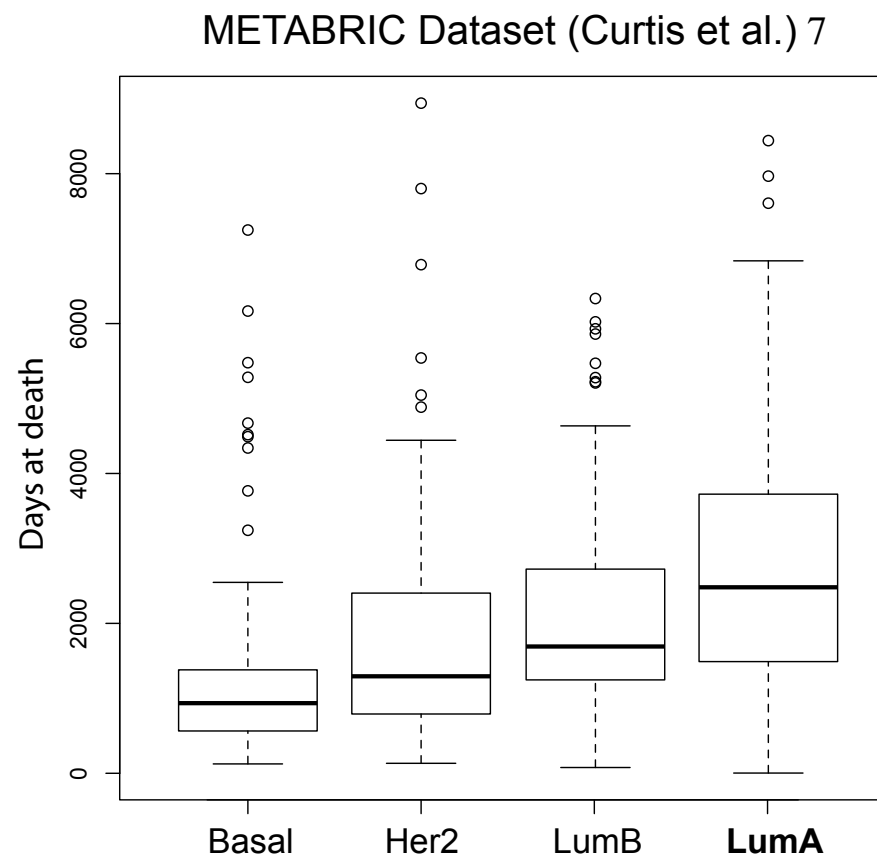
(TCGA, Ellis et al., Banerji et al)



# Luminal A Clinical Heterogeneity

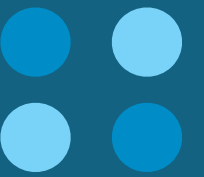


- Luminal A tumors have heterogenous outcome

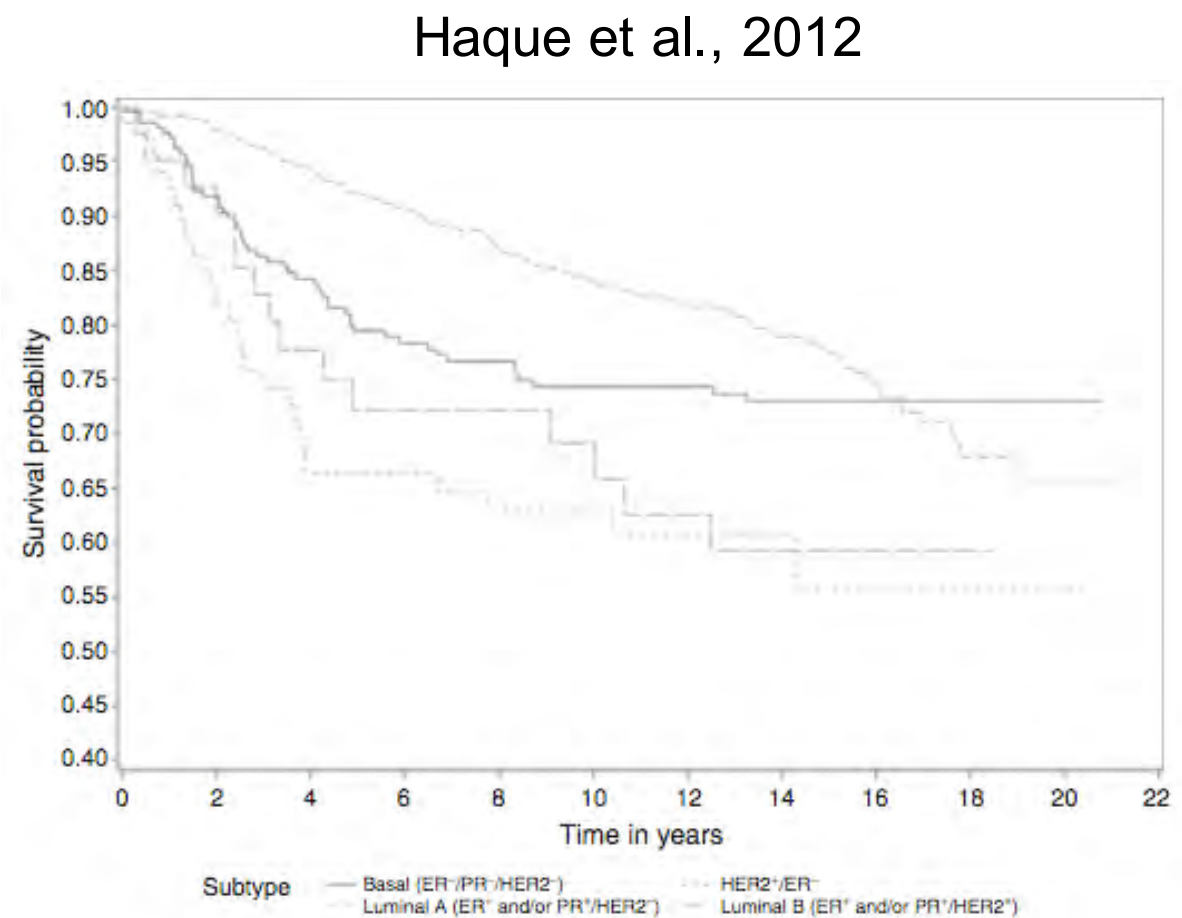
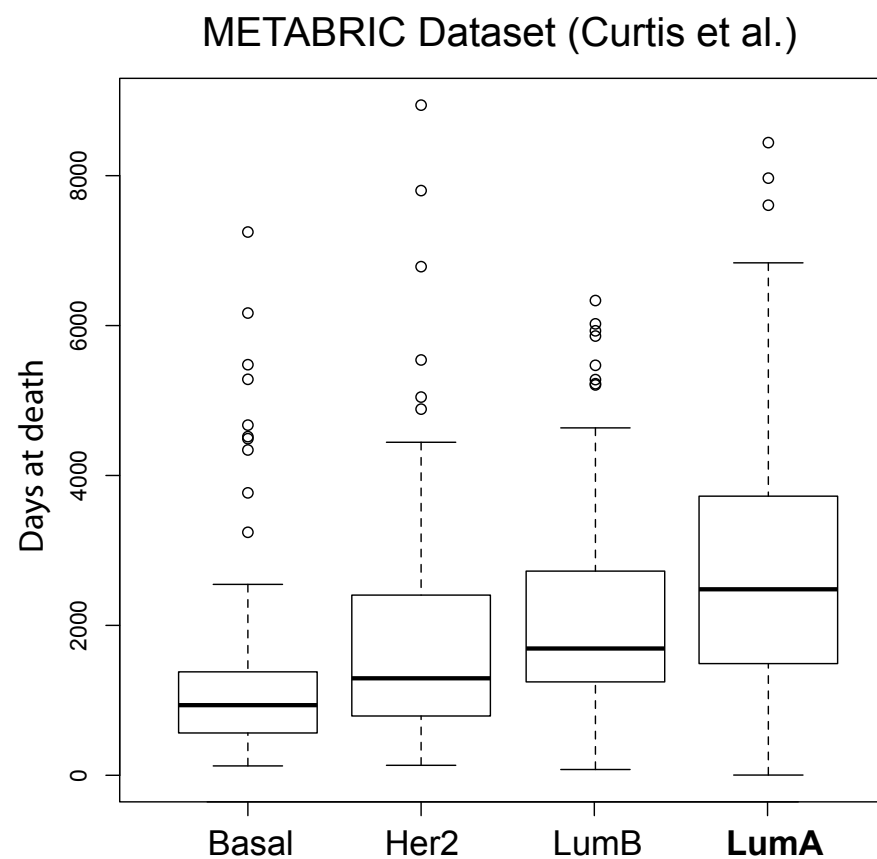




# Luminal Heterogeneity

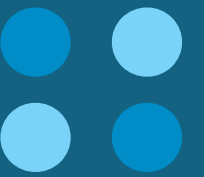


- Luminal A tumors have heterogenous outcome



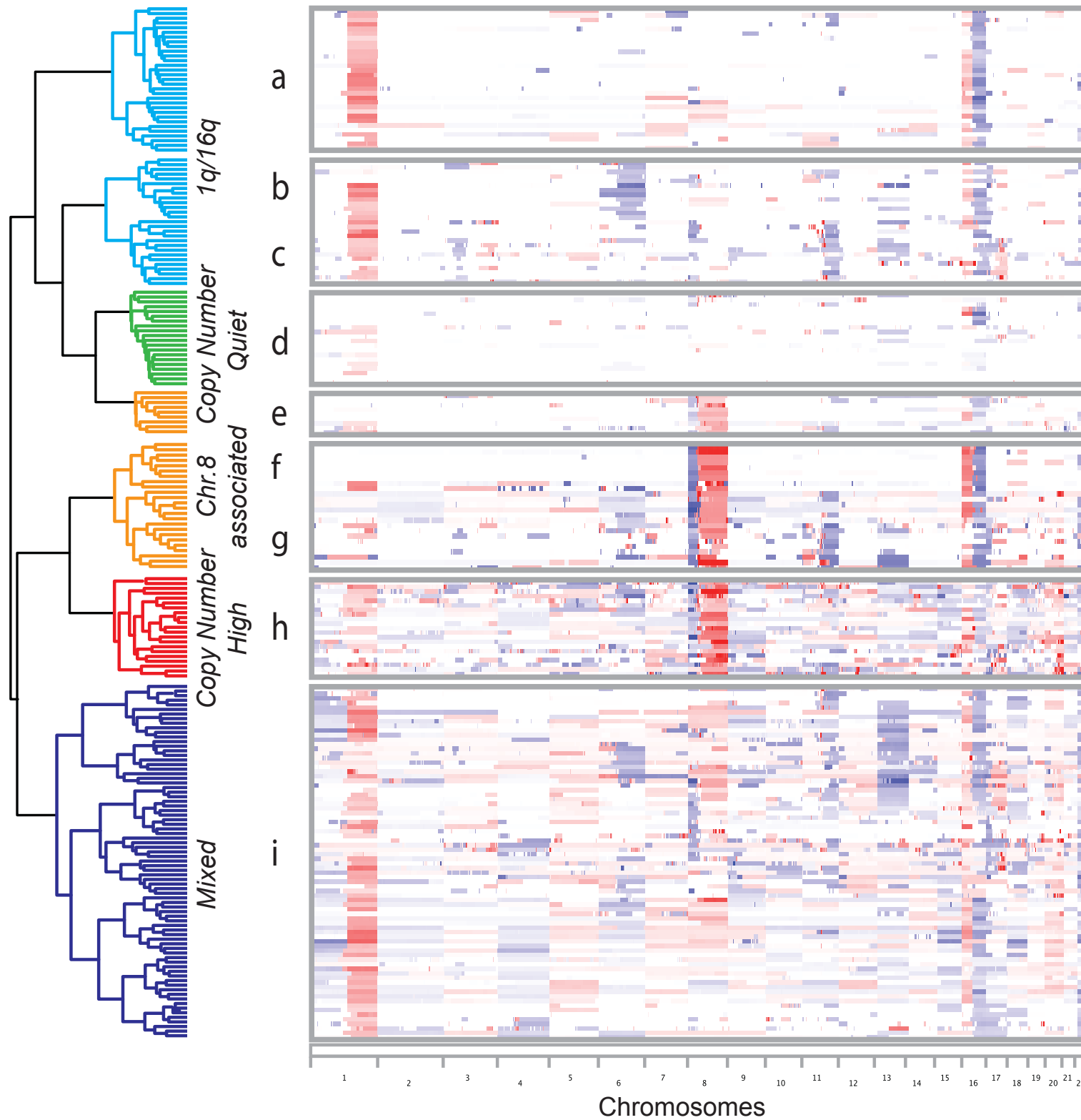
**Luminal A is molecularly and clinically heterogeneous**  
**Can we link outcome variability to molecular diversity?**

# Luminal A Heterogeneity



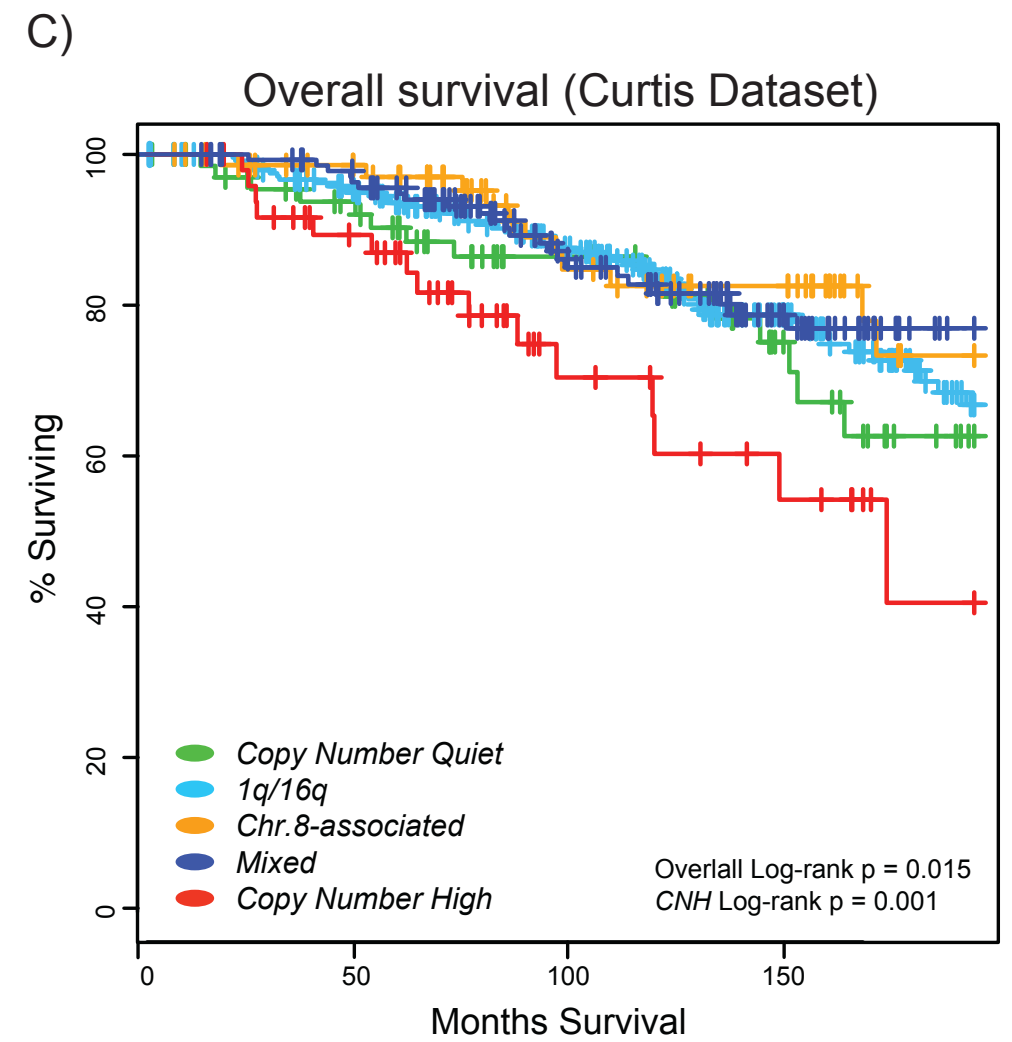
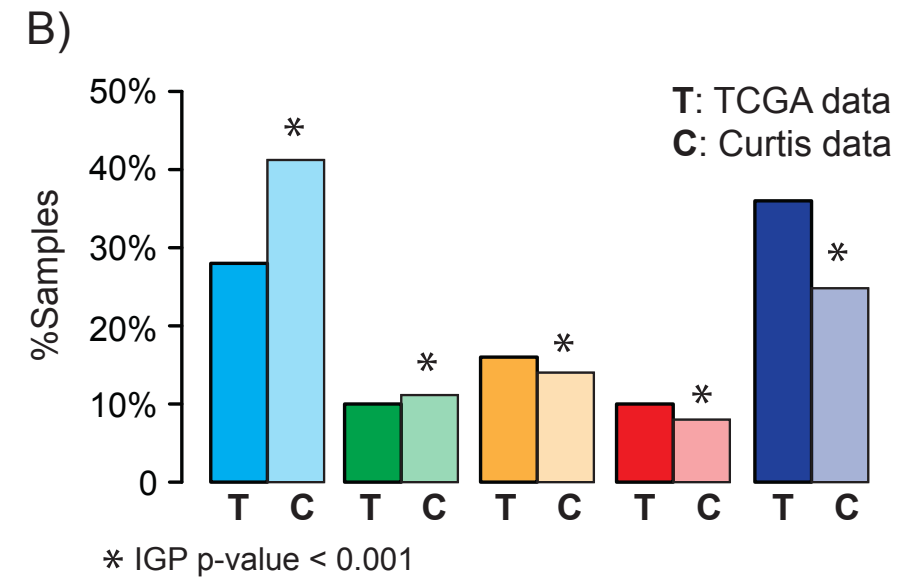
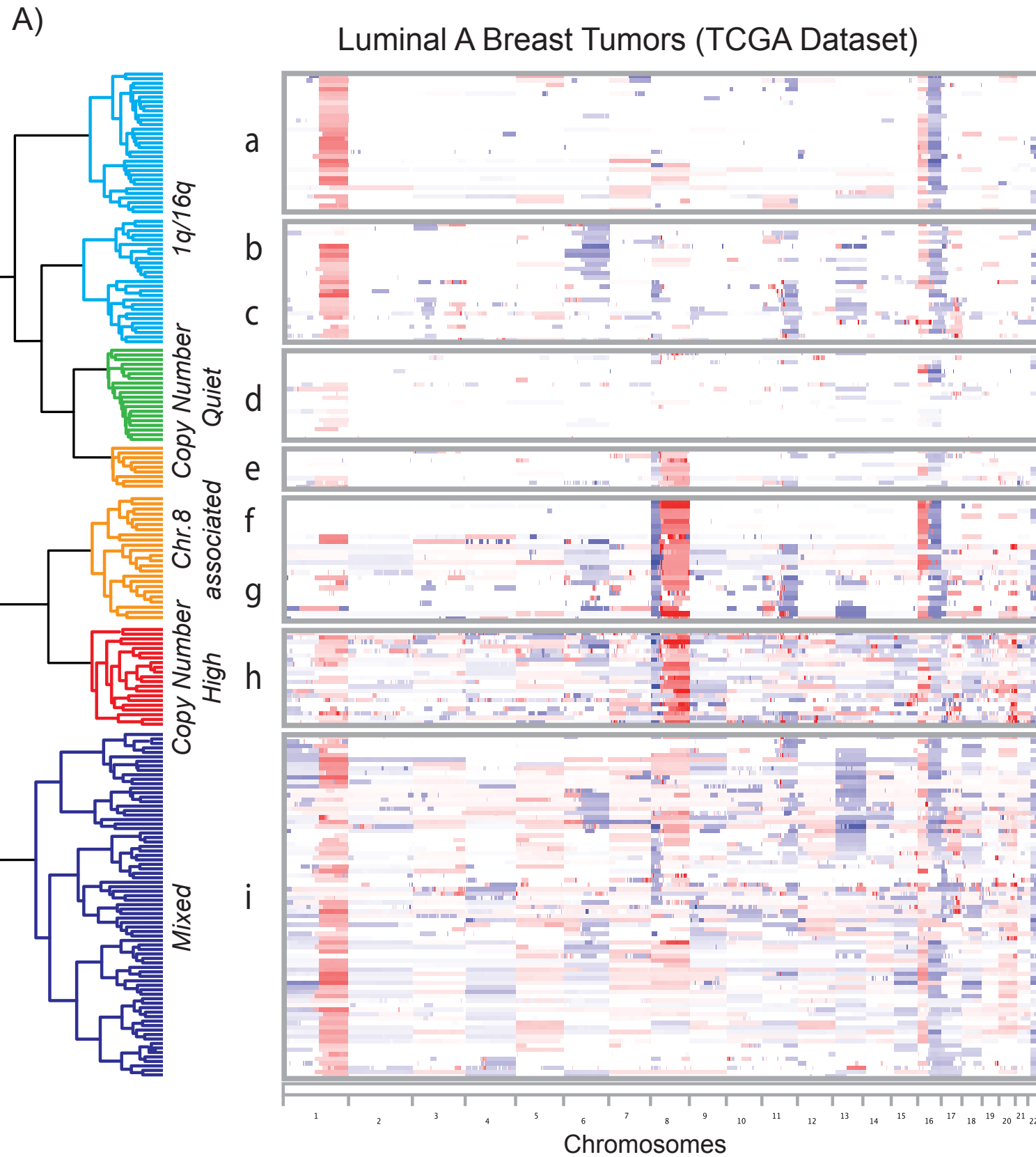
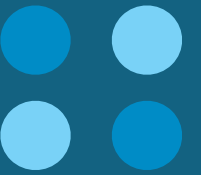
A)

Luminal A Breast Tumors (TCGA Dataset)

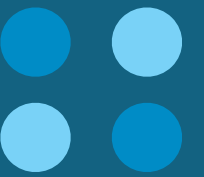


Copy Number Alterations identify five major subgroups

# Luminal A Heterogeneity

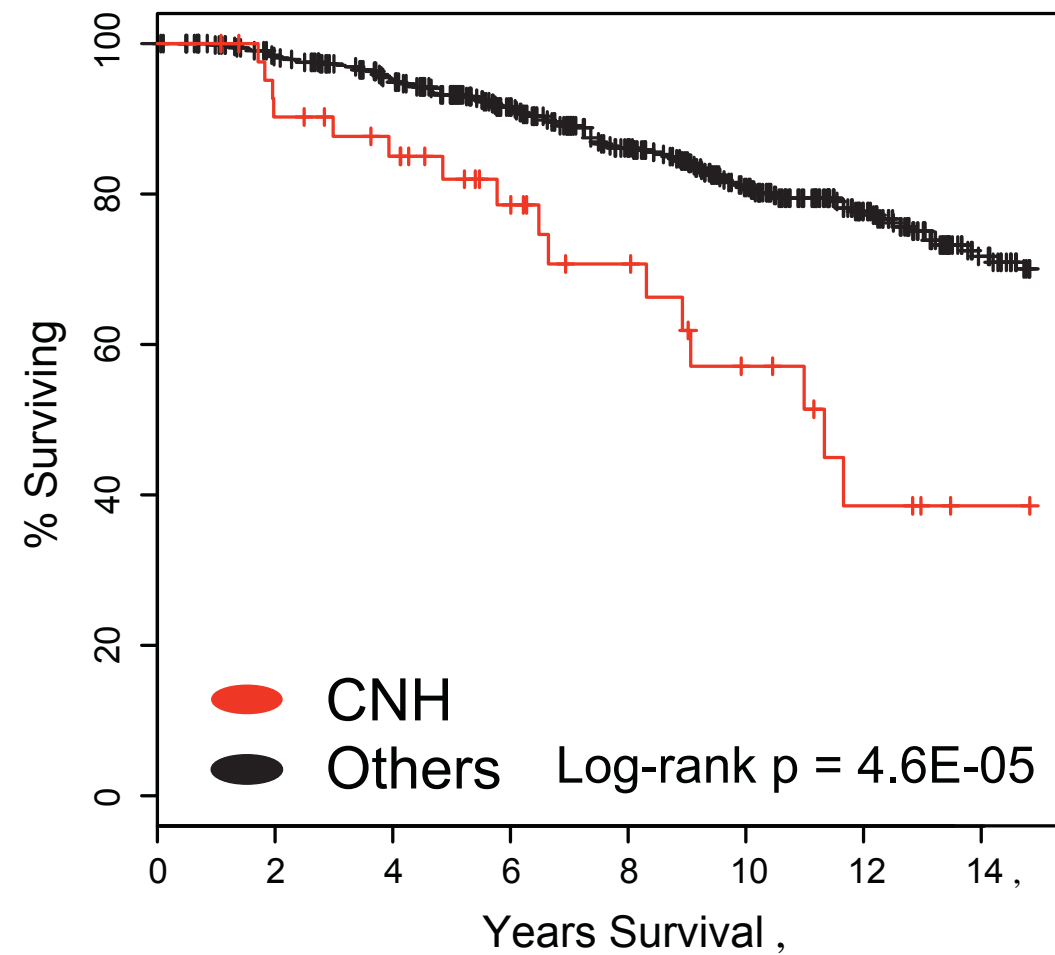


# Genomic Instability correlates with poor prognosis



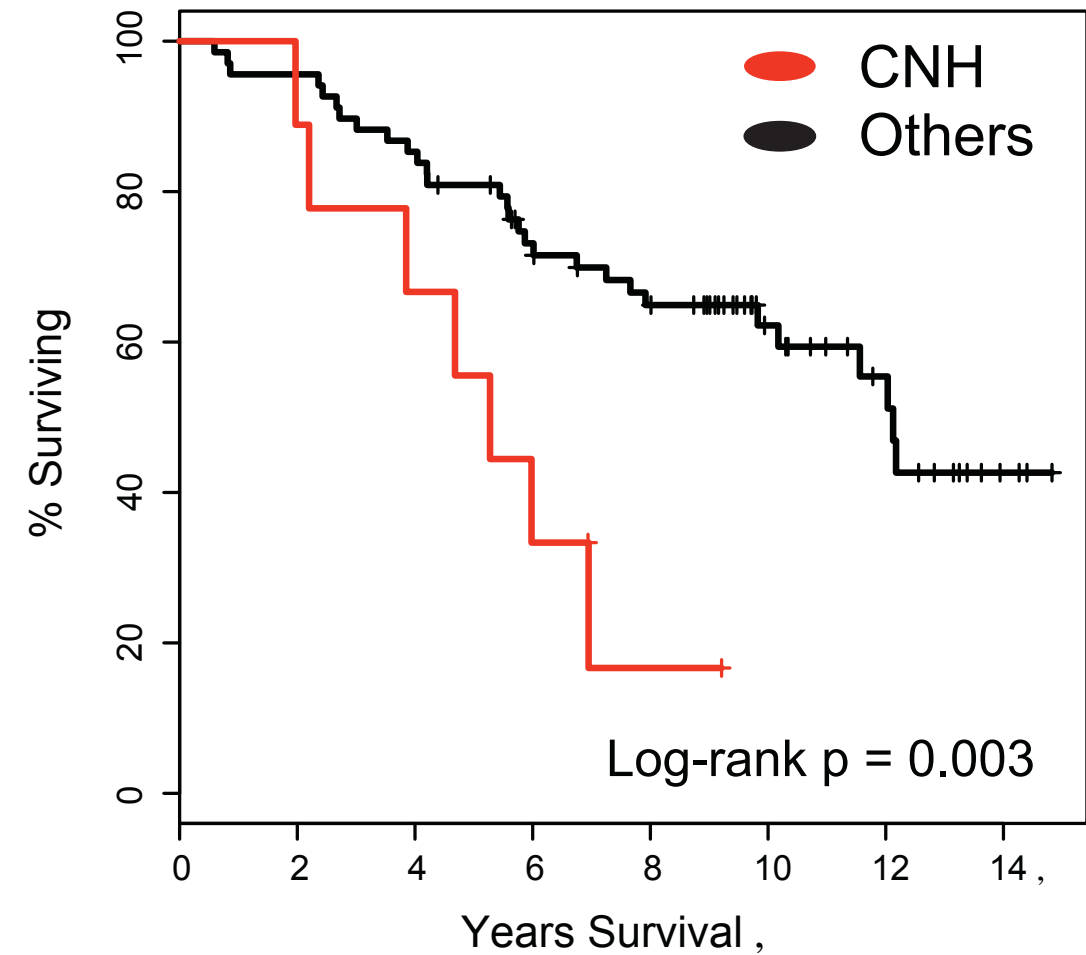
A)

CNH survival (Curtis et al.)

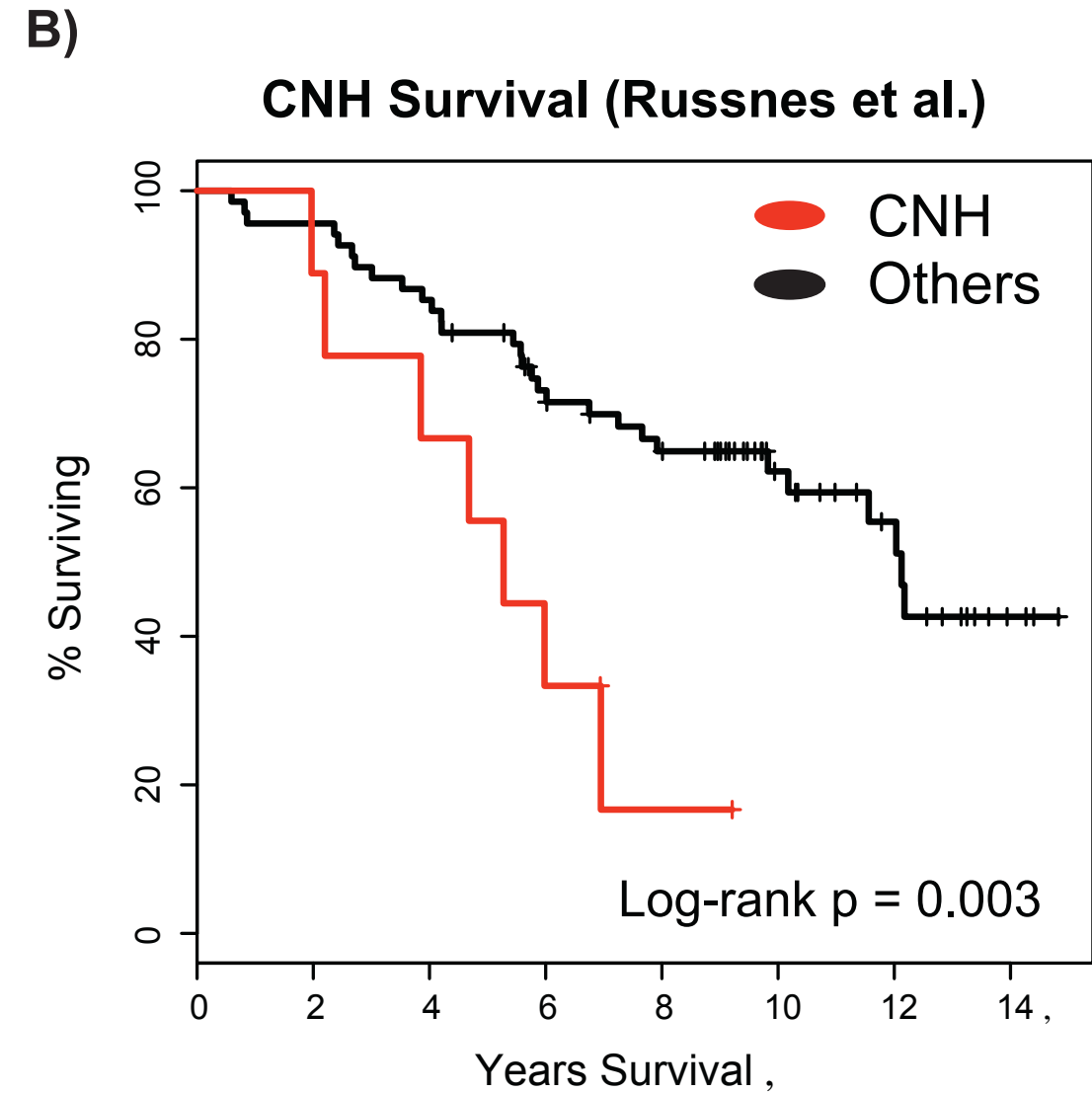
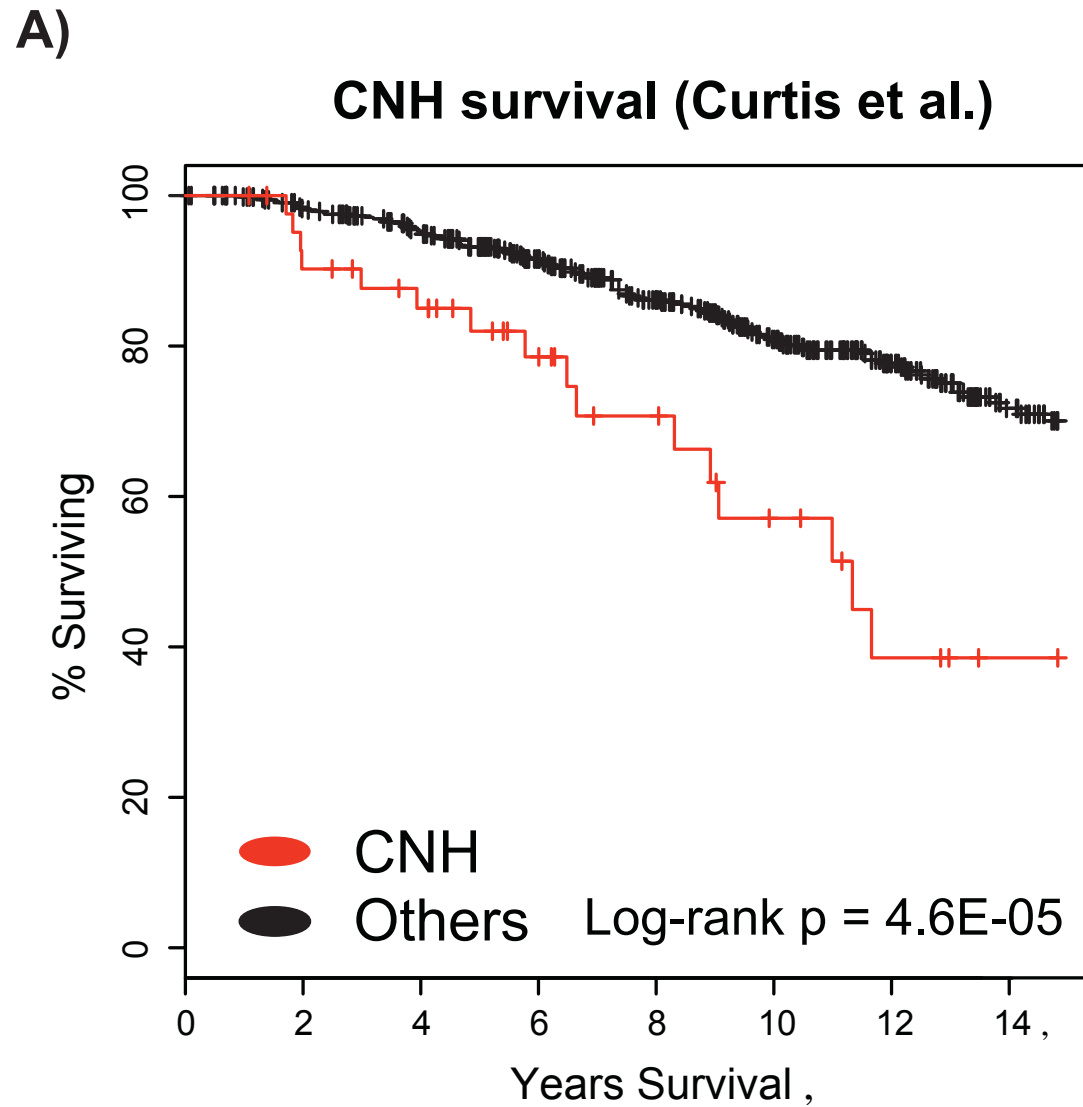
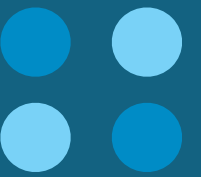


B)

CNH Survival (Russnes et al.)

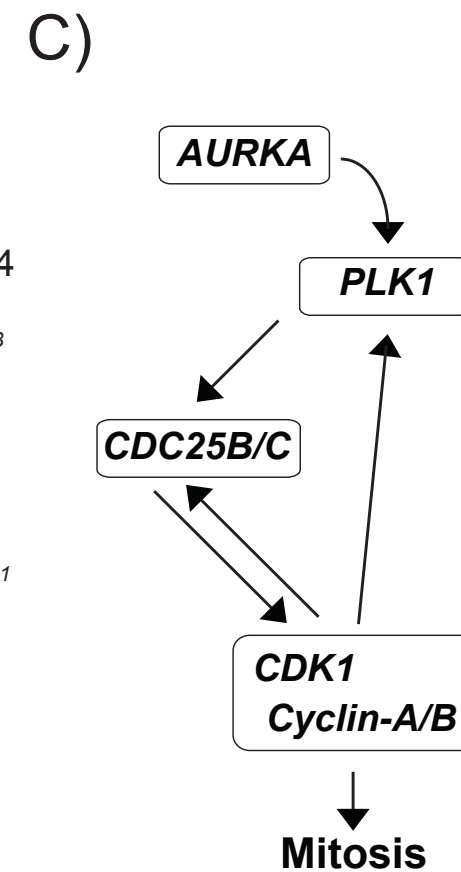
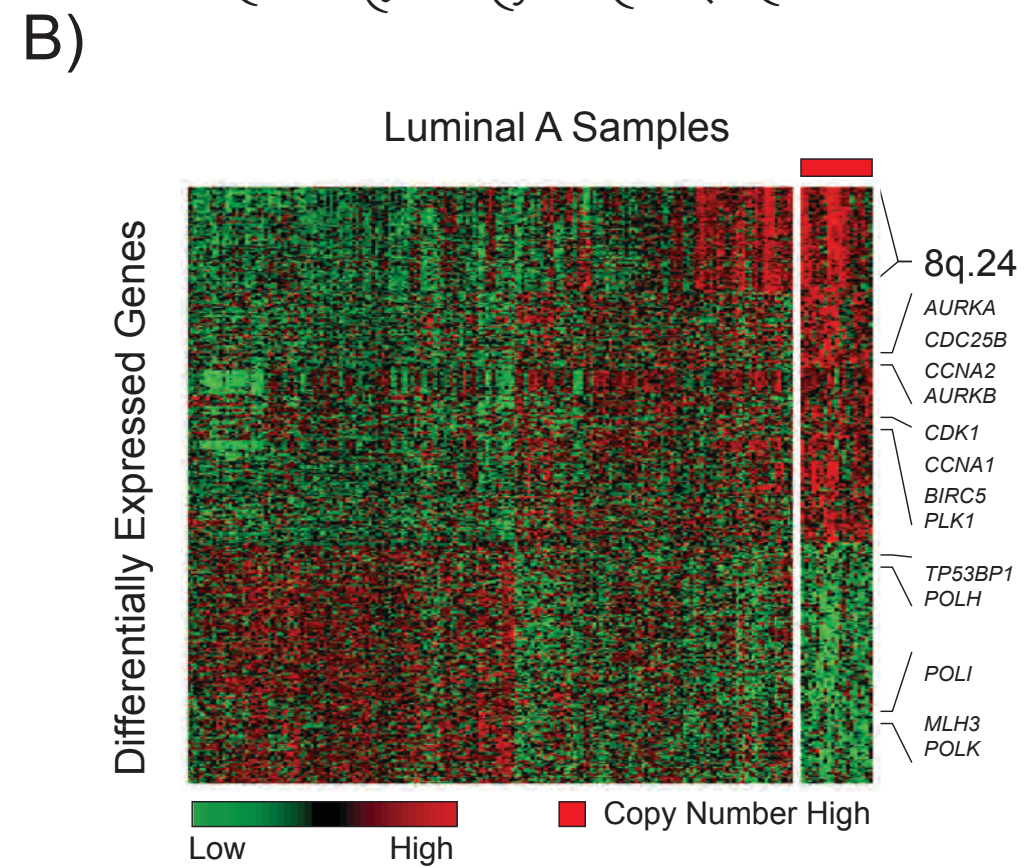
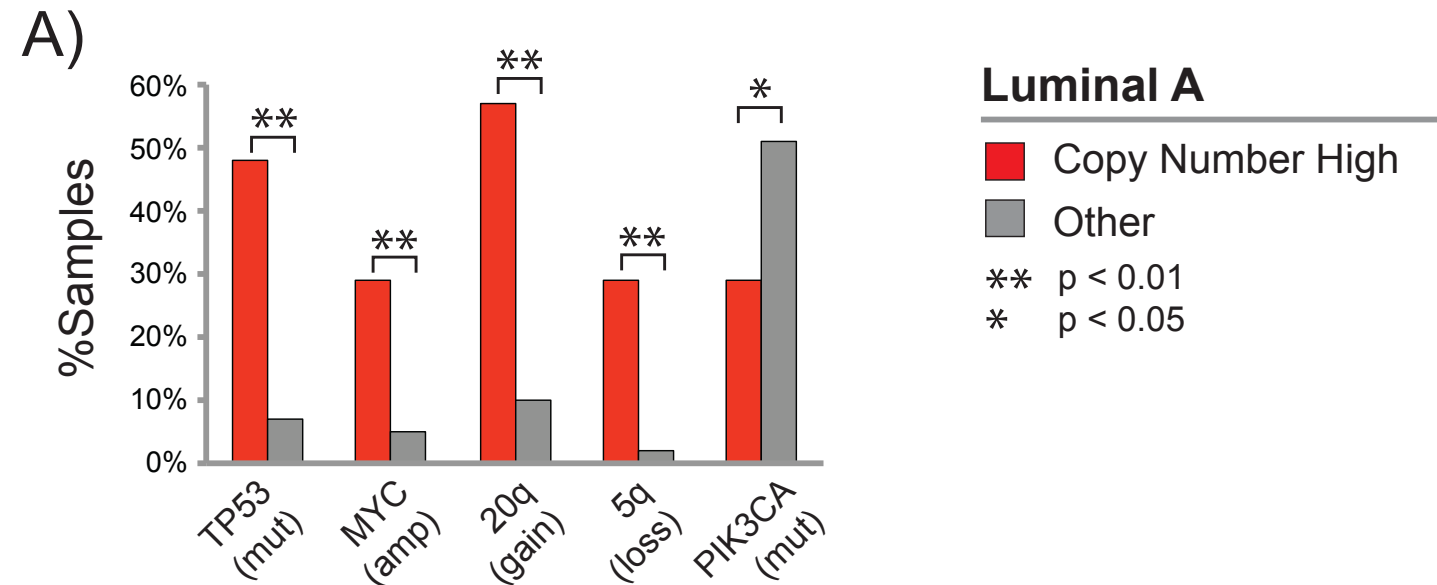
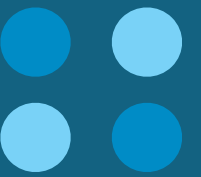


# Genomic Instability correlates with poor prognosis

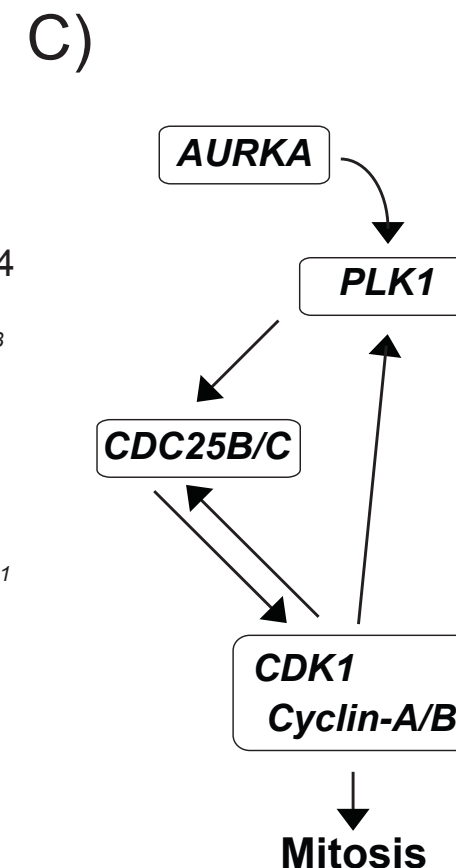
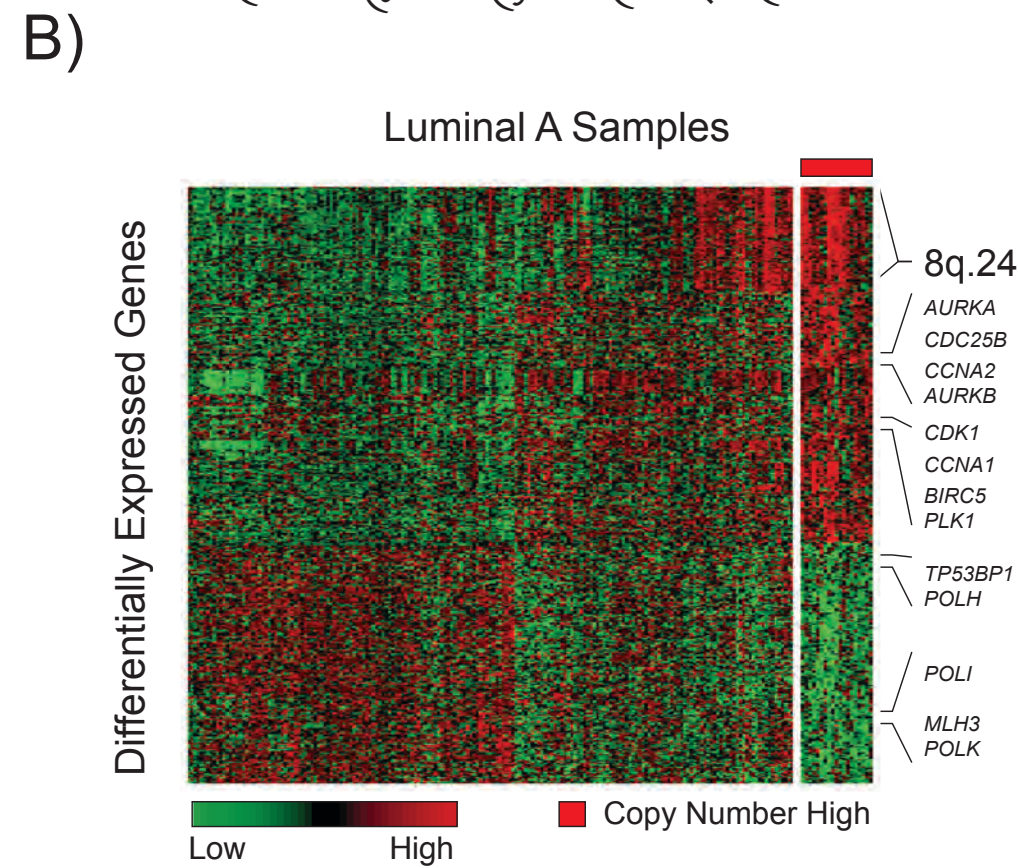
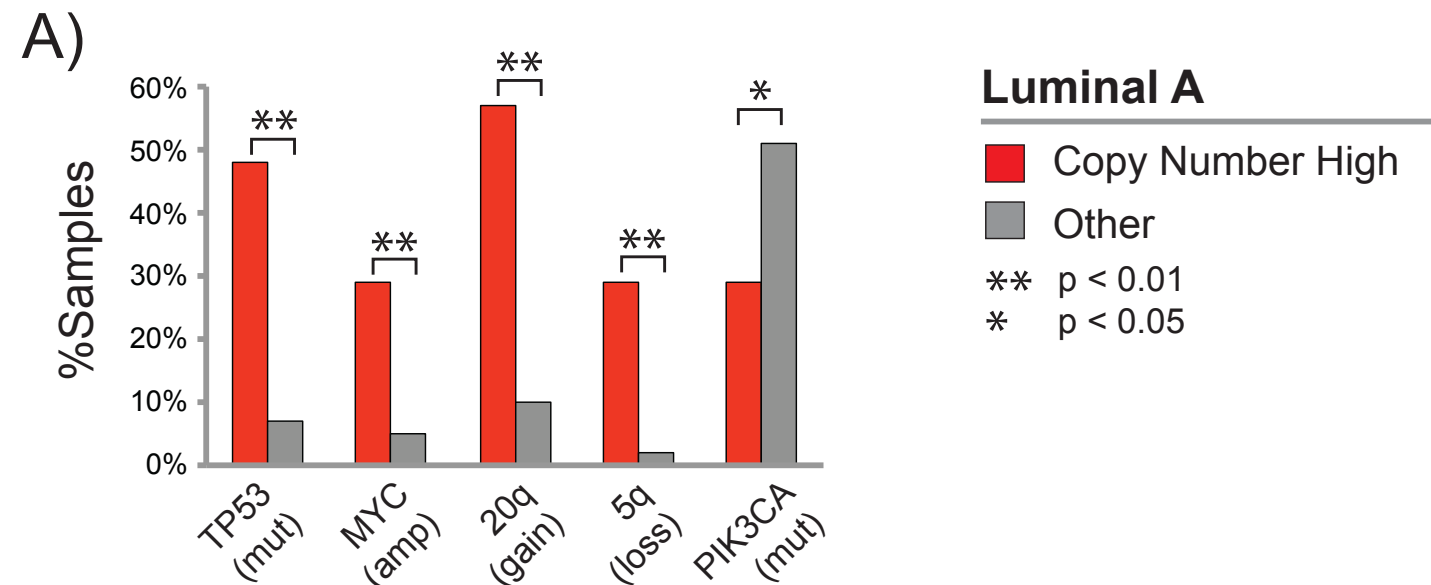
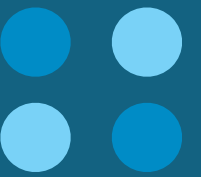


**What are the molecular features of these tumors?**

# CNH Molecular Features

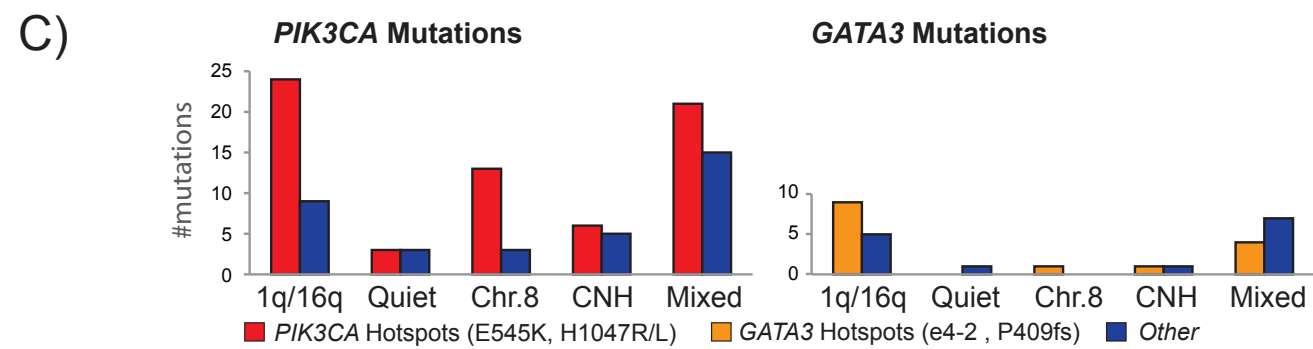
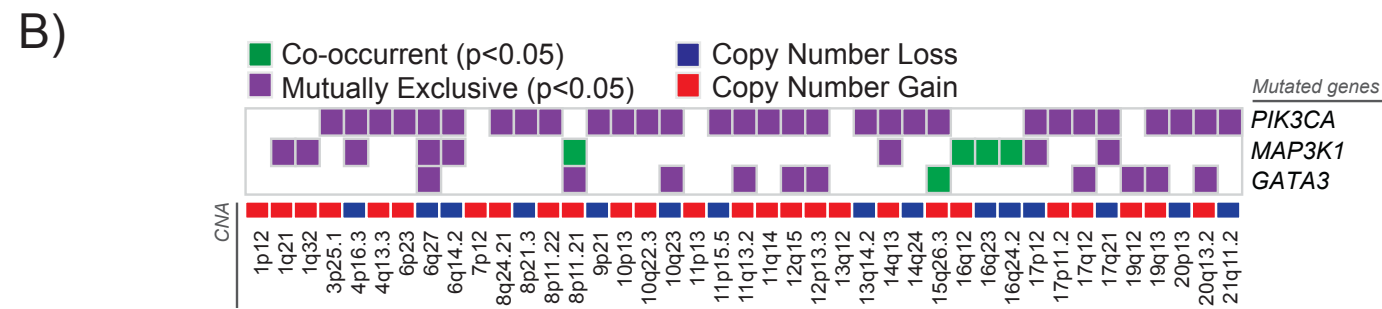
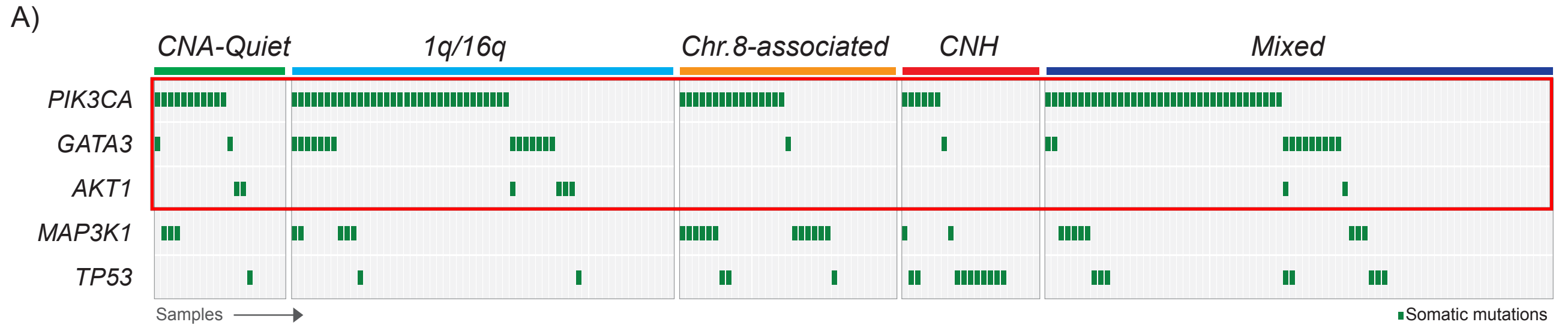
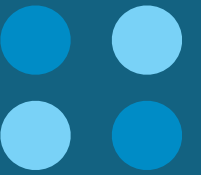


# CNH Molecular Features



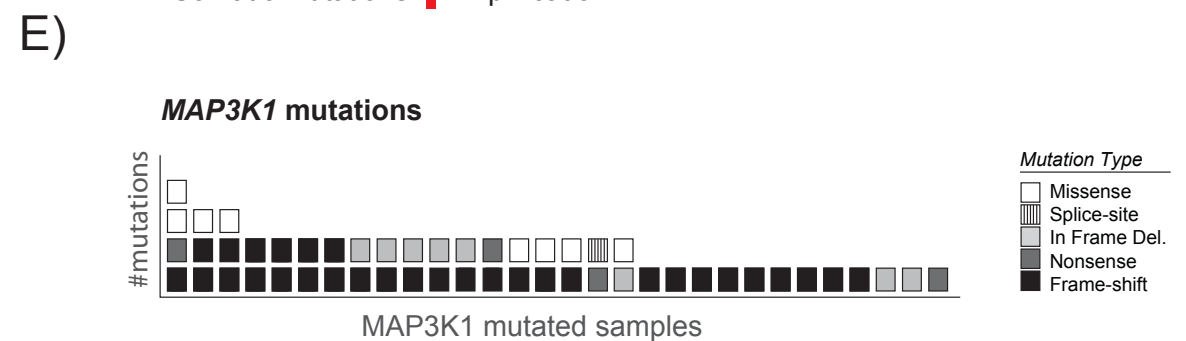
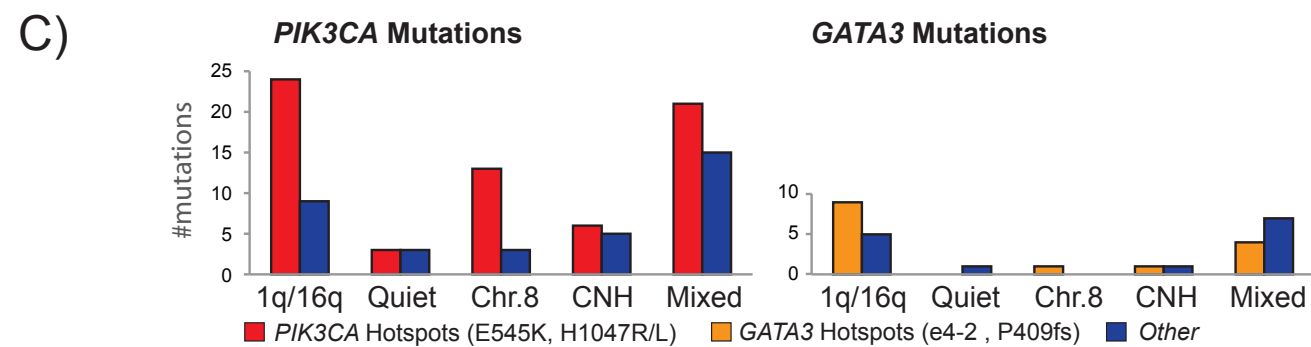
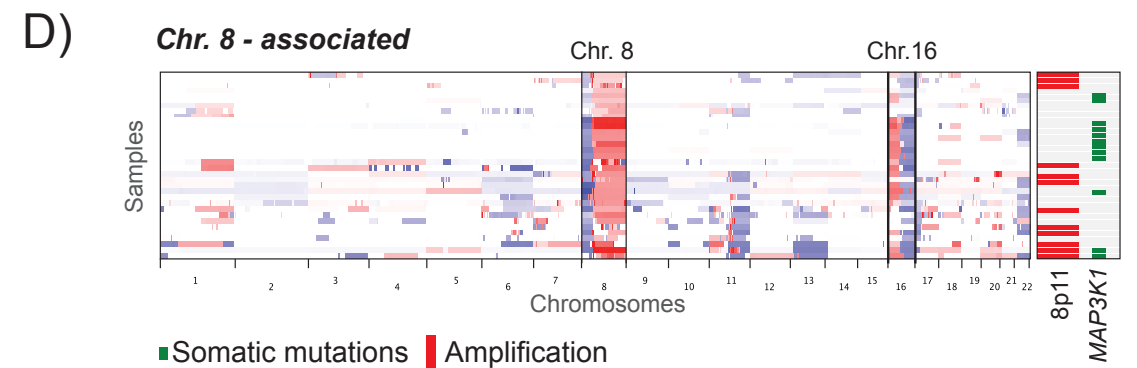
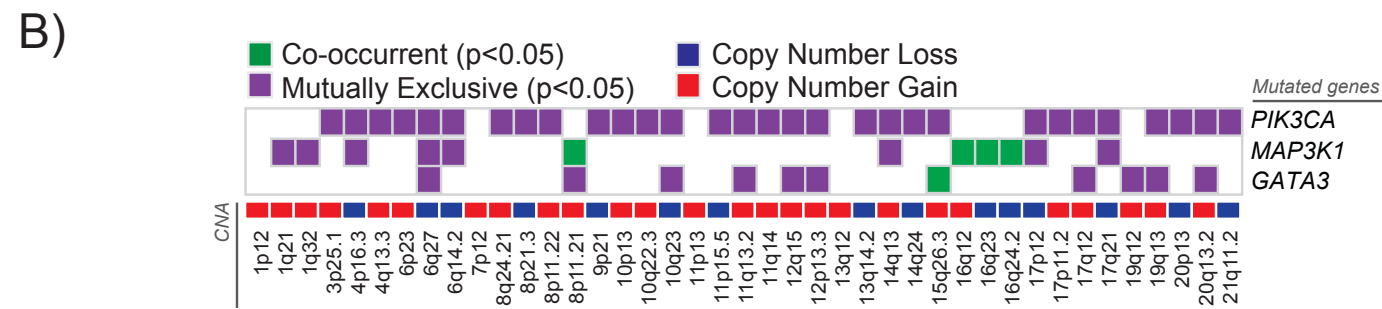
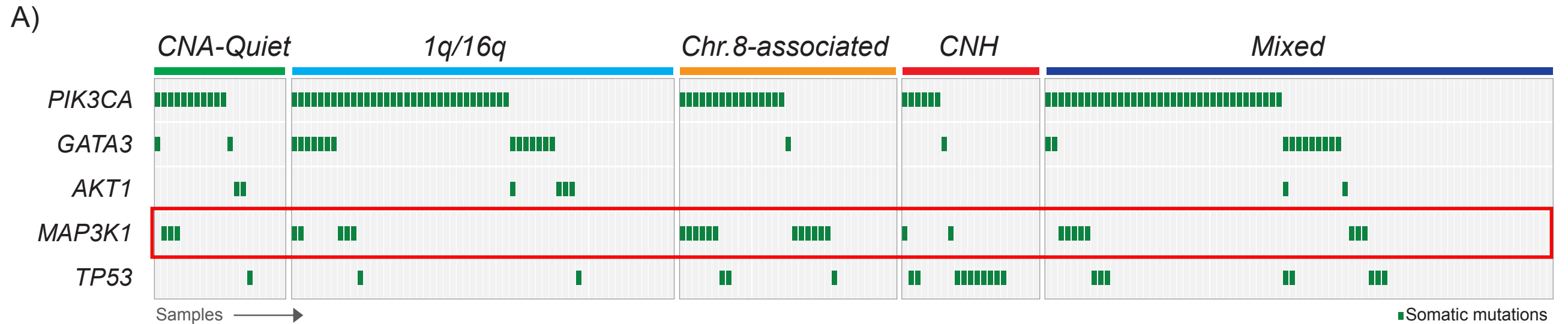
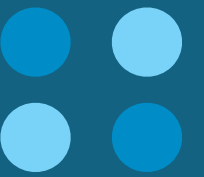
**What characterizes the other Luminal A subtypes?**

# Luminal A Somatic Mutations

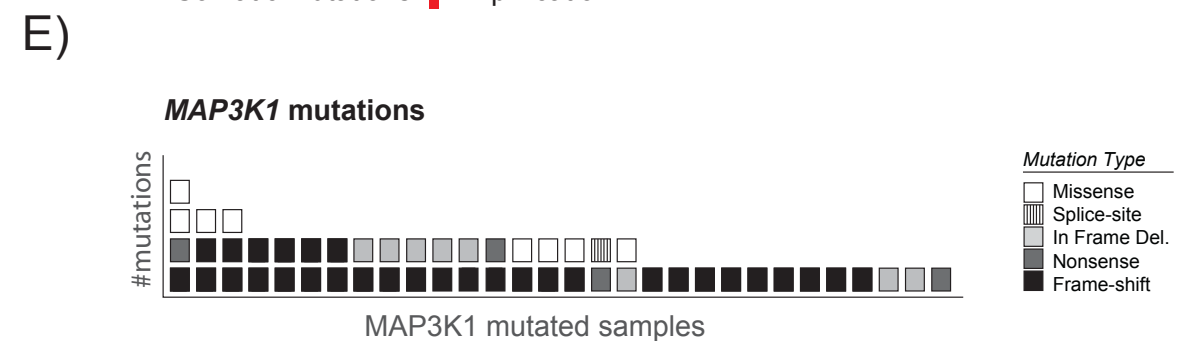
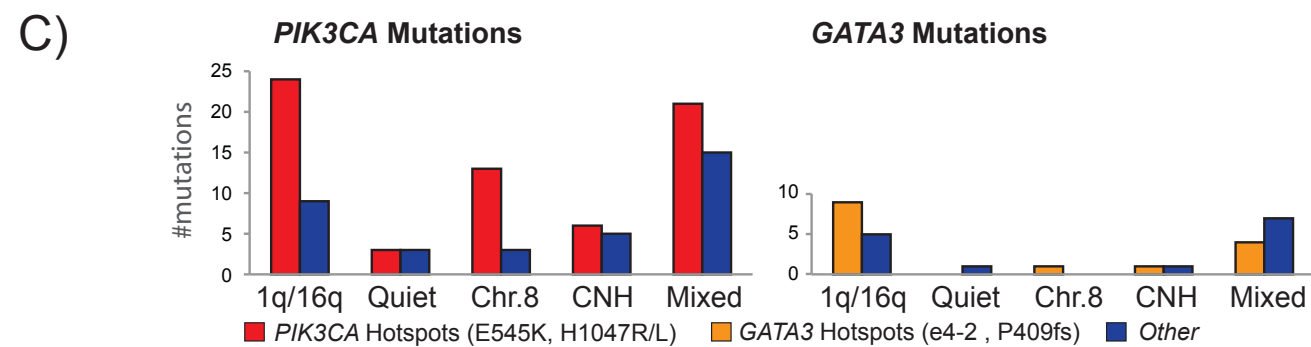
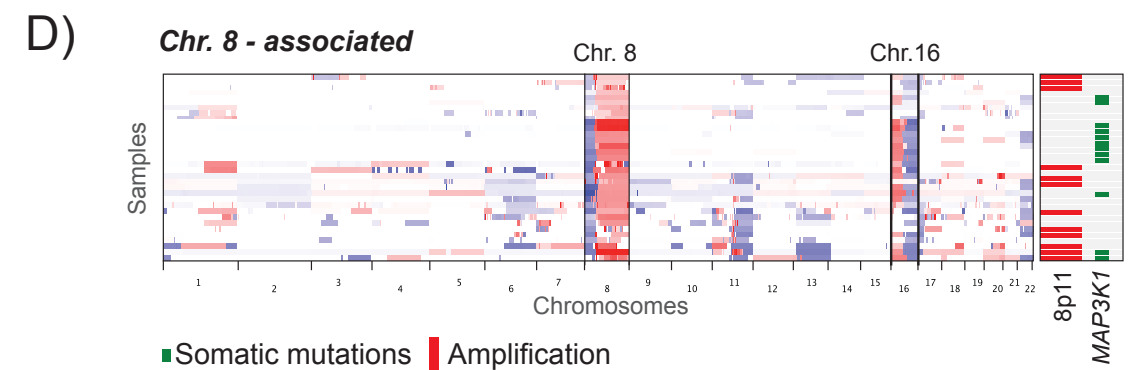
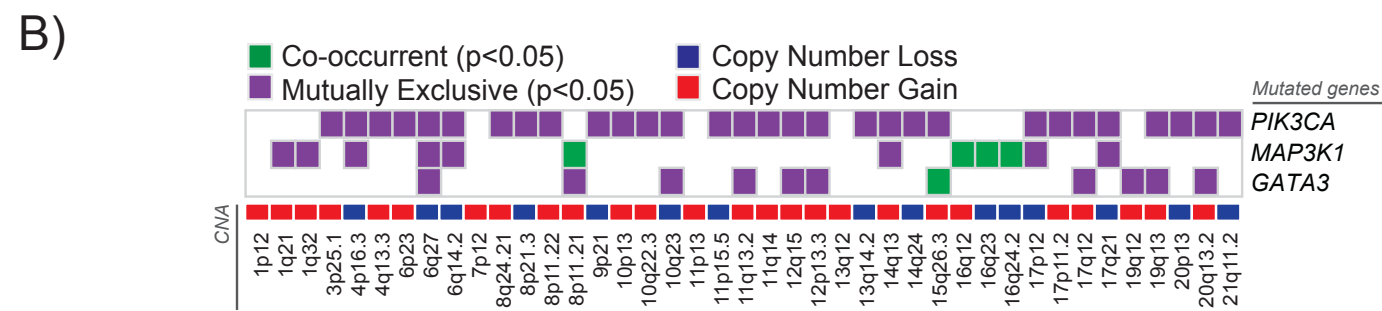
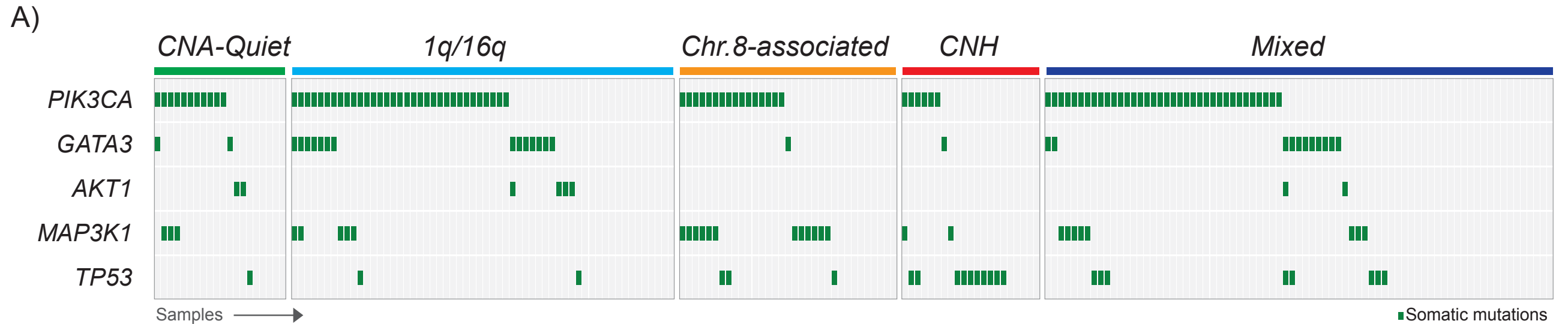
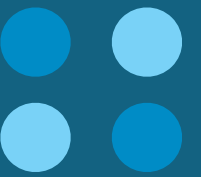




# Luminal A Somatic Mutations

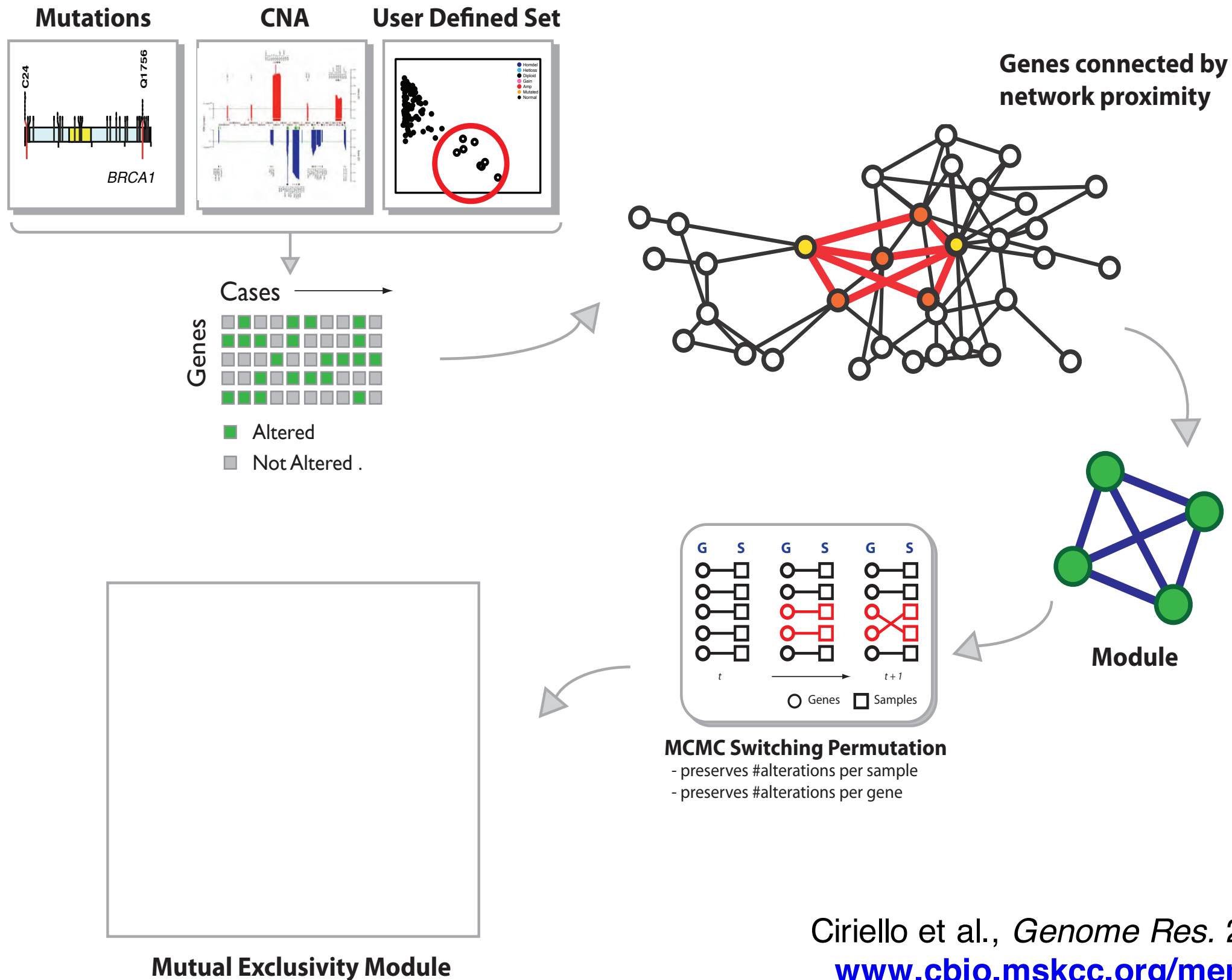


# Luminal A Somatic Mutations

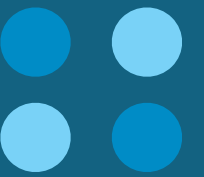


**Which pathways are most de-regulated?**

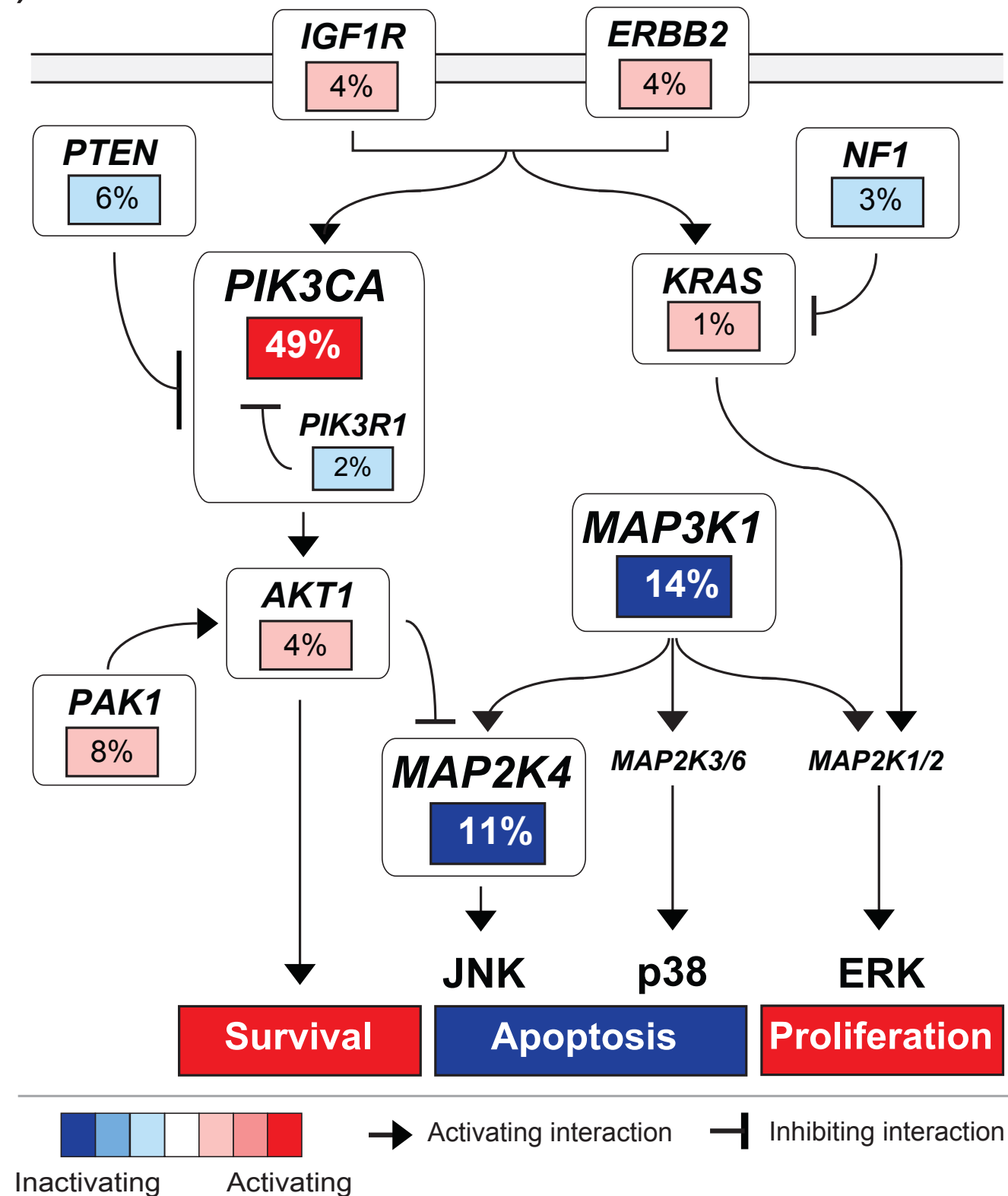
# MEMo: Mutual Exclusivity Modules



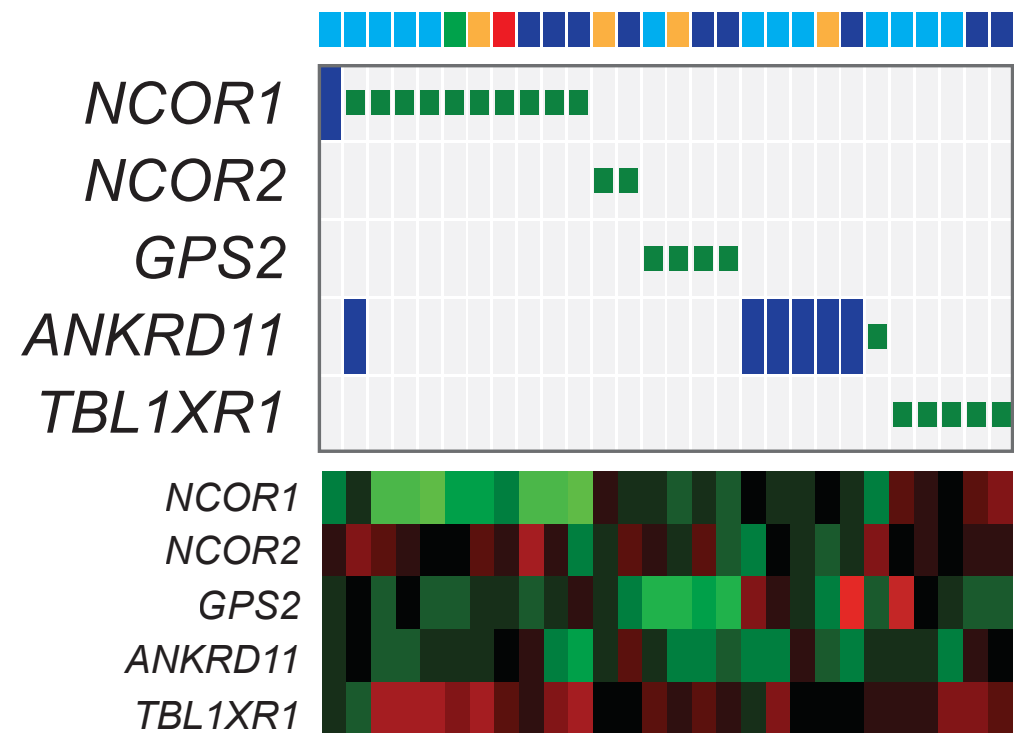
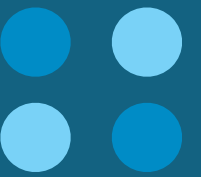
# Luminal A Pathways (MEMo)



A) 2



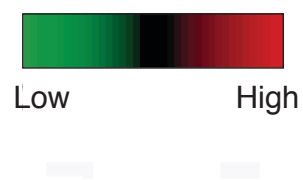
# Alterations to NCor/SMRT components



## Fingerprint

- Hom. Del
- Somatic mutation

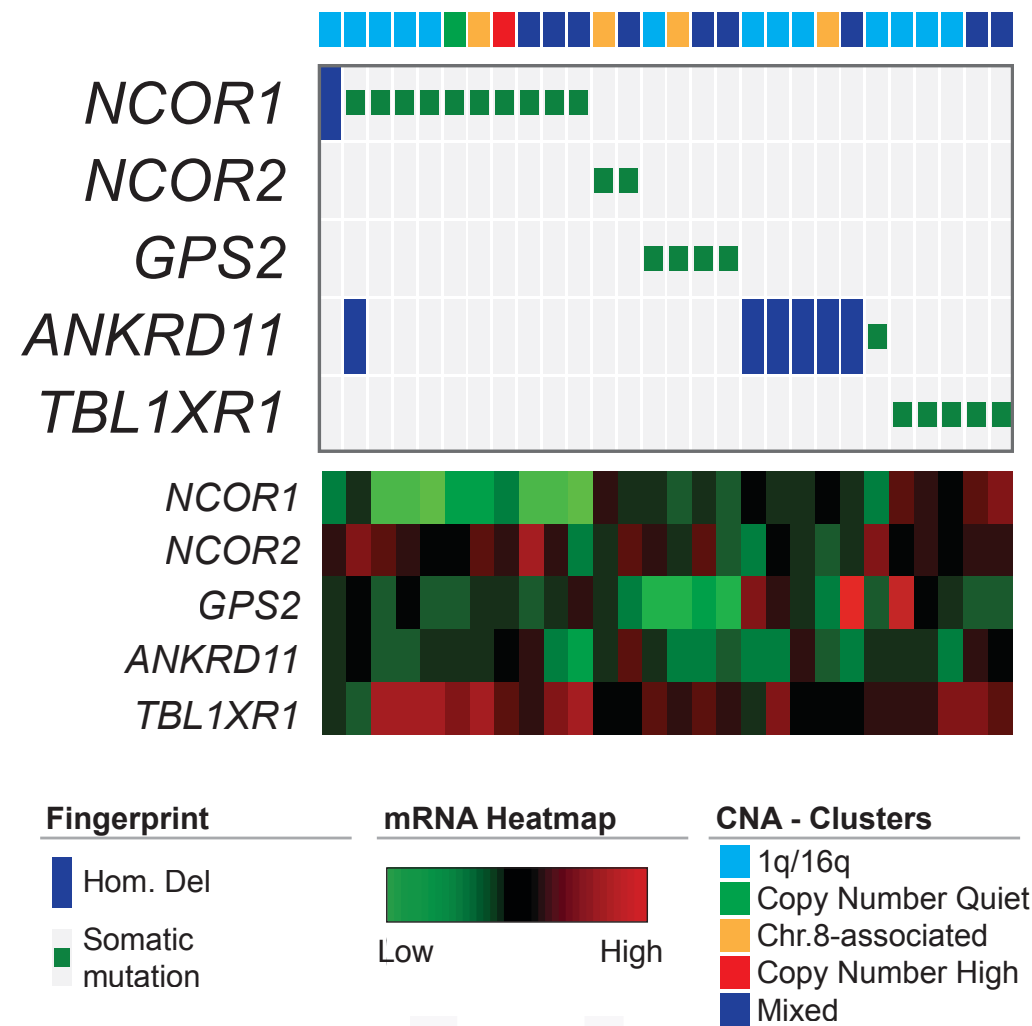
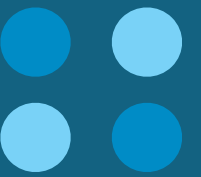
## mRNA Heatmap



## CNA - Clusters

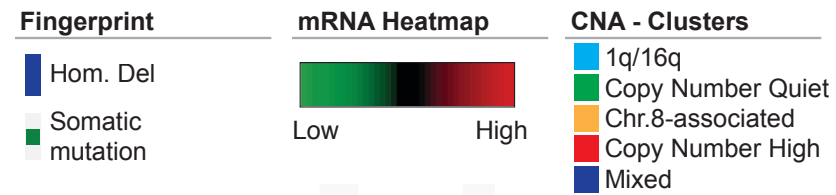
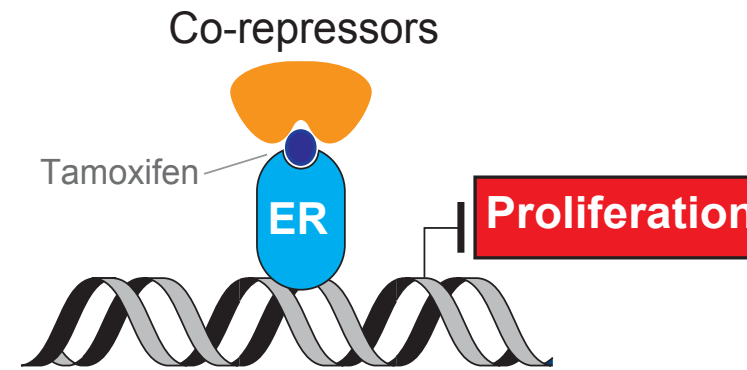
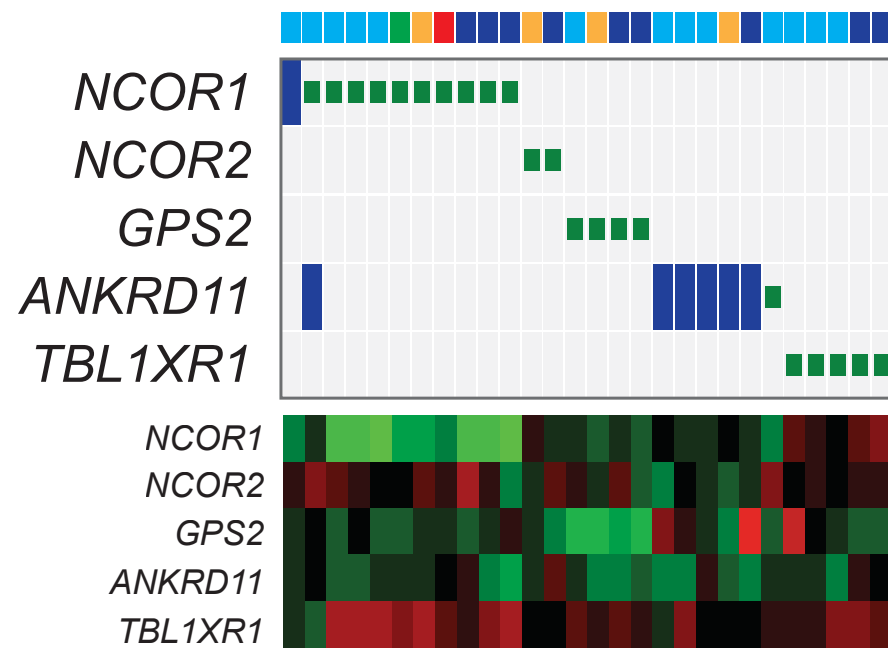
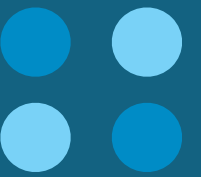
- 1q/16q
- Copy Number Quiet
- Chr.8-associated
- Copy Number High
- Mixed

# Alterations to NCor/SMRT components

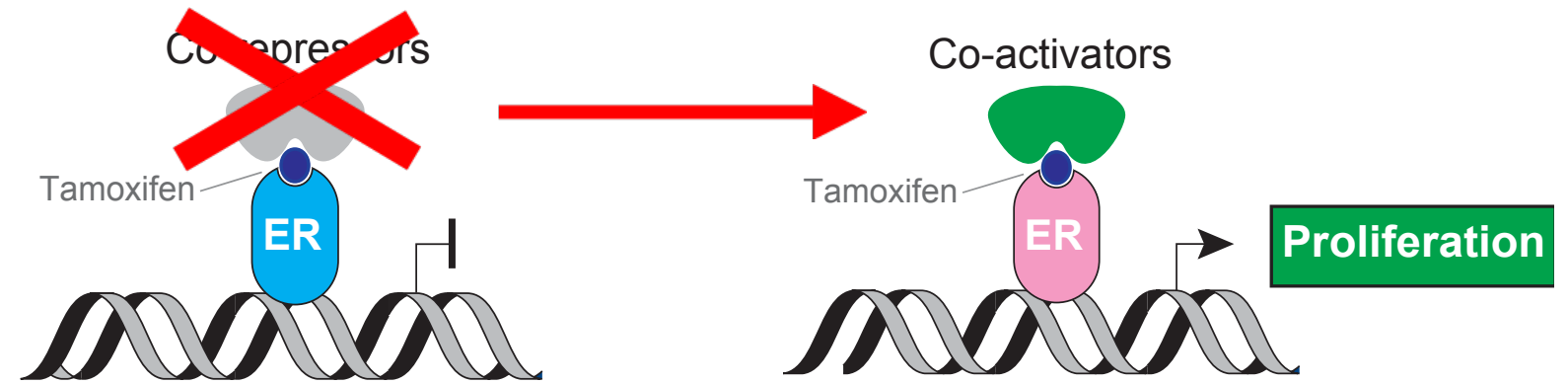
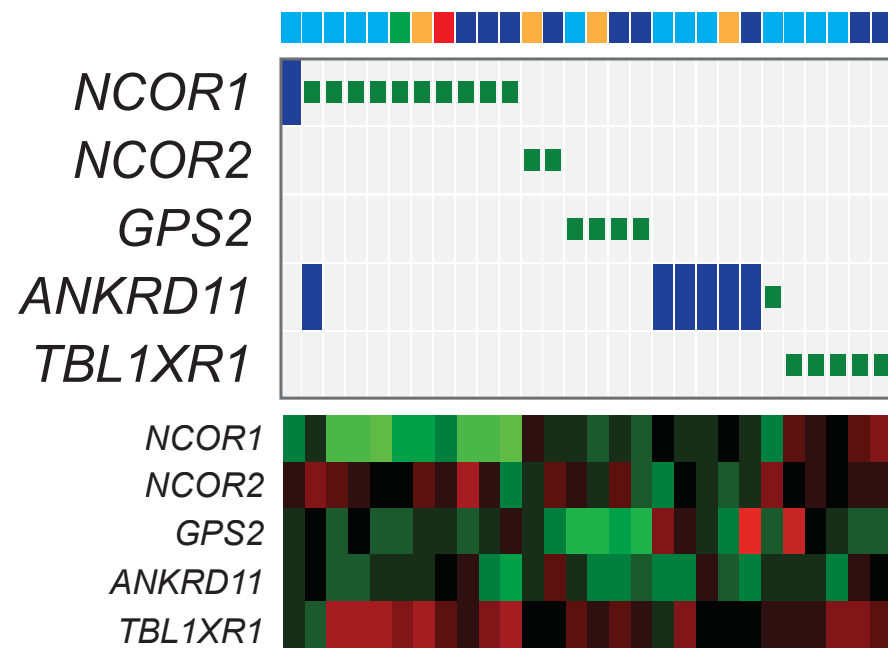
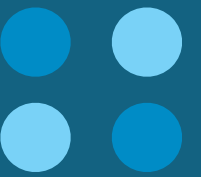


**Why are co-repressor complexes important in ER+ tumors?**

# NCor/SMRT are required for Tamoxifen effects



# NCor/SMRT are required for Tamoxifen effects



## Fingerprint

- Hom. Del
- Somatic mutation

## mRNA Heatmap

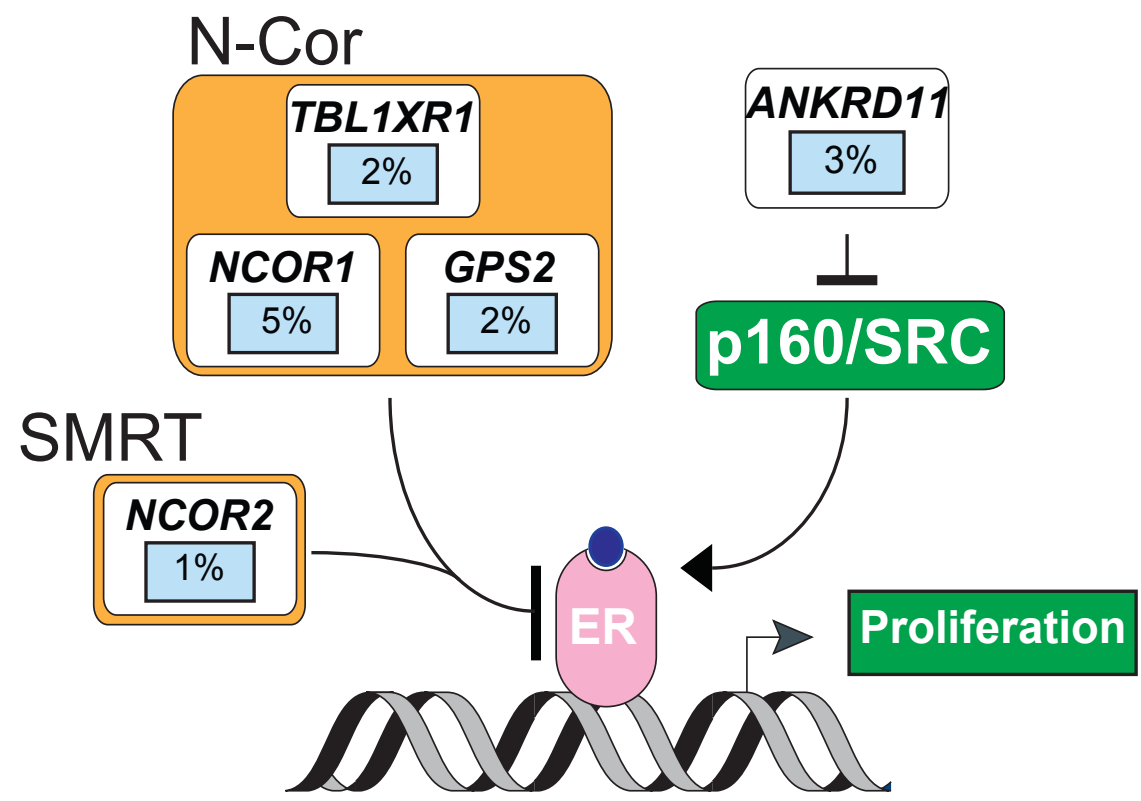
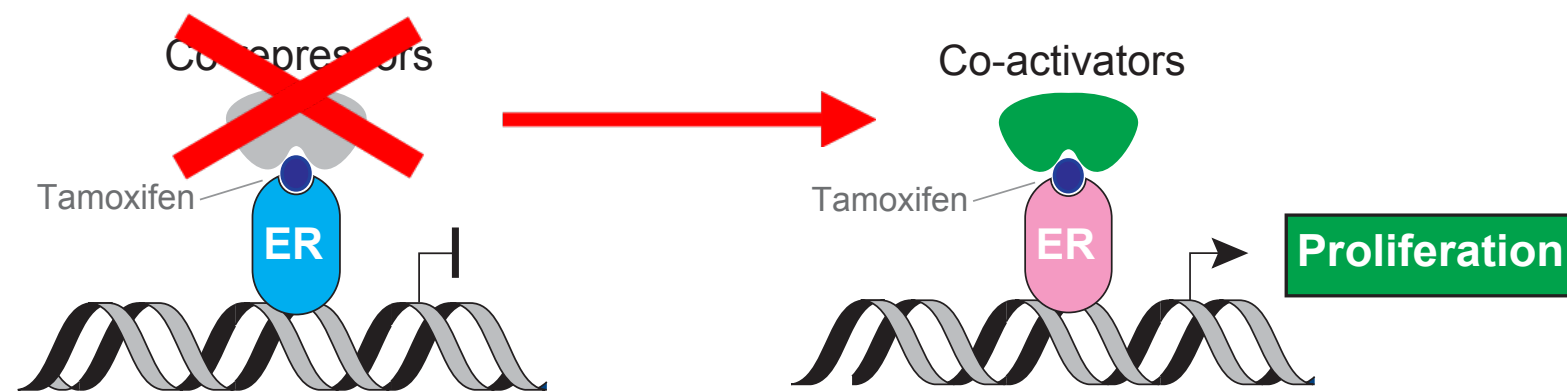
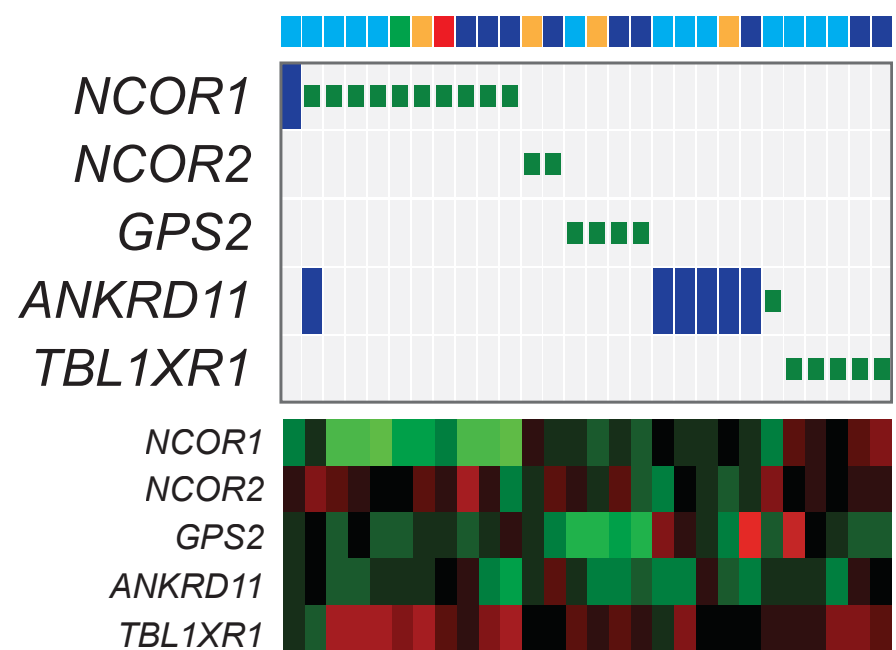
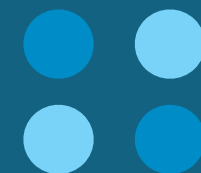


## CNA - Clusters

- 1q/16q
- Copy Number Quiet
- Chr.8-associated
- Copy Number High
- Mixed



# Loss of NCor/SMRT predicts resistance

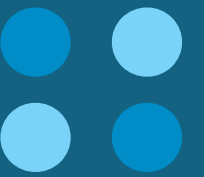


**Fingerprint**  
 Hom. Del  
 Somatic mutation

**mRNA Heatmap**  
 Low High

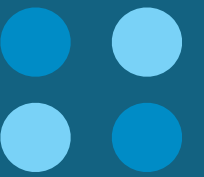
**CNA - Clusters**  
 1q/16q  
 Copy Number Quiet  
 Chr.8-associated  
 Copy Number High  
 Mixed

# Conclusions



- We dissected the genomics of **Luminal A tumors** in multiple datasets to explain their **molecular and clinical heterogeneity**
- **Four major subtypes** of Luminal A tumors
- **Atypical Luminal subtype** characterized by:
  - high genomic instability
  - p53 mutations
  - Aurora kinases up-regulation
  - poor prognosis
- Luminal A hallmark mutations are prevalent in tumors characterized by low copy number alterations
- We identified multiple rare, but mutually exclusive alterations associated with loss **NCor/SMRT**
  - These alterations may predict lack of response to endocrine therapy

# Thanks!



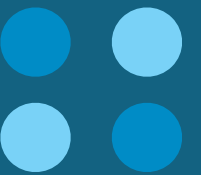
**Chris Sander**  
**Niki Schultz**  
**Rileen Sinha**  
Anders Jacobsen  
Boris Reva  
Xiaohong Jing  
Wei-Qing Wang



**Chuck Perou**  
**Katie Hoadley**

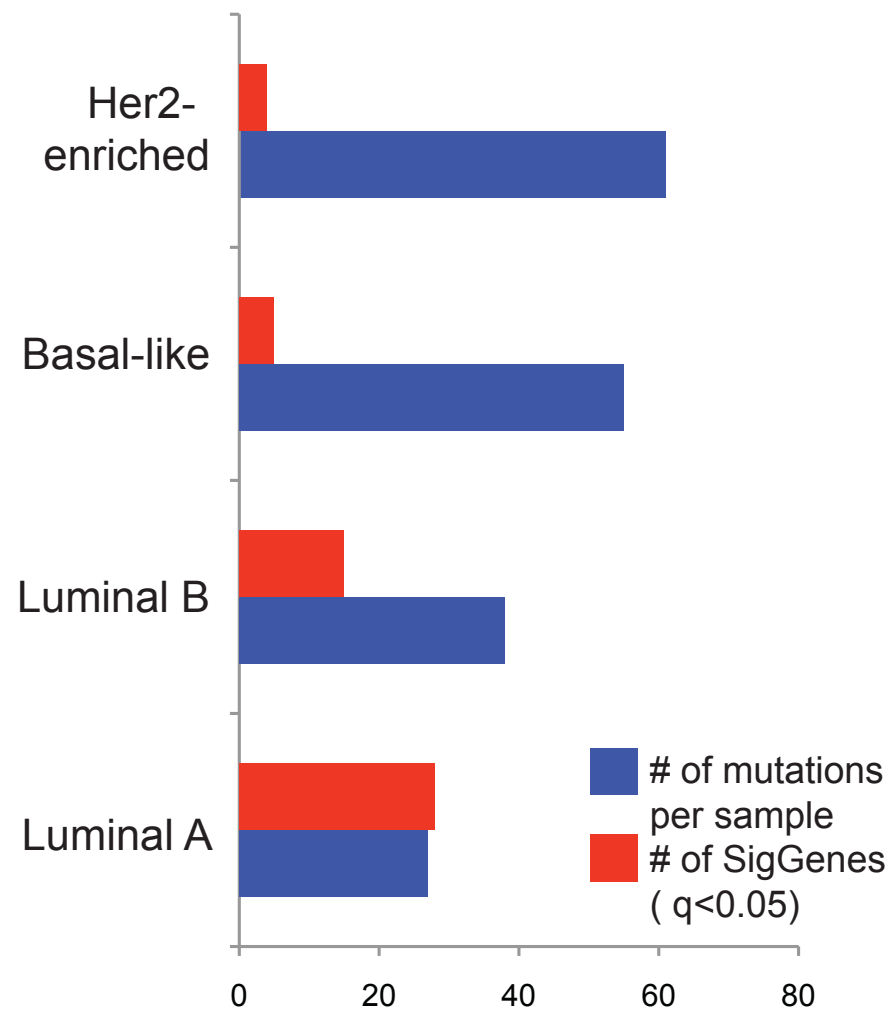
**...and the whole TCGA Breast AWG!**

# Appendix A



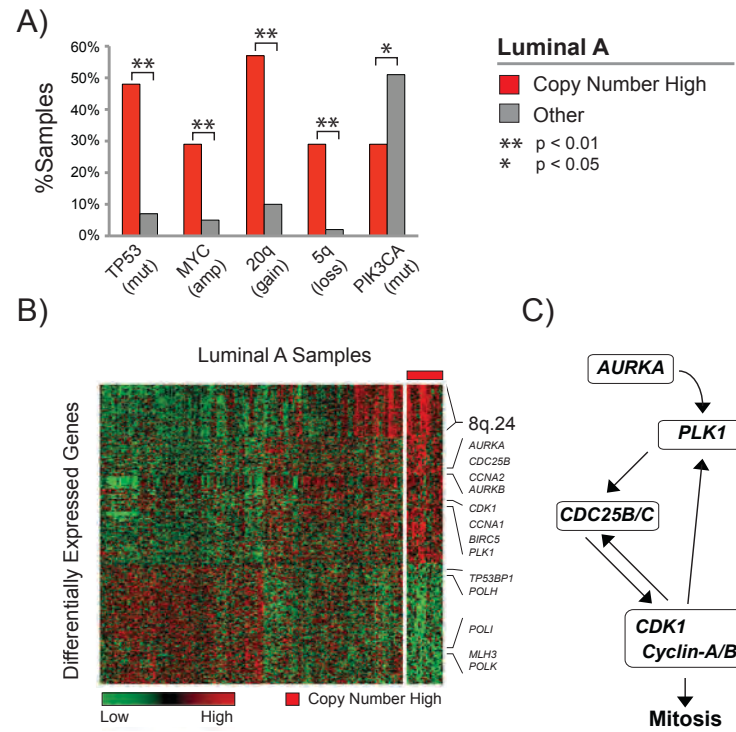
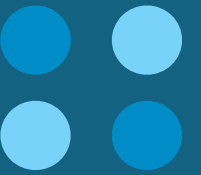
## Luminal A Recurrently Mutated Genes ( $q < 0.05$ )

data from TCGA, Ellis et al., Banerji et al



*PIK3CA*      *RUNX1*      *DGKG*  
*MAP3K1*      *CTCF*      *SMCHD1*  
*GATA3*      *CBFB*      *KRAS*  
*TP53*      *SF3B1*      *CCND3*  
*CDH1*      *MED23*      *NKAIN4*  
*MLL3*      *WNT7A*      *HIST2H2BE*  
*MAP2K4*      *TBL1XR1*      *HIST1H3B*  
*NCOR1*      *TBX3*      *SHD*  
*AKT1*      *GPS2*      *GPR32*  
*PTEN*      *FOXA1*

# Appendix B



**CNH tumors are ER+**

**ER Positive Targets (BRCA\_ER\_POS)**

ClassA (positively correlated)    ClassB (negatively correlated)

$p < 10^{-3}$ , FDR = 0.03

# Appendix B

