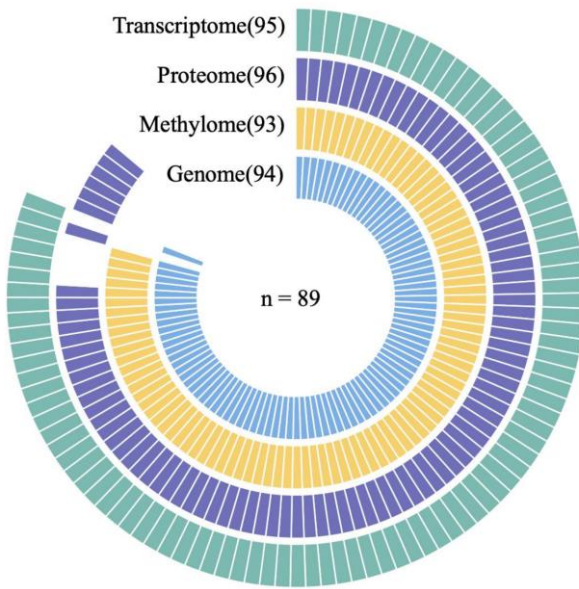
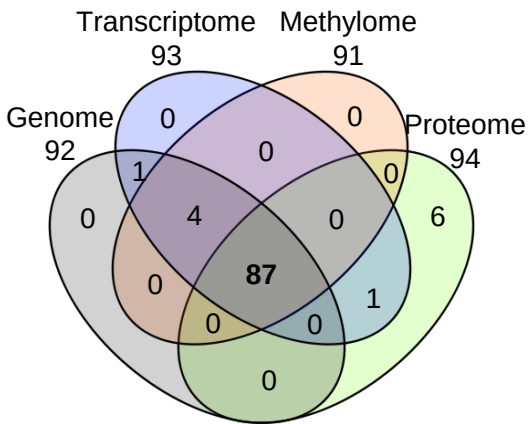
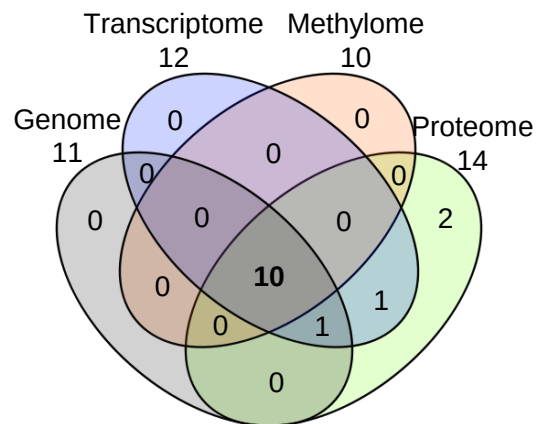


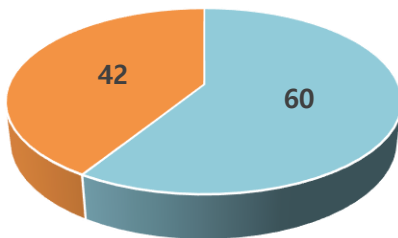
a

**Data status**

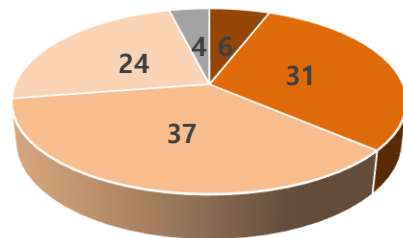
b

**Primary tumor (patients)****Recurrent tumor (patients)**

c

**Gender (patients)**

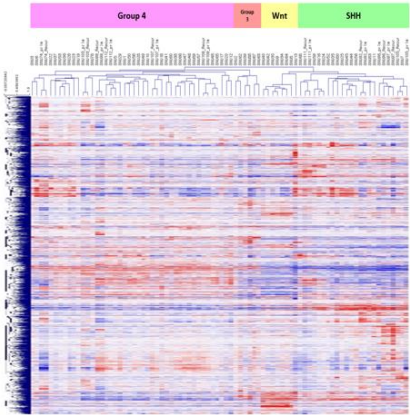
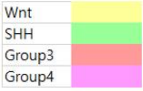
Male Female

**Age (patients)**

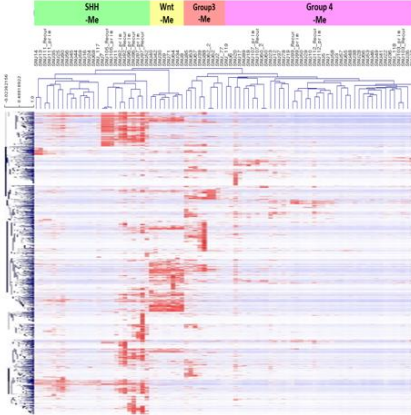
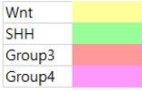
15+ 10~15 5~10 0~5 Unknown

a  
Unsupervised hierarchical clustering

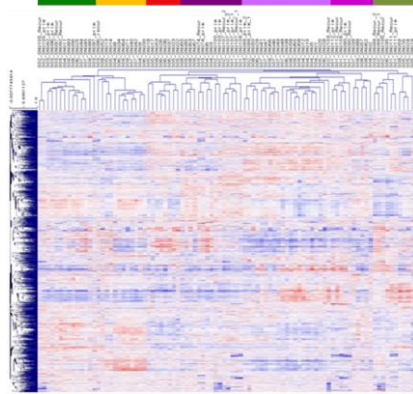
Transcriptome



DNA methylome

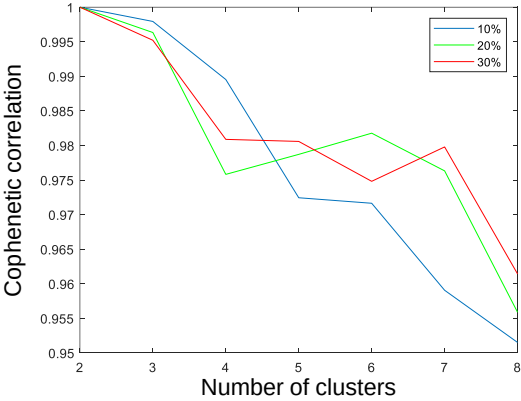


Proteome

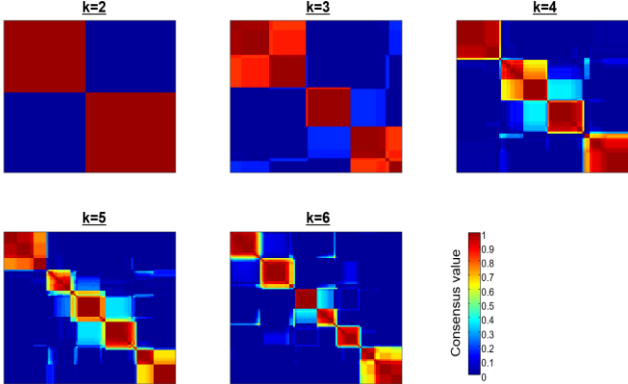


b  
NMF clustering

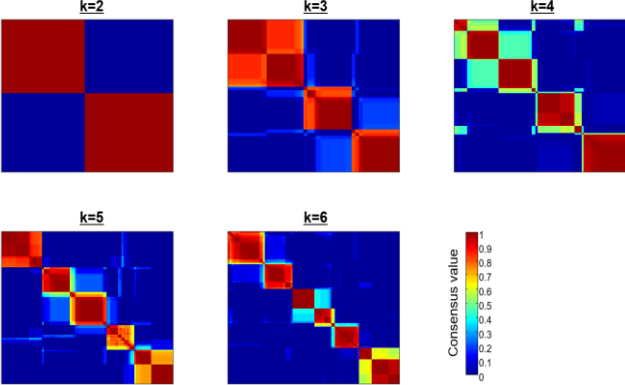
Cophenetic correlation  
- 1356, 2712, and 4067 genes (MAD>10%, 20%, and 30%)



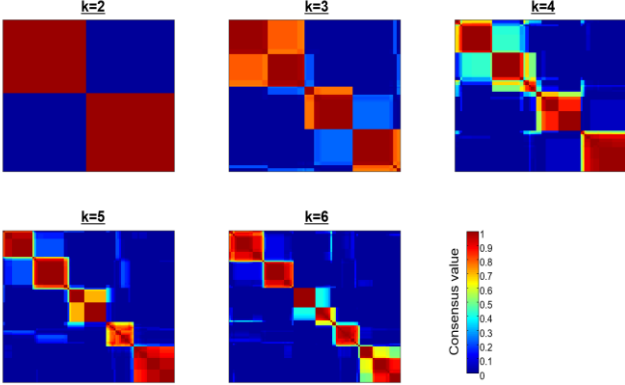
Cophenetic correlation (MAD>10%)



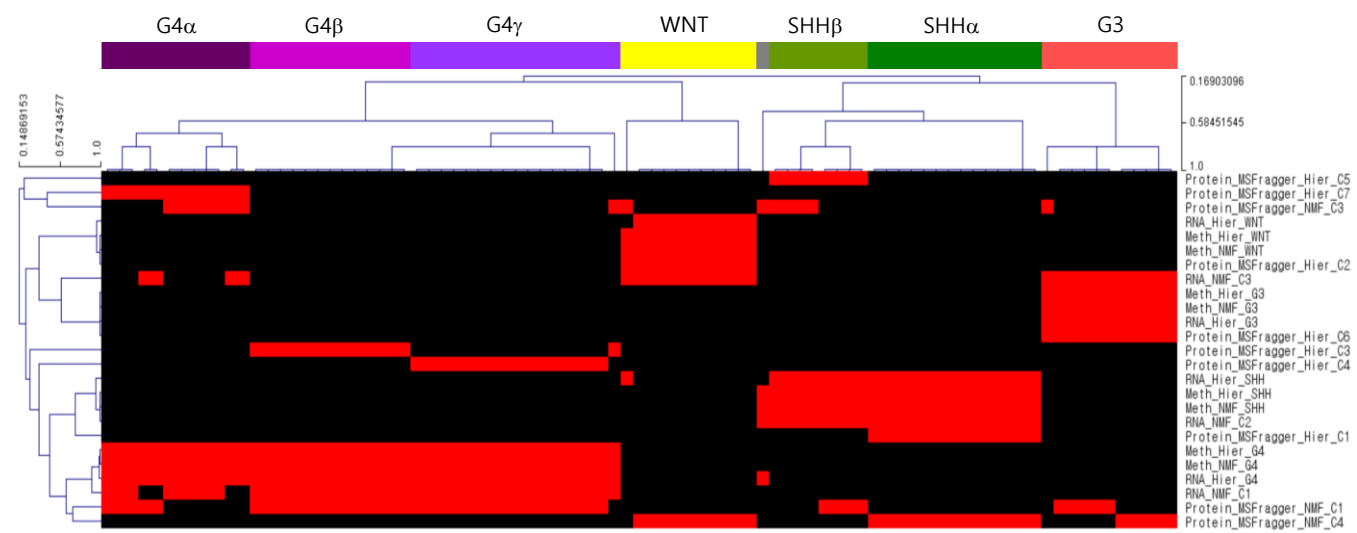
Cophenetic correlation (MAD>20%)



Cophenetic correlation (MAD>30%)

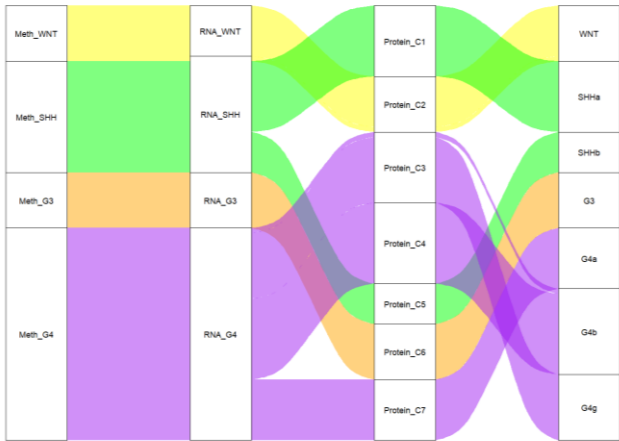


Subtyping with multiome analysis

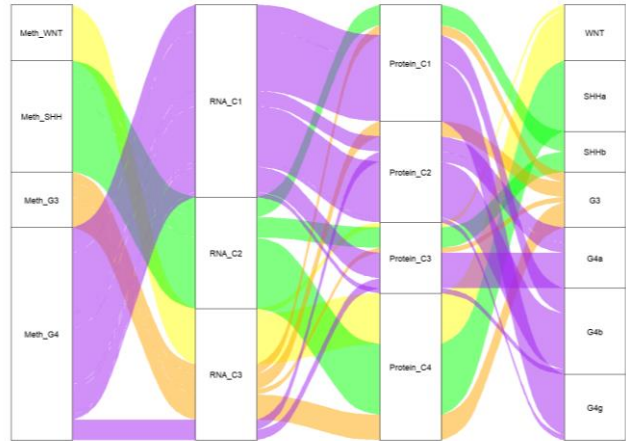


Sample migration by single platform clusters

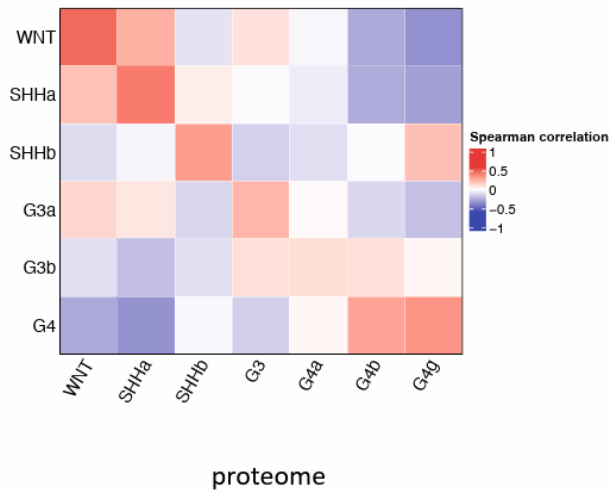
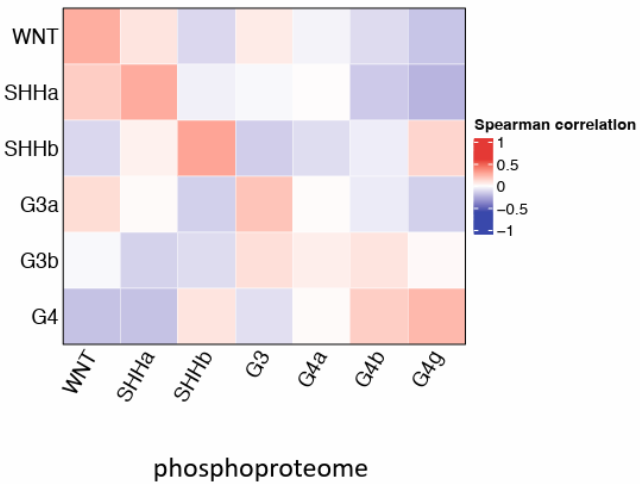
Hierarchical clustering



NMF clustering

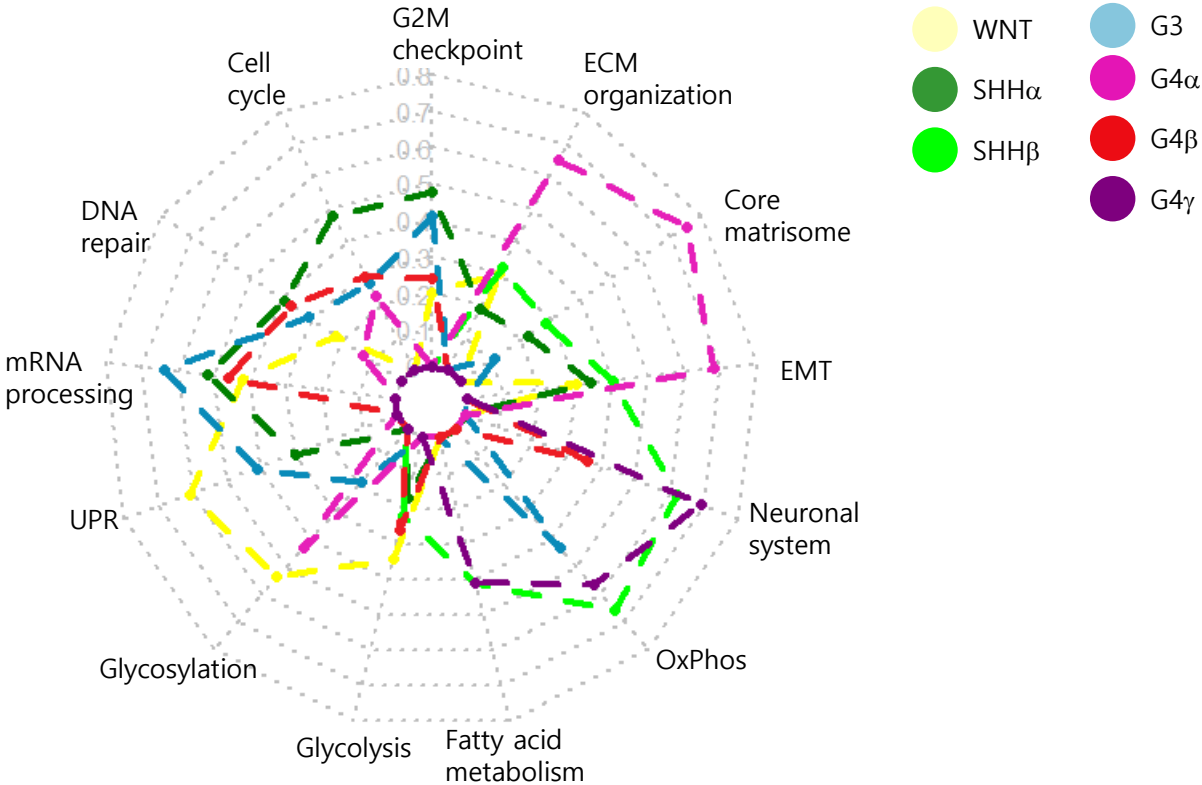


Correlation between subtypes  
(our own data vs. public dataset)  
(Archer et al.,2018)



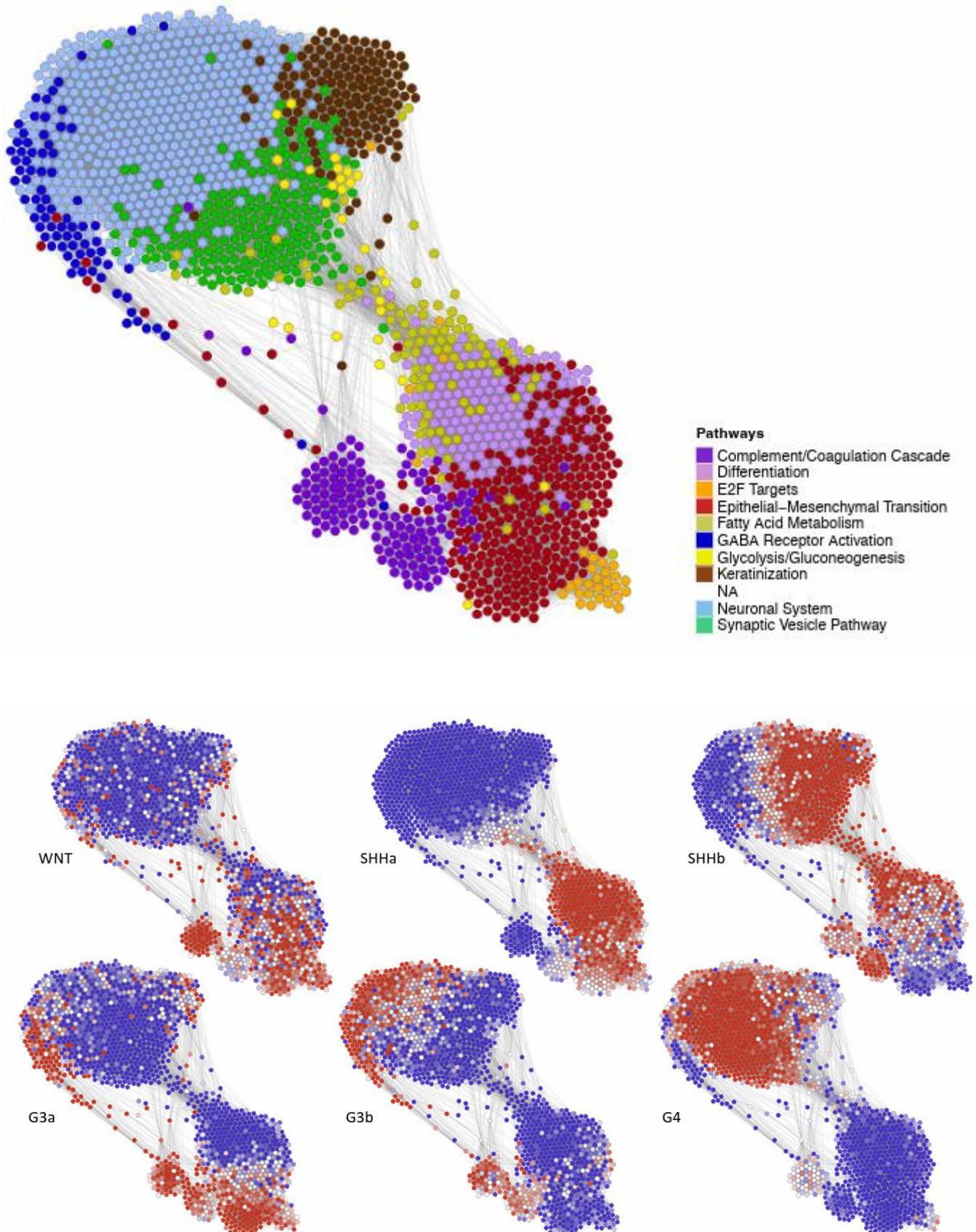


Function by subtype

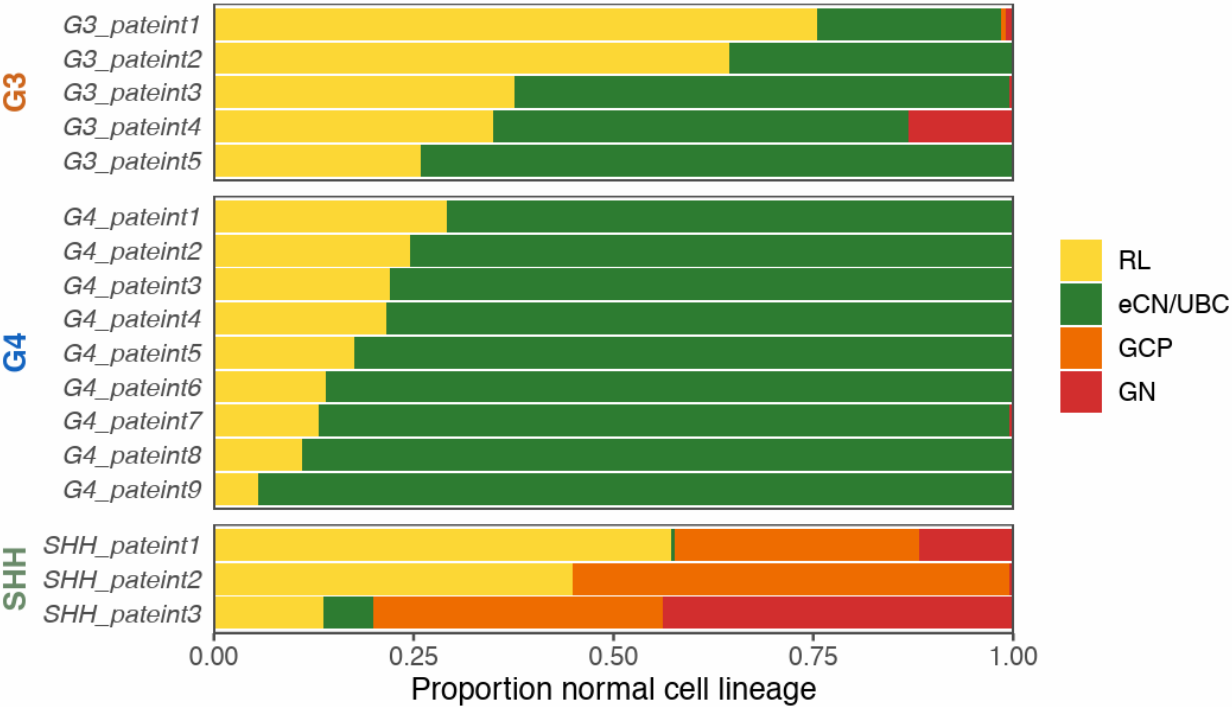




Correlation network and subtype-specific expression in public dataset  
(Archer et al.,2018)

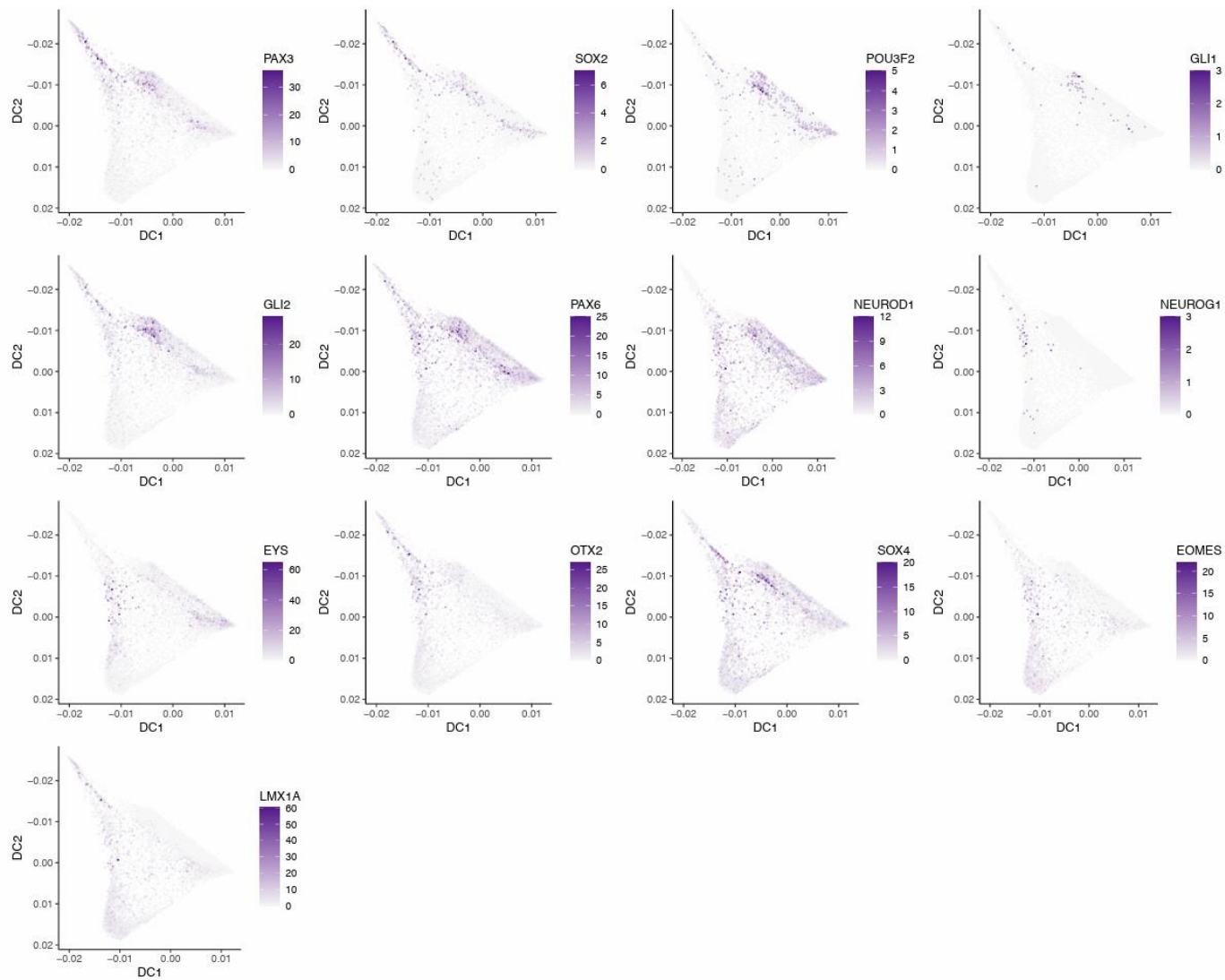


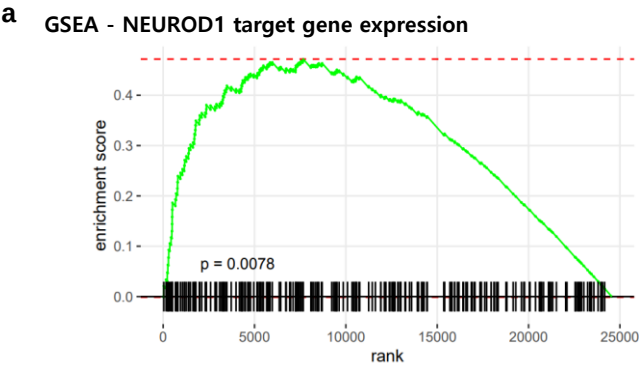
Proportion of cell lineage in medulloblastoma tissues  
(scRNA-seq from Michael Taylor's group)



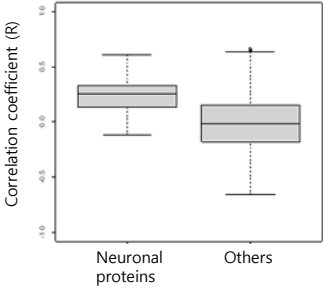


Lineage-related gene expression on Diffusion map  
(scRNA-seq, Smith et al., 2022)

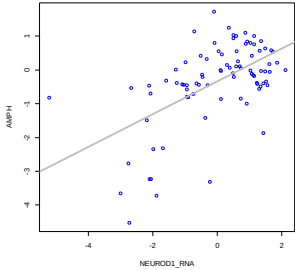




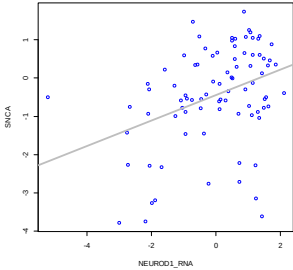
**b** NEUROD1 RNA-neurotype 86 protein correlation (R)  
 $p < 2.2 \times 10^{-16}$  by t-test



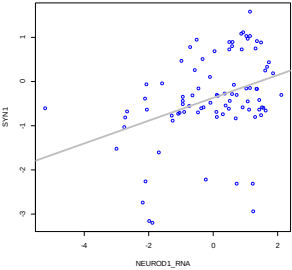
**c** AMPH – NEUROD1 RNA  
 $R = 0.5669745$   
 $p = 1.262 \times 10^{-8}$



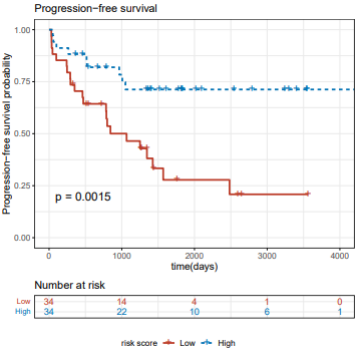
SCNA – NEUROD1 RNA  
 $R = 0.3653281$   
 $p = 0.0005428$



SYN1 – NEUROD1 RNA  
 $R = 0.3676445$   
 $p = 0.0004971$



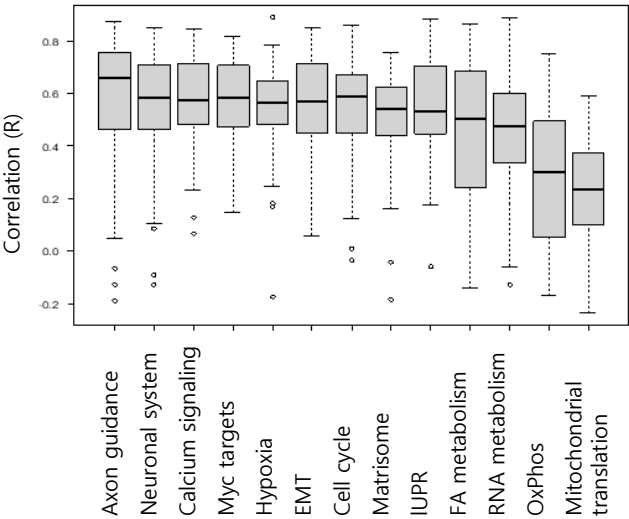
**d** PFS in non-WNT patients  
NEUROD1 RNA



a

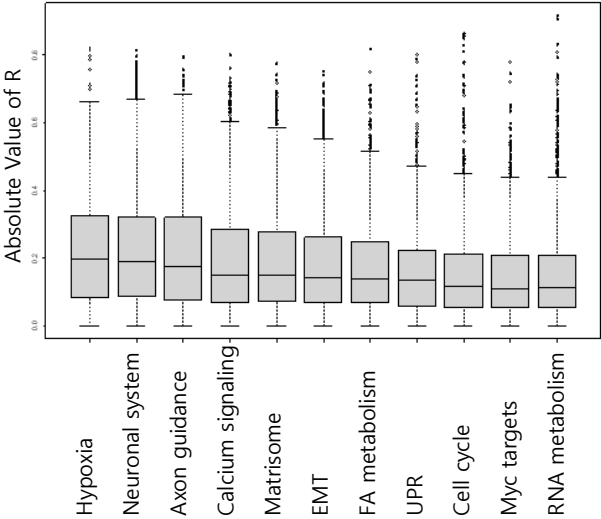
Correlation

Protein expression - RNA expression

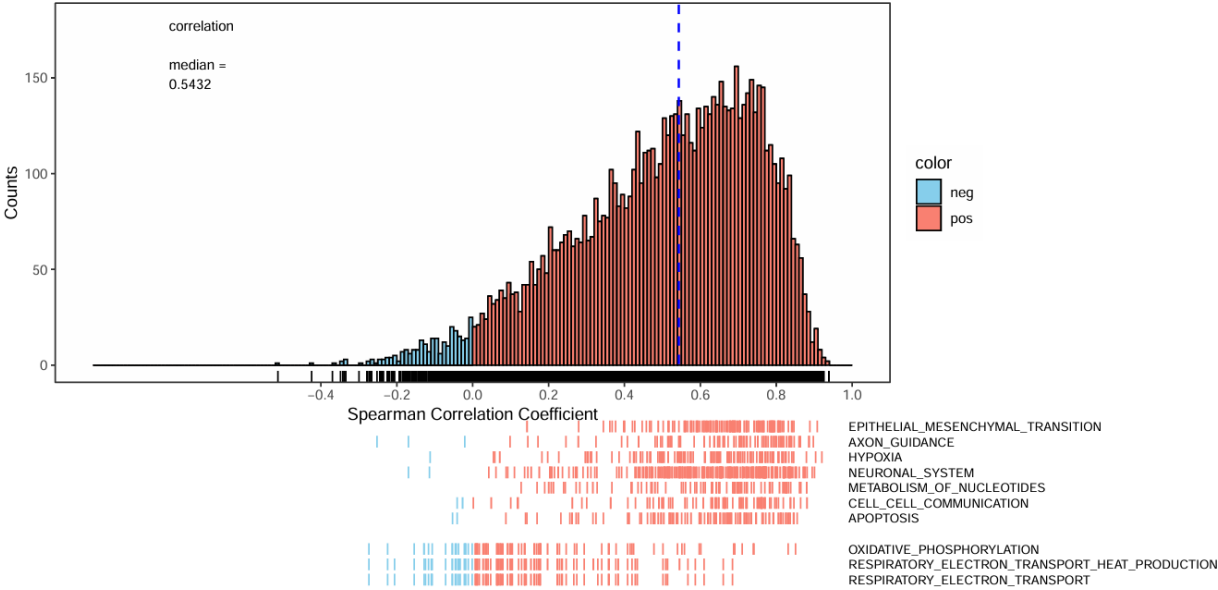


b

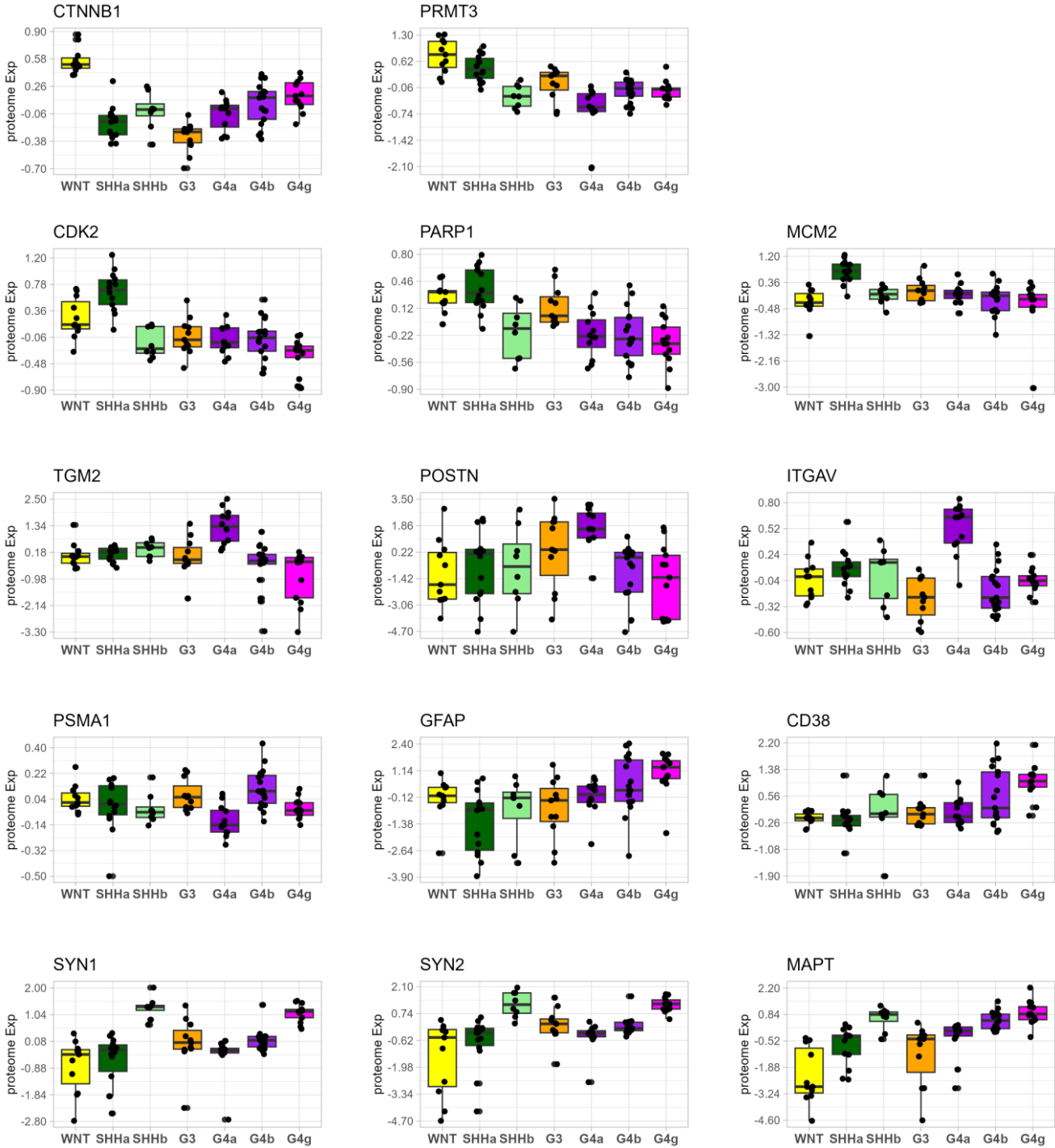
DNA methylation – RNA expression

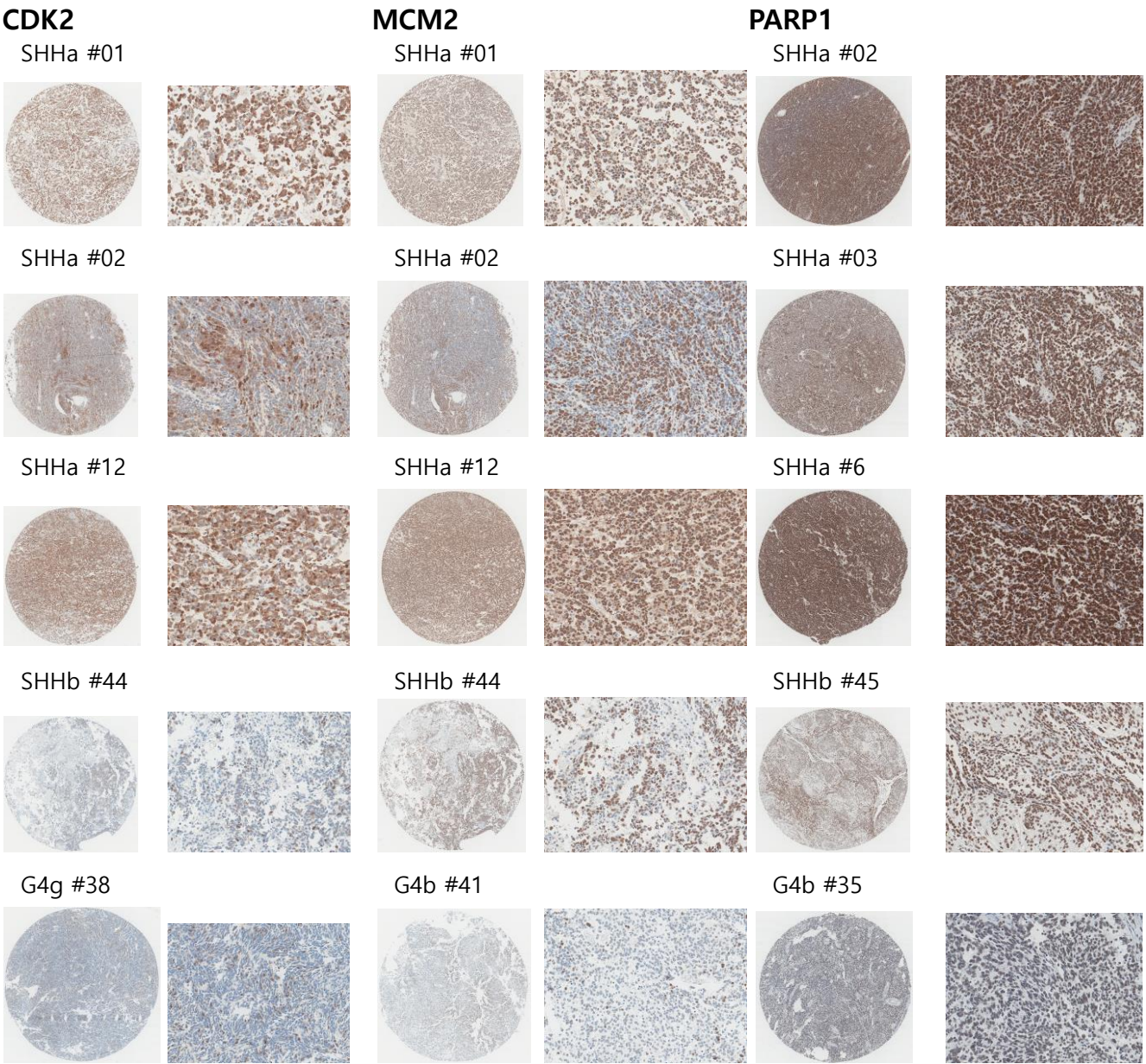


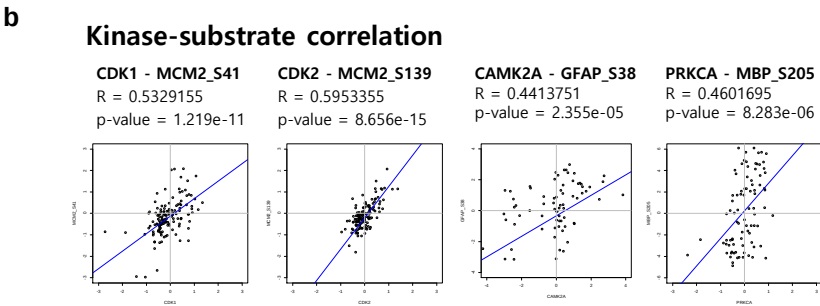
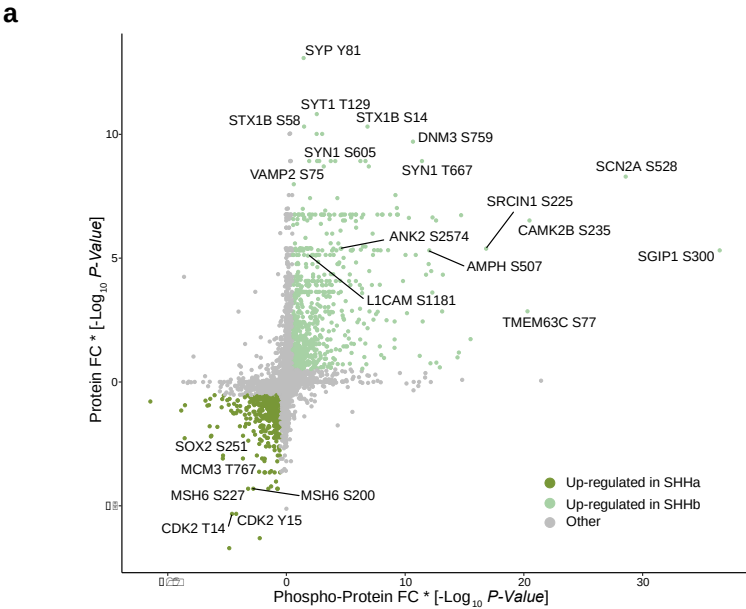
c



Subtype-specific protein expression

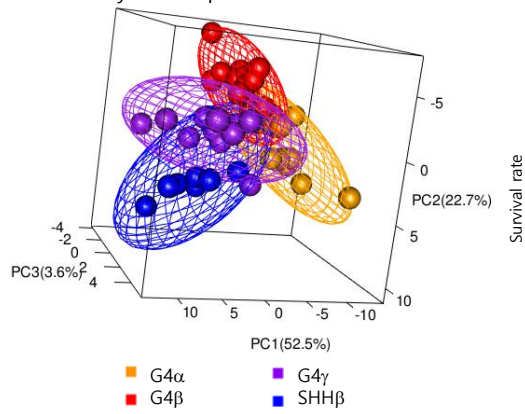




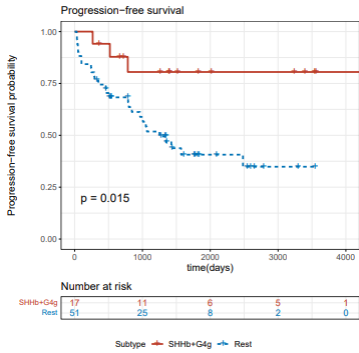




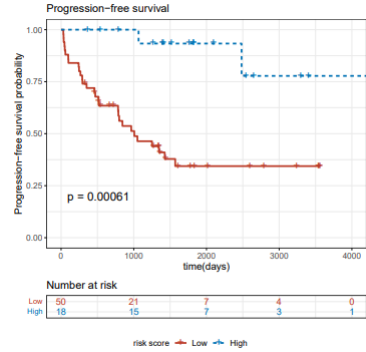
**a** PCA analysis with proteome



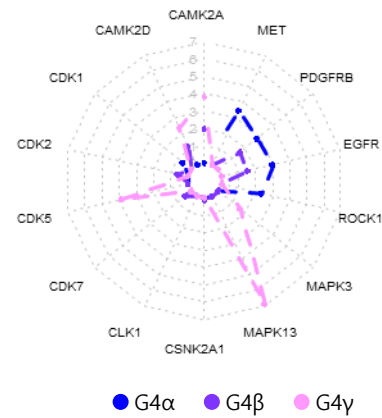
**b** Non-WNT medulloblastoma



**c** Non-WNT medulloblastoma  
Synaptic signaling proteins

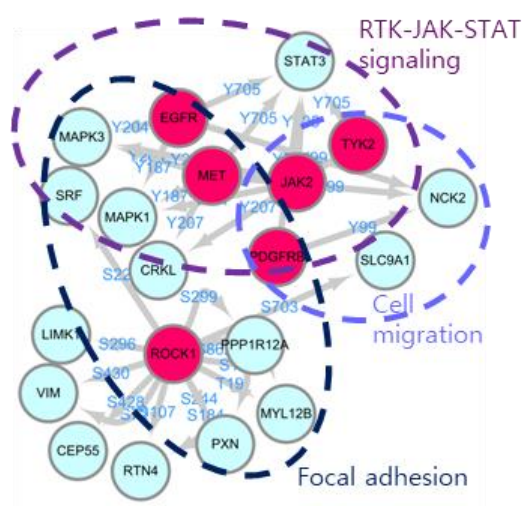


Kinase z-score (KSEA)

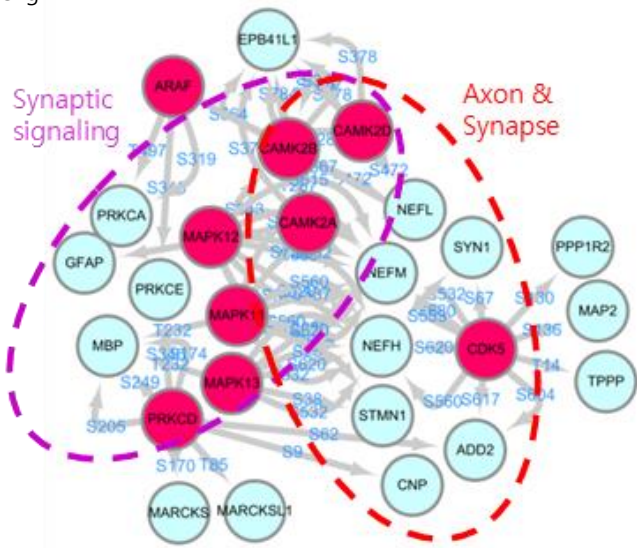


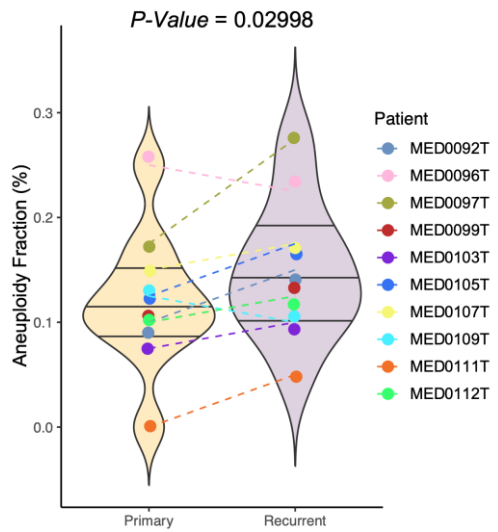
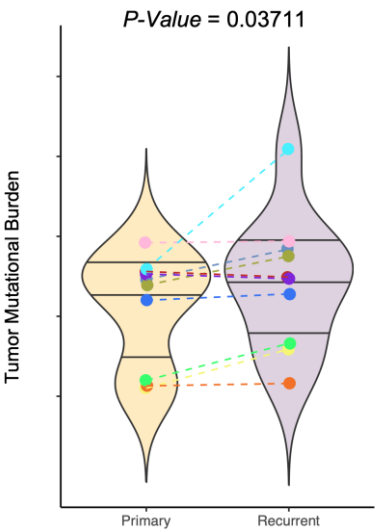
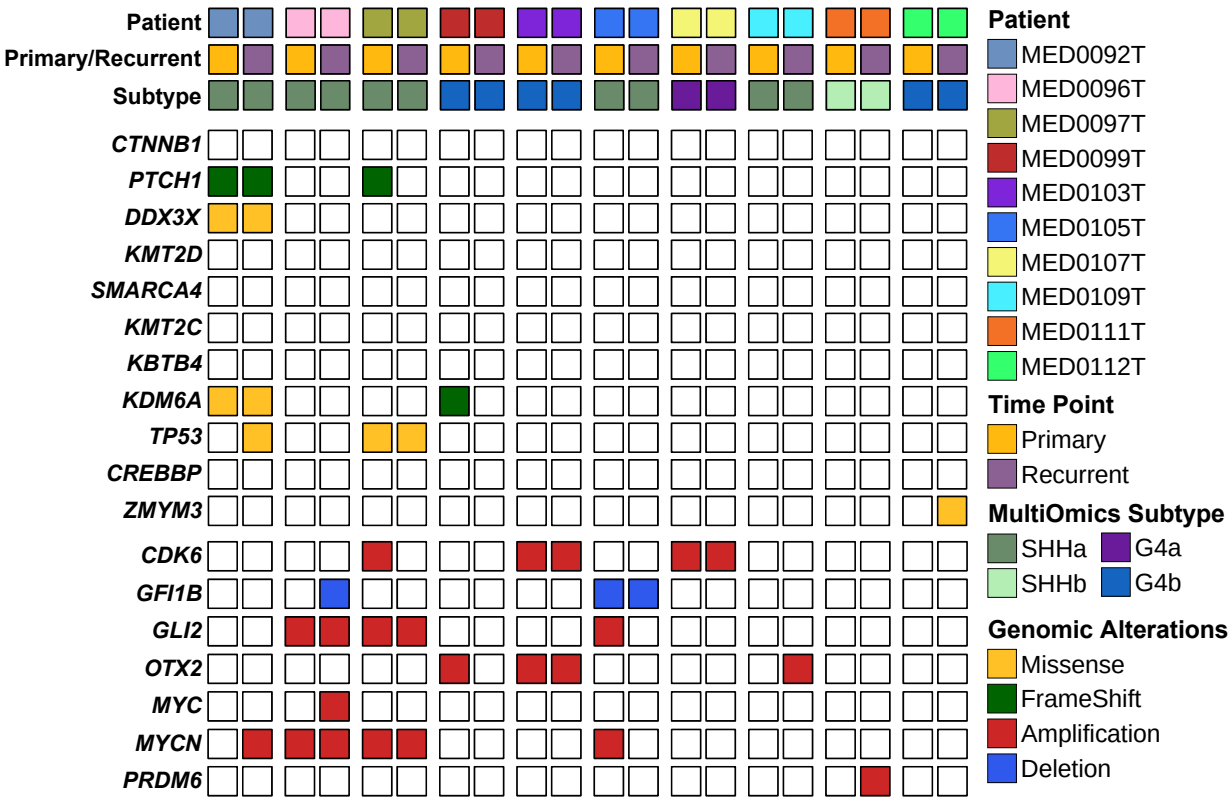
Kinase-substrate network

G4a

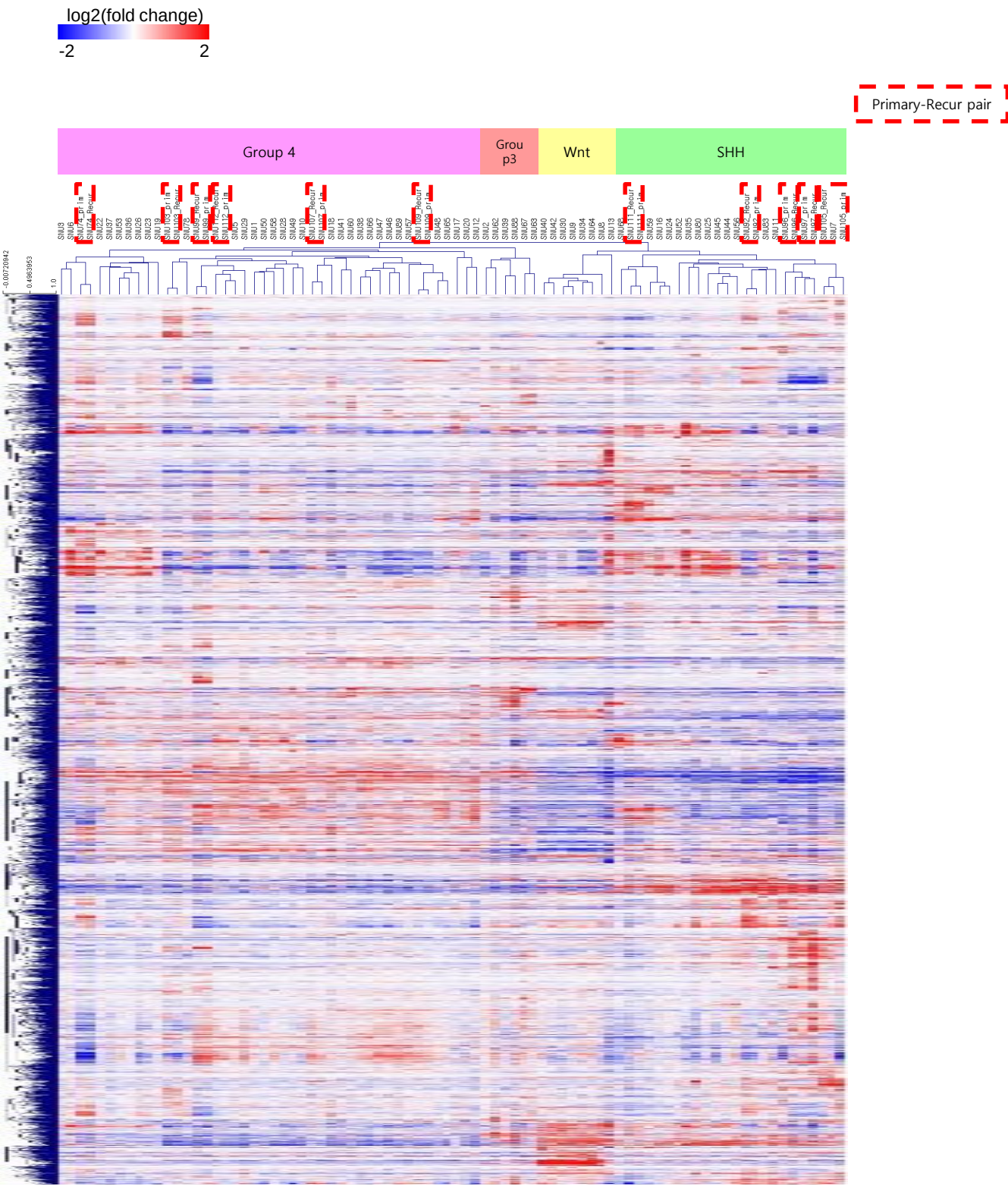


G4g



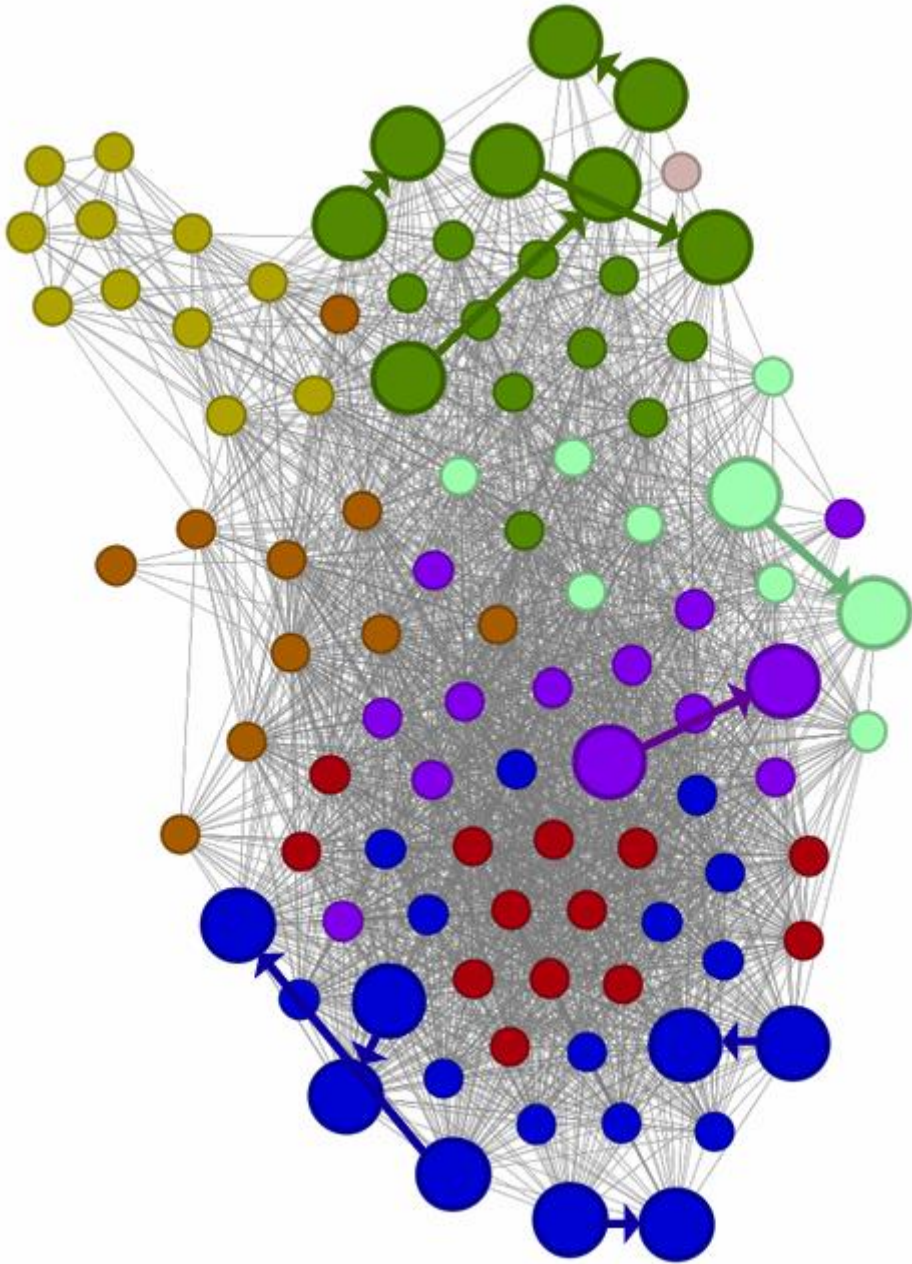


RNA-seq (Hierarchical clustering)

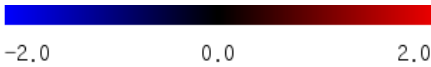




Cell type migration by recurrence on correlation network (RNA)

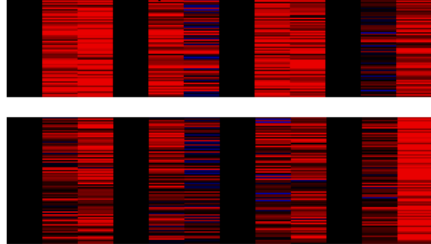


Recurrence patterns (Proteome)

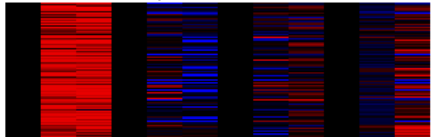


SHHa\_NRP  
SHHa\_RPP  
SHHa\_Recur  
SHHb\_NRP  
SHHb\_RPP  
SHHb\_Recur  
G4a\_NRP  
G4a\_RPP  
G4a\_Recur  
G4b\_NRP  
G4b\_RPP  
G4b\_Recur

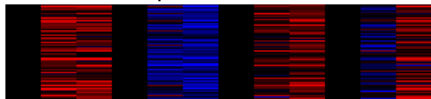
Recurrence promotion



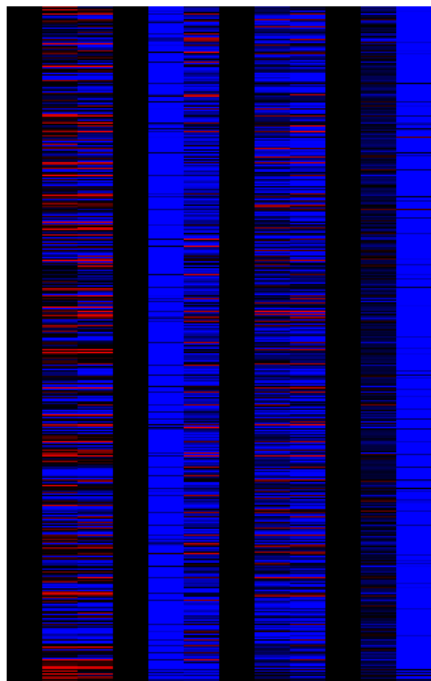
SHHa-specific  
Recurrence promotion



SHHa-, G4a-specific  
Recurrence promotion

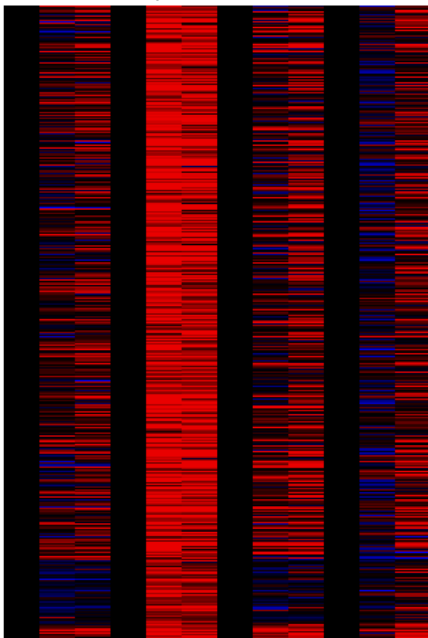


Recurrence inhibition

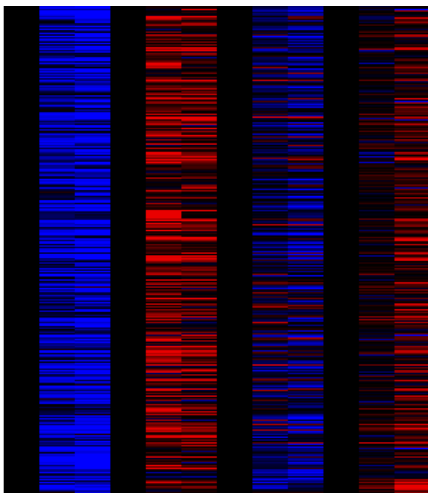


SHHa\_NRP  
SHHa\_RPP  
SHHa\_Recur  
SHHb\_NRP  
SHHb\_RPP  
SHHb\_Recur  
G4a\_NRP  
G4a\_RPP  
G4a\_Recur  
G4b\_NRP  
G4b\_RPP  
G4b\_Recur

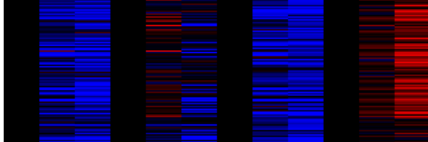
SHHb-specific  
Recurrence promotion



SHHa-specific  
Recurrence inhibition

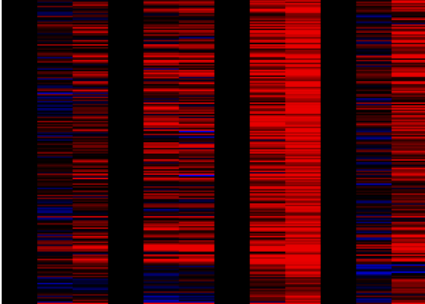


SHHa-, G4a-specific  
Recurrence inhibition

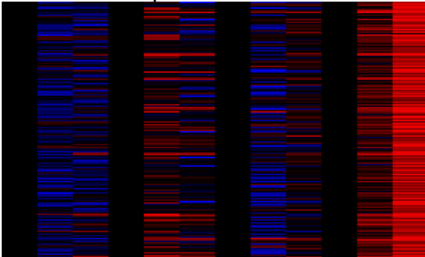


NRP: non-recurrence primary  
RPP: recurrence-potent primary

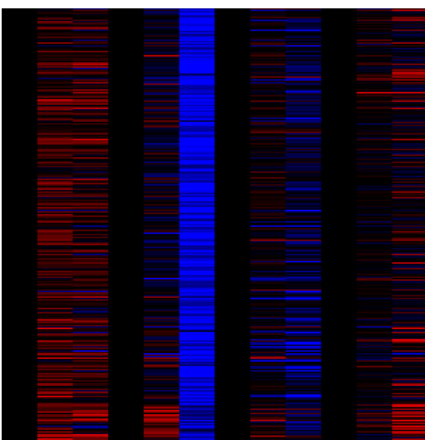
G4a-specific  
Recurrence promotion



G4b-specific  
Recurrence promotion



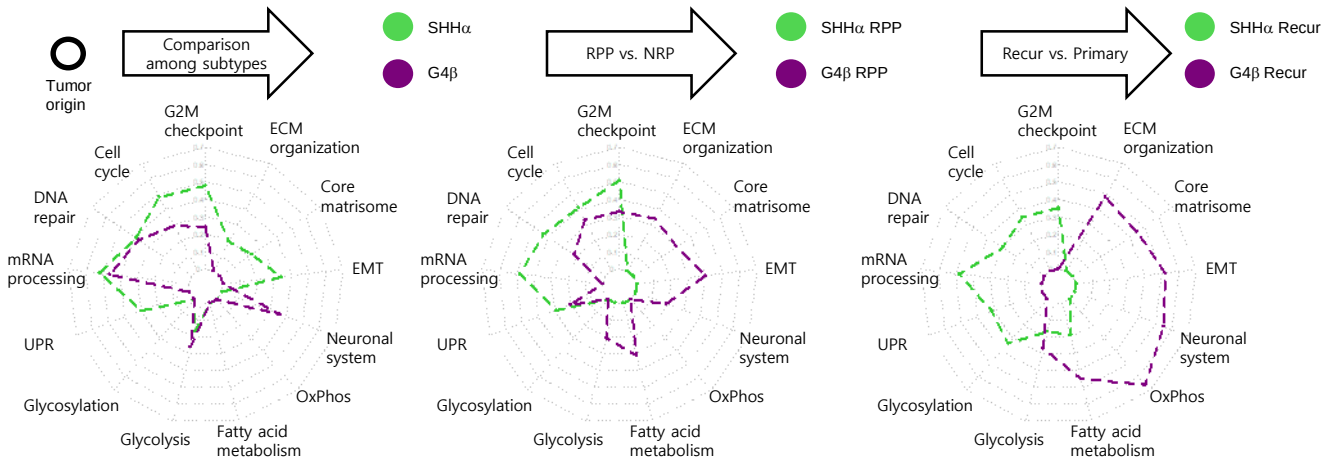
SHHb-specific  
Recurrence inhibition





Normalized Enrichment Score (GSEA)

NRP: non-recurrence primary  
RPP: recurrence-potent primary



Representative protein expression by recurrence

