

# SUPPLEMENTAL INFORMATION

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## Insights into cancer severity from biomolecular interaction mechanisms

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## Supplemental figure legends

### Figure S1

- a) Degree of homology for the templates used for the predictions.
- b) Most perturbed interfaces directionality

### Figure S2

Extended cancer type specific interface perturbation matrix: for each of the most abundant 24 cancer types (columns), the 48 most frequently perturbed interfaces are shown (rows). Each dot represents perturbed interfaces, with the diameter being proportional to the sample frequency and the colour corresponding to the median of the mechismo scores.

### Figure S3

Mechismo score distribution of most significantly diverging interfaces mediated by the same gene in a given cancer type.

### Figure S4

Mechismo score distribution of interfaces most significantly diverging between different cancer types.

### Figures S5

Mutational spectra of the CTNNB1 gene in four different cancer types. Interactors whose interfaces are perturbed are listed in green at the bottom of the plot.

### Figures S6

a) Mutational spectra of NRAS and KRAS in skin malignant melanoma and pancreas carcinoma. b) Structure caption and mechismo score distributions of variant predicted effects towards K and NRAS interfaces with SOS1 (top) and RASA1 (bottom). c) Predicted effect for Q61R mutation to H,K in NRAS. Red and green lines indicate disabling and enabling effects respectively. Solid, dashed and dotted lines indicate the level of confidence of the prediction (respectively high, medium and low) while the line thickness is proportional to

the score magnitude. **d)** Same representation as in c) for predicted effects of mutations Q209 P, L of GNAQ and GNA11

### **Figures S7**

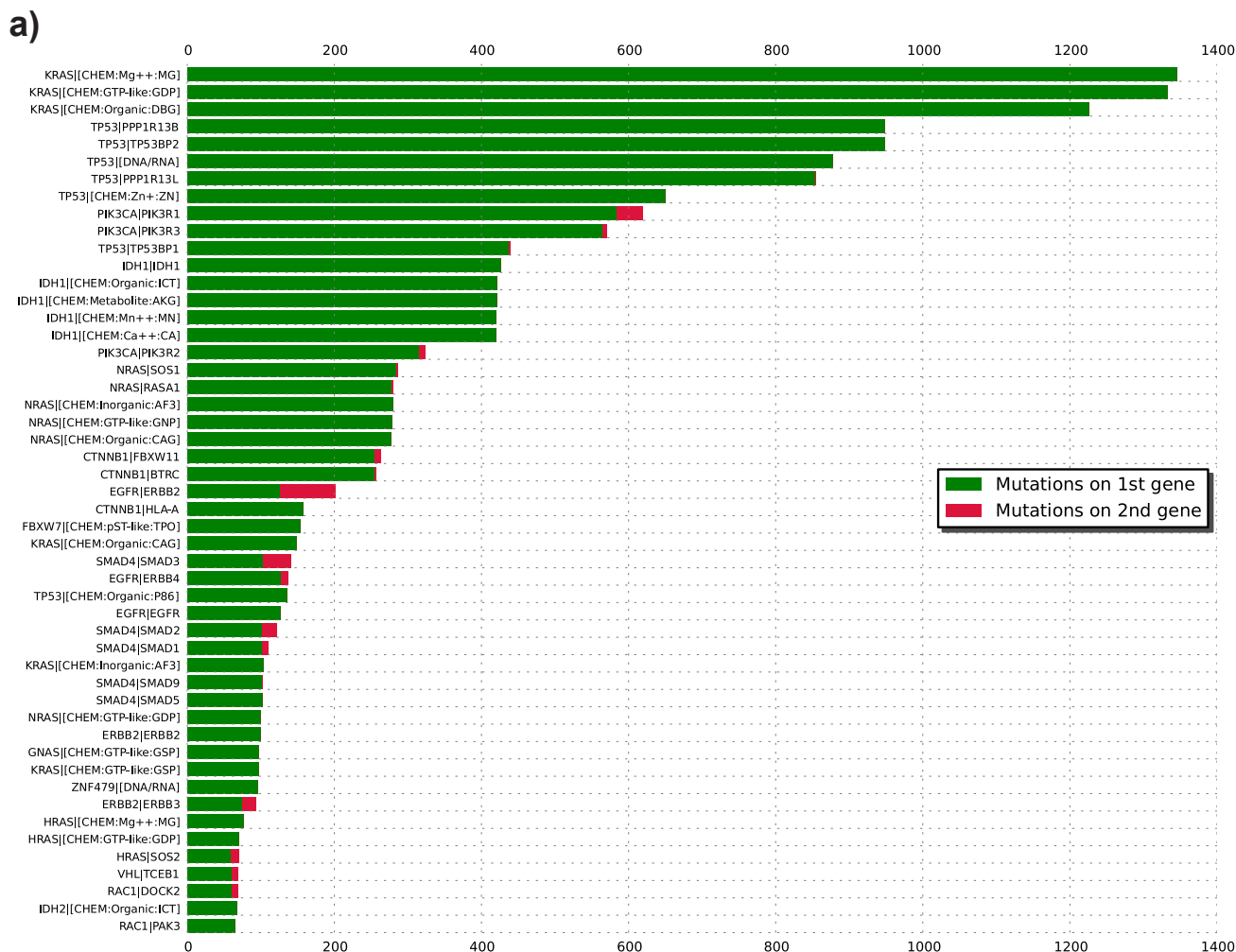
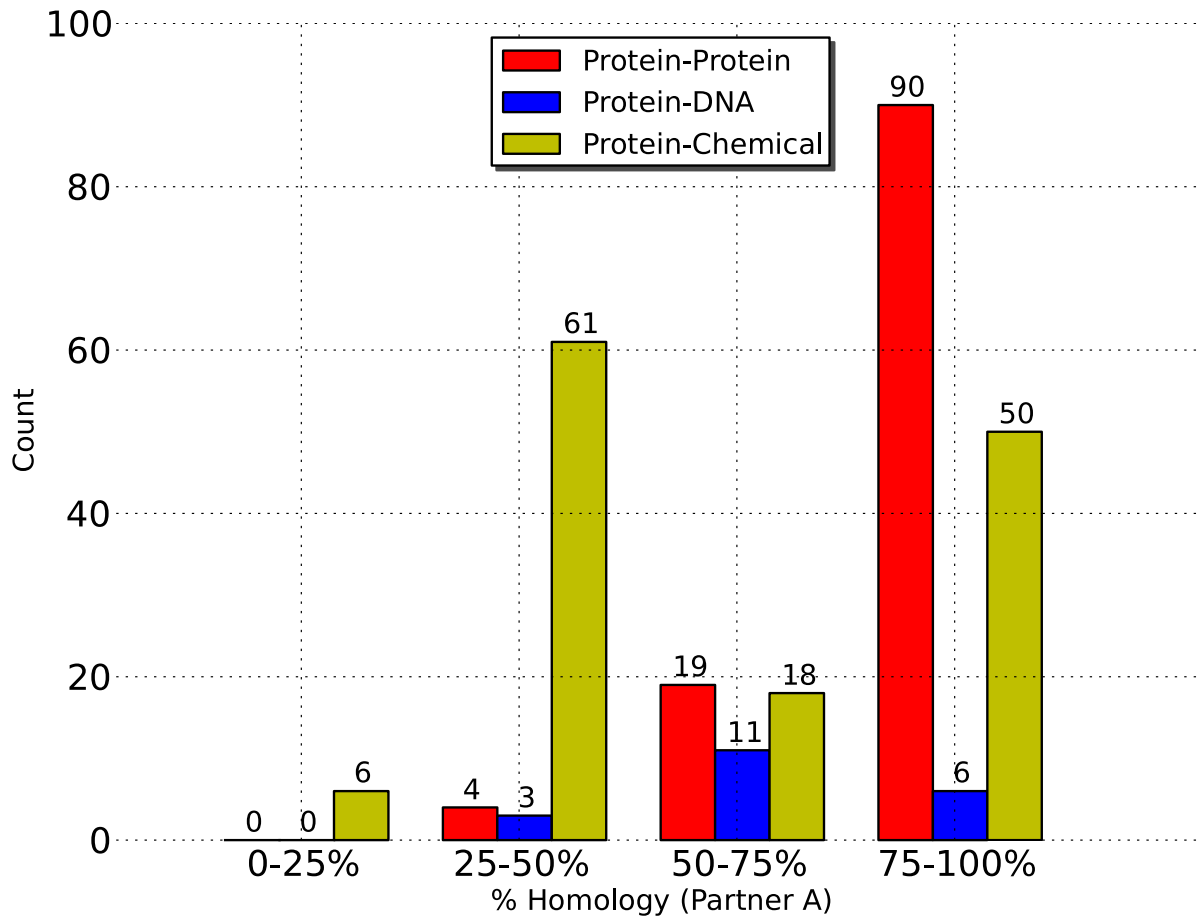
Matrix representation of the clustering obtained by considering samples from all cancer types.

### **Figures S8**

Clustering matrix of four major cancer types showing the mutual exclusivity between TP53 interfaces mediated with ZN++ compared to DNA /co-regulation of transcription proteins.

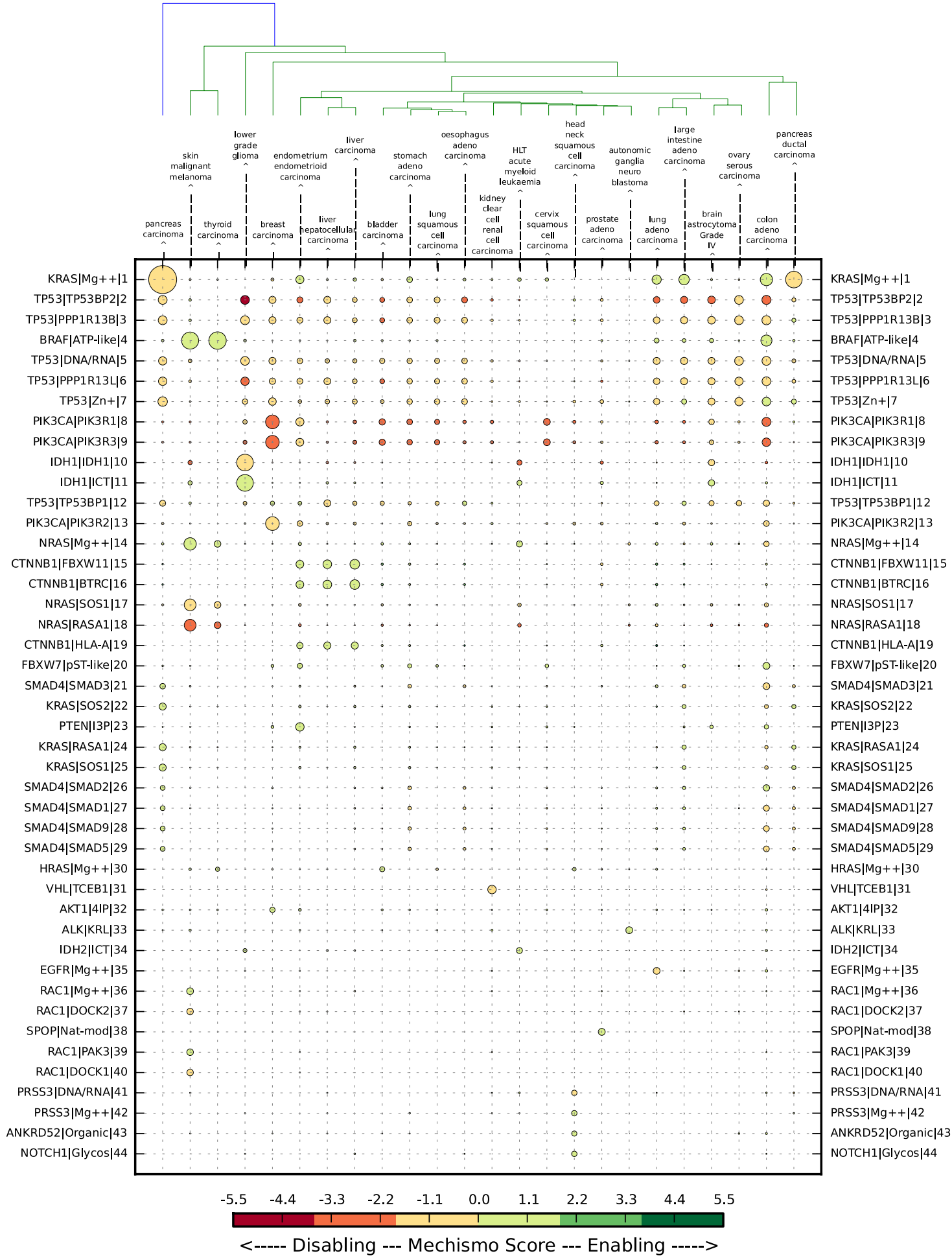
### **Figures S9**

Comparison of Kaplan-Meier survival plots for KRAS and CTNNB1 perturbed interfaces (green and red) and genes only (lime and orange).

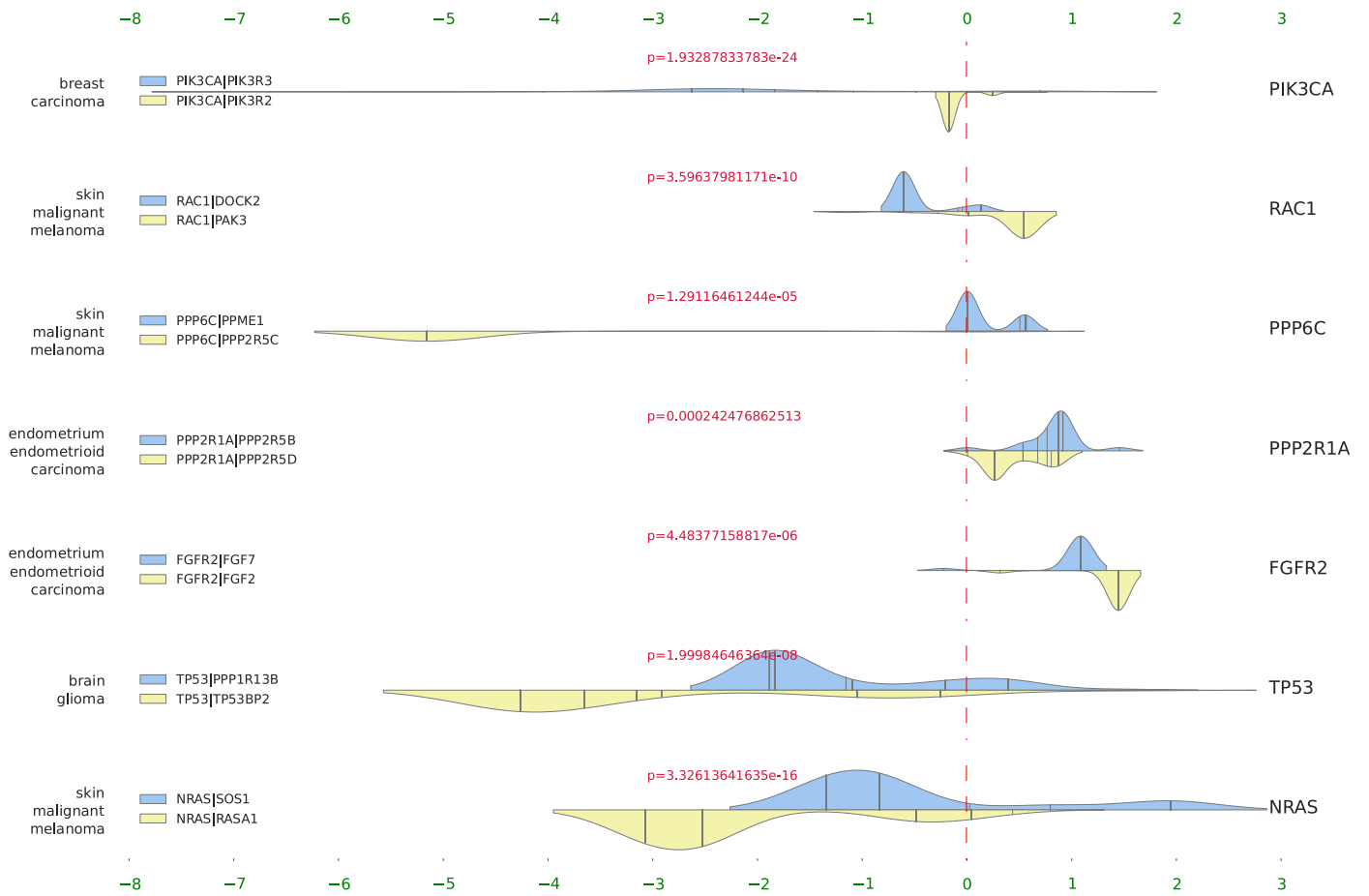


b)

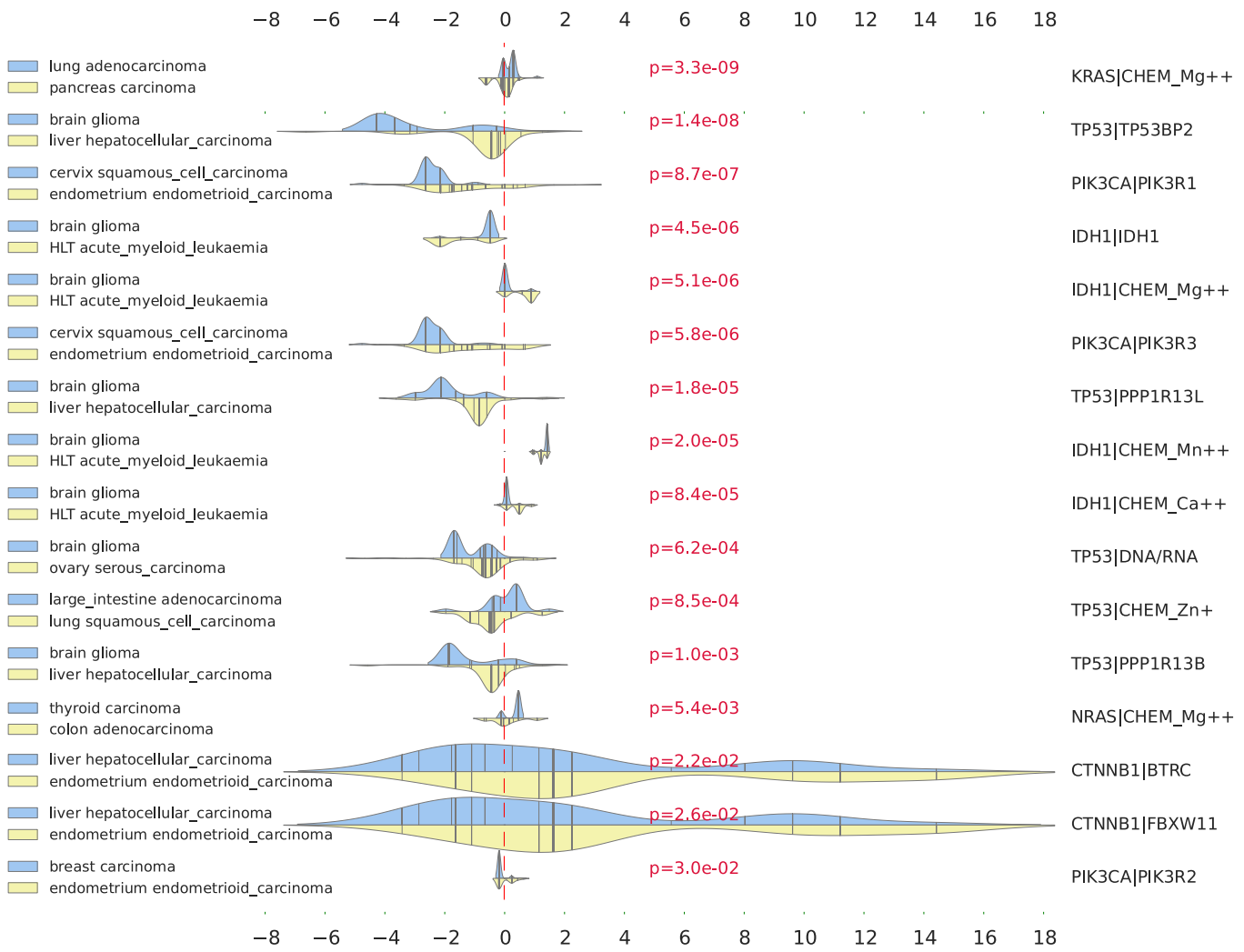
Figure S1



**Figure S2**

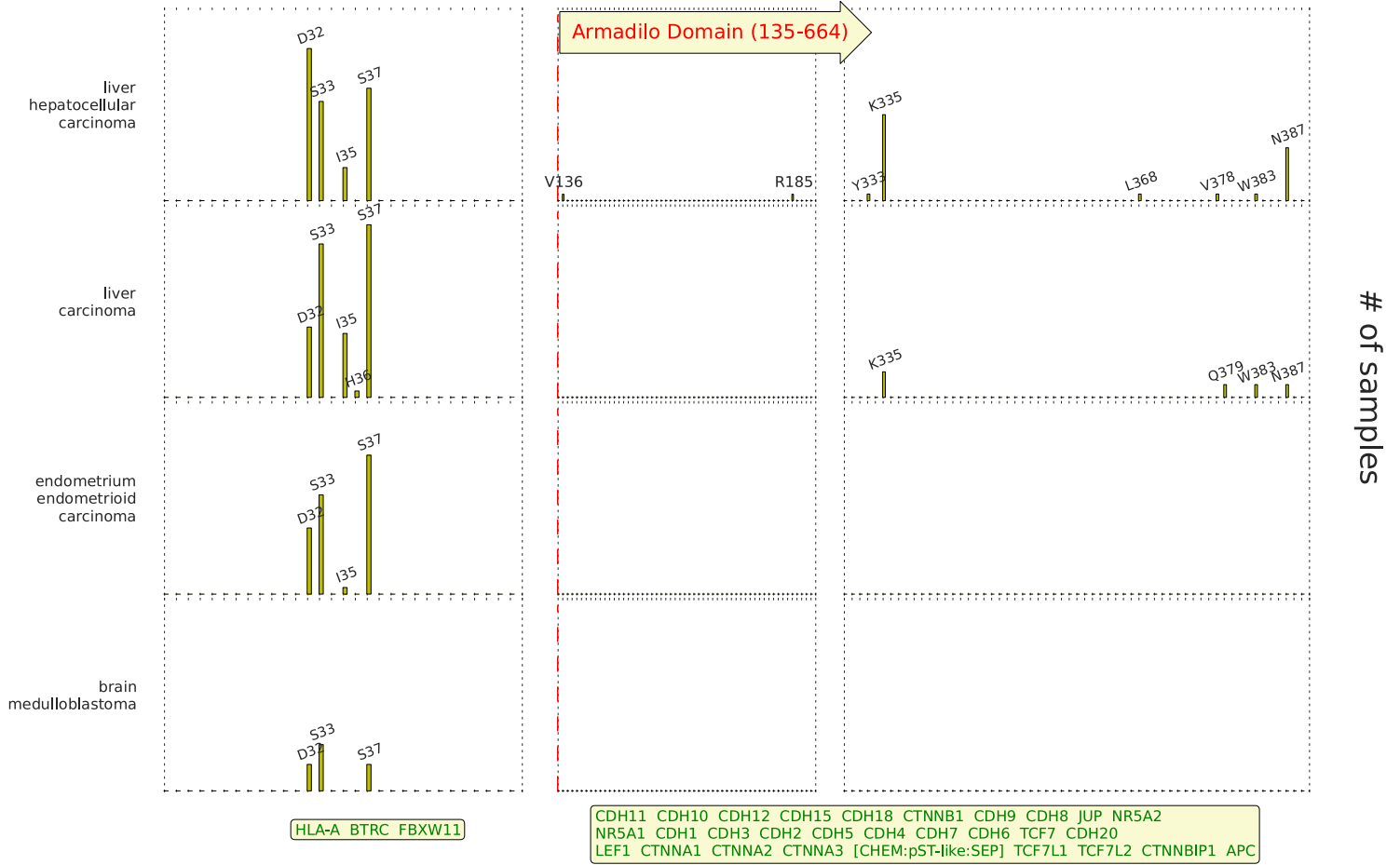


**Figure S3**



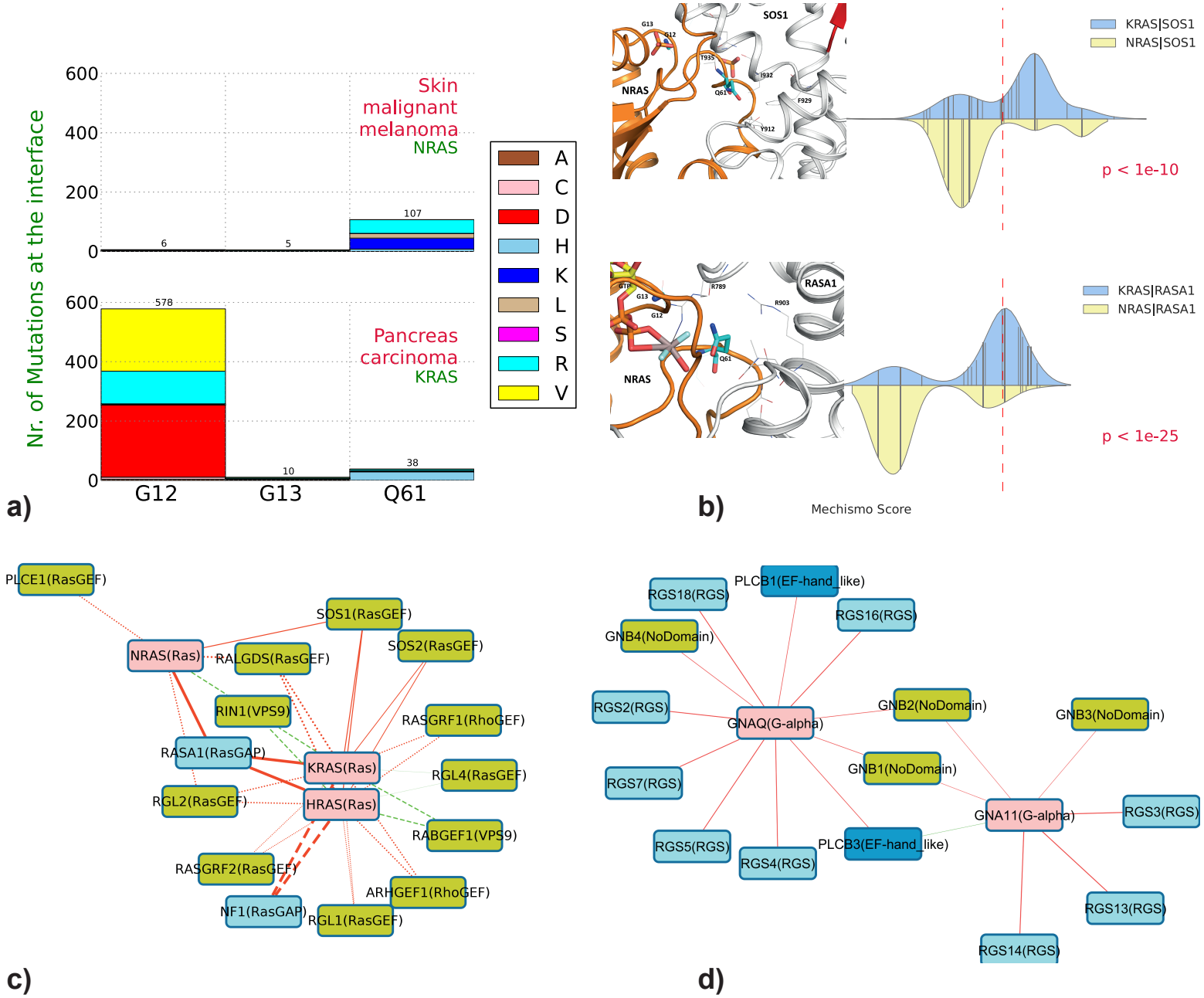
**Figure S4**

# CTNNB1



**Figure S5**





**Figure S6**

Pan cancer

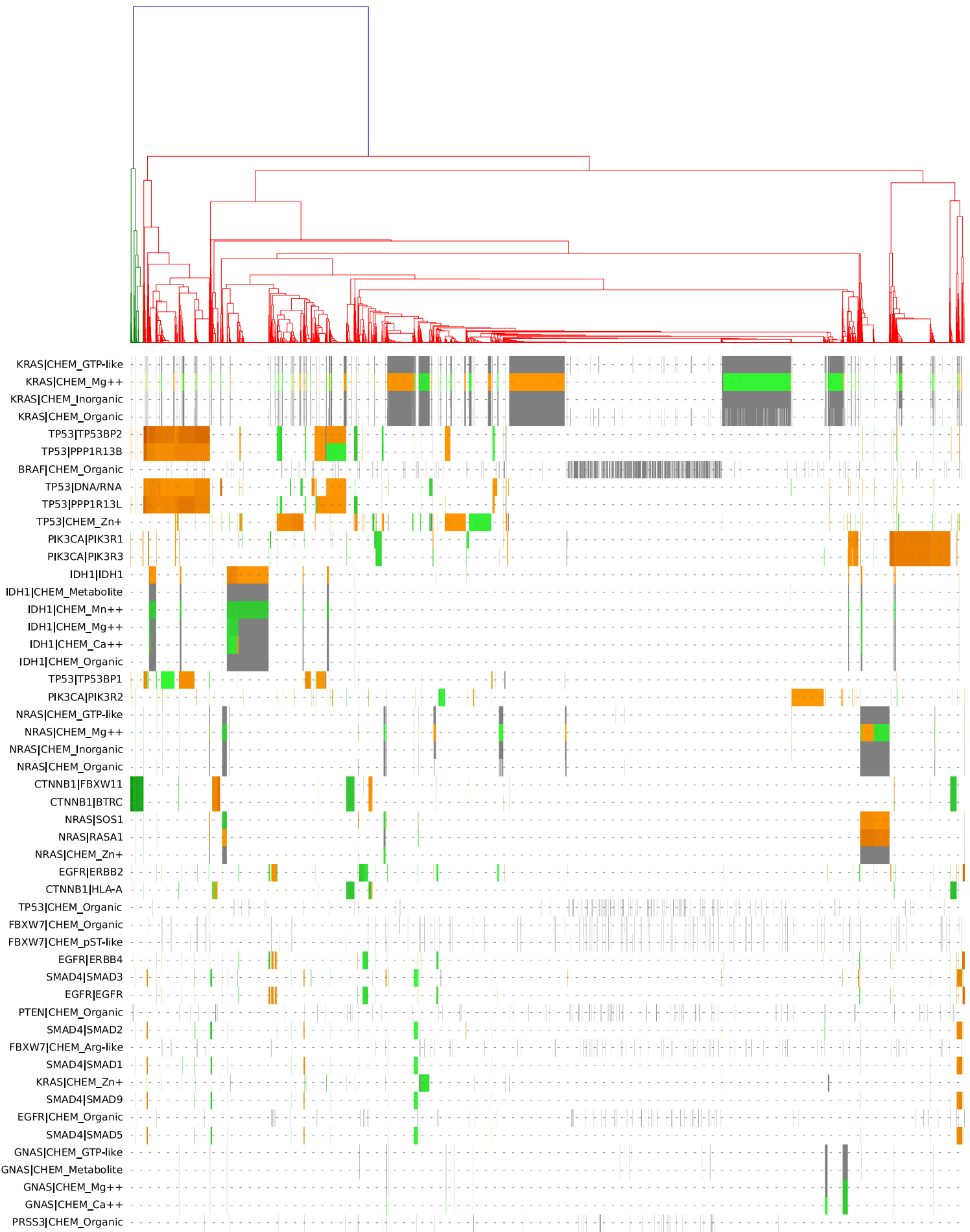
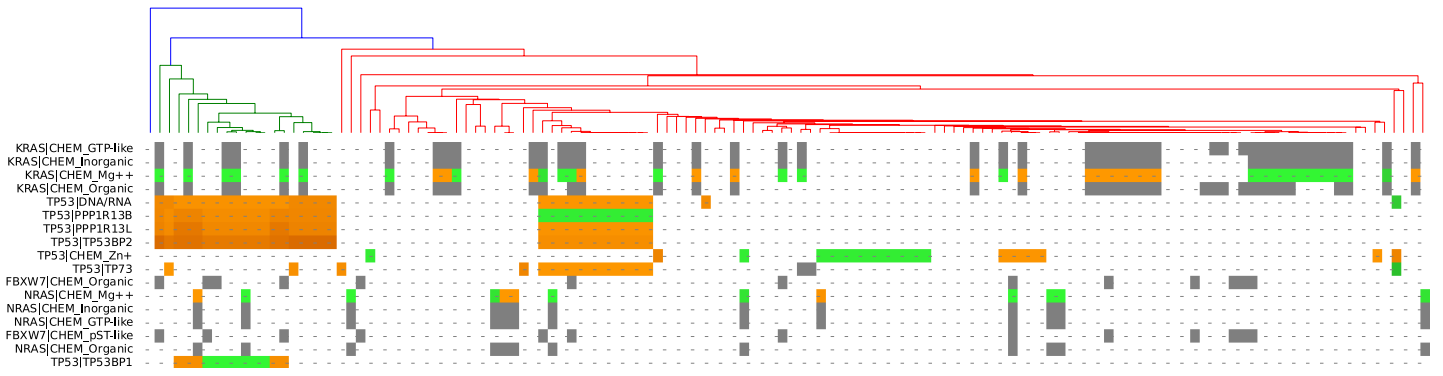
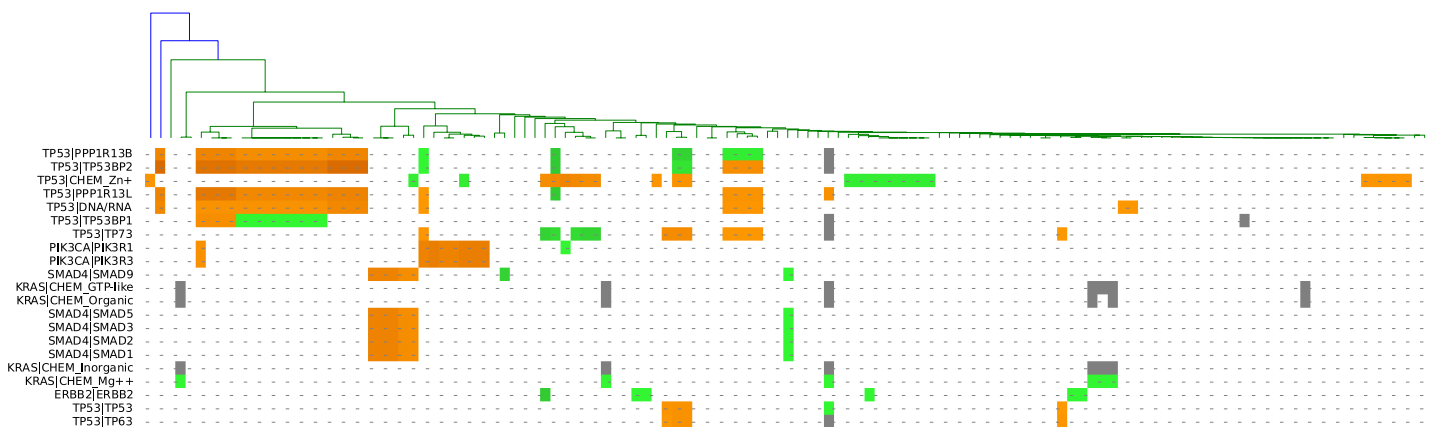


Figure S7

### Rectum adenocarcinoma



### Oesophagus adenocarcinoma



### Ovary serous\_carcinoma

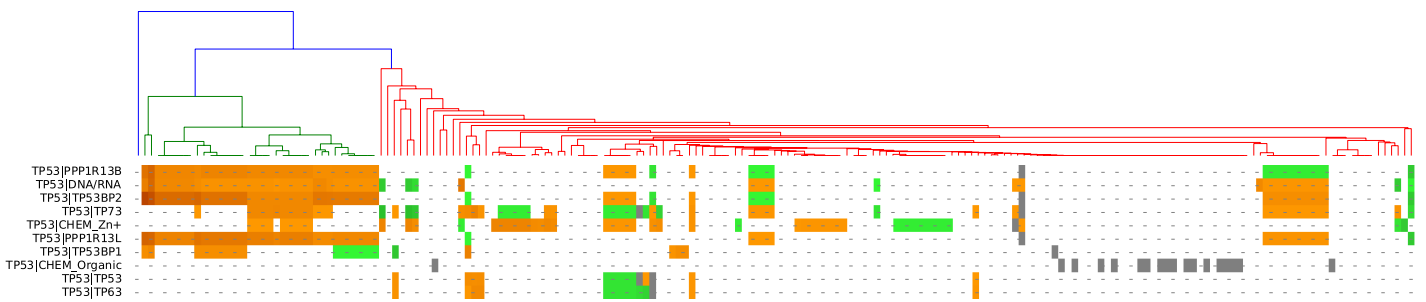


Figure S8

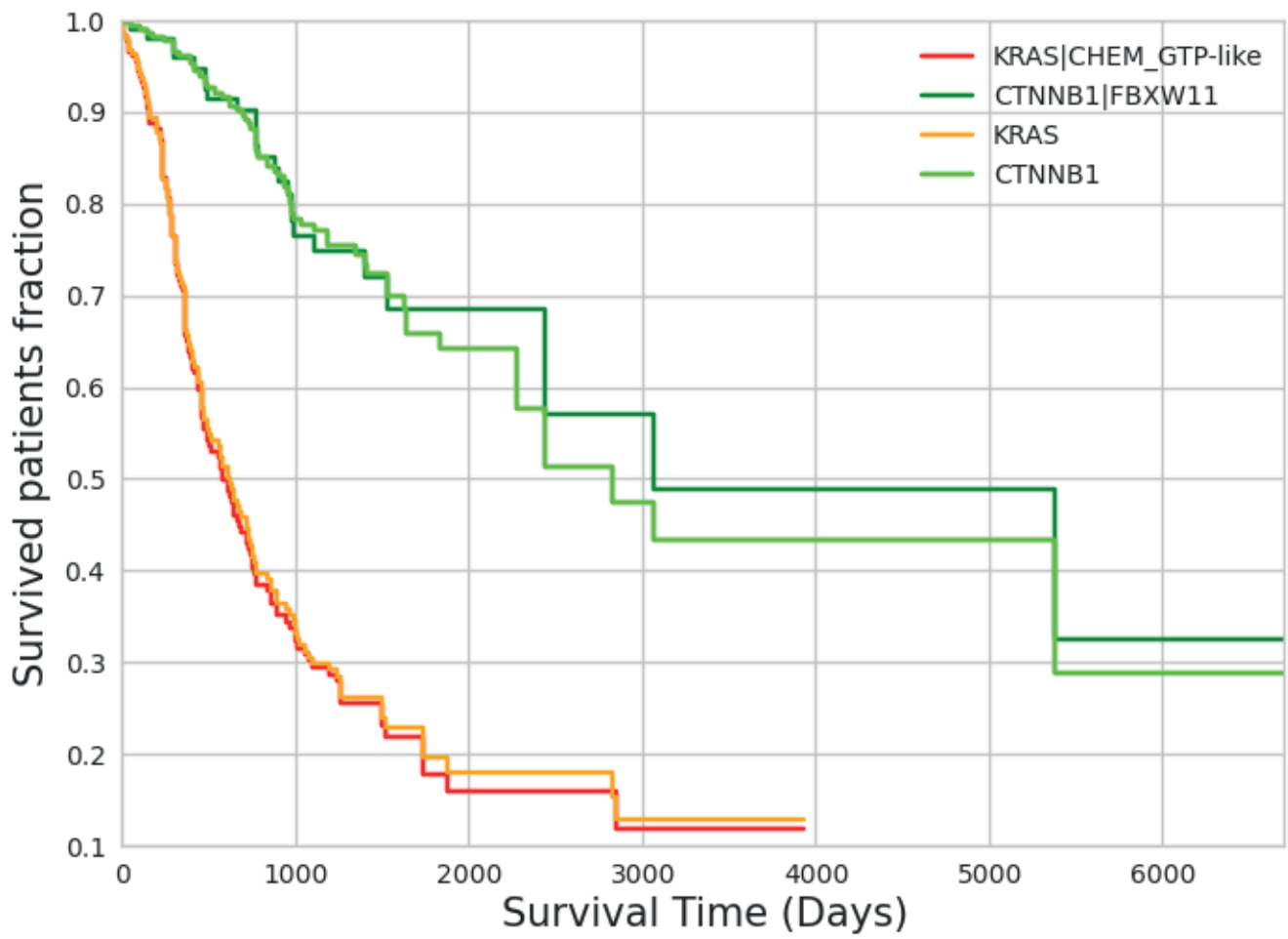


Figure S9