

Description of Additional Supplementary Files

File Name: Supplementary Data 1 -

Description: Tissues types represented in the GEO dataset

File Name: Supplementary Data 2

Description: Tissues types represented in the TCGA dataset

File Name: Supplementary Data 3

Description: Tissues types represented in the CCLE dataset

File Name: Supplementary Data 4

Description: Tissues types represented in the GDSC dataset

File Name: Supplementary Data 5

Description: Genes located in a marked genomic region of at least one CNA-CES

File Name: Supplementary Data 6

Description: Colocalization of borders of marked genomic regions of CNA-CESs with common fragile sites

File Name: Supplementary Data 7

Description: Correlations between the weight of genes in CNA-CESs across datasets

File Name: Supplementary Data 8

Description: Correlations between GSEA results in the GEO-dataset and TCGA-dataset

File Name: Supplementary Data 9

Description: Gene set enrichment analysis per cytoband on the degree of transcriptional adaptation*

File Name: Supplementary Data 10

Description: Gene set enrichment analysis on TACNA expression levels in the TCGA dataset using the protein complex geneset database from CORUM*

File Name: Supplementary Data 11

Description: Significance of pearson correlation coefficients between TACNA expression levels of genes from protein complex subunits

File Name: Supplementary Data 12

Description: Presence of individual genes in marked genomic regions of CNA-CESs in the GEO and TCGA datasets

File Name: Supplementary Data 13

Description: Average degree of transcriptional adaptation of oncogenes

File Name: Supplementary Data 14

Description: Spearman correlations between average TACNA profiles per tumor type

File Name: Supplementary Data 15

Description: Correlations between inferred CNA burden and expression-based immune metric per tumor type

File Name: Supplementary Data 16

Description: Spearman correlations between TACNA expression levels and inferred immune cell type abundance

File Name: Supplementary Data 17

Description: Gene set enrichment analysis on correlations between TACNA expression levels and inferred CD8+ T cell abundance