

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Subtype-specific gene signatures

Subtype-specific gene signatures were derived from the top 500 contributors to PC1 (for SCNC-Y) and PC2 (for SCNC-A and SCNC-N) (see PCA plot in Fig S10a). The SCNC-Y gene signature is composed of the top 217 negative contributors to PC1. The SCNC-A gene signature is composed of the top 179 negative contributors to PC2. The SCNC-N gene signature is composed of the top 321 positive contributors to PC2. Abbreviations: PC: principal component; SCNC: small cell neuroendocrine cancers

File Name: Supplementary Data 2

Description: Enriched GO terms in SCNC subtypes

The GO enrichment analysis was performed for each subtype, using the subtype-specific gene lists. Abbreviations: FDR: false discovery rate; GO: gene ontology; SCNC: small cell neuroendocrine cancers

File Name: Supplementary Data 3

Description: Metabolic pathway enrichment analysis

Pathway ID: Metabolic pathways from KEGG, Hallmark, Reactome and biocarta; Pearson R: Pearson correlation between NE score and metabolic pathway ssGSEA enrichment score

File Name: Supplementary Data 4

Description: PDX gene expression data