

Supplemental Figures for:

Comprehensive characterization of the genomic landscape in Chinese pulmonary neuroendocrine tumors reveals prognostic and therapeutic markers

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Figure S1. The comparison of prognosis in different histological sub-cohorts. A. Progression-free survival in patients treated with systemic treatment; B. Overall survival in patients with systemic treatment; C. Disease-free survival in patients treated with surgery; D. Overall survival in patients treated with surgery.



Figure S2. The oncoprint of genomic alterations identified in pulmonary neuroendocrine tumor (**n=148).** Only genes with mutated number > 5 were presented except for *MEN1*, *STK11*, *MYCL*, and *EGFR*.



Figure S3. The comparison of genomic features in different LCNEC subsets. A. Gene mutated frequency; B. Tumor mutational burden (TMB); C. Copy number variation (CNV) (*P<0.05, **P<0.01, ****P<0.001, ****P<0.0001). SCLC-like refers to LCNEC harboring concomitant *TP53/RB1* alterations; NSCLC-like refers to LCNEC harboring no *RB1* alteration but harboring alteration(s) in *STK11*, *ERBB2*, *MET*, *KRAS*, *KEAP1* or *EGFR*.



Figure S4. The association of alteration in homologous recombination (HR) signaling pathway with prognosis in LCNEC and SCLC patients treated with platinum-based chemotherapy.



Figure S5: The association of tumor stage with survival outcomes in resected SCLC patients. A. Disease-free survival in resected SCLC patients; B. Overall survival in resected SCLC patients.



Figure S6. The association of TERT/KEAP1 mutation with prognosis in SCLC patients with systemic treatment.



Figure S7. The comparison of prognosis in different LCNEC subsets and SCLC. A. Progression-free

survival in patients treated with systemic treatment; B. Overall survival in patients with systemic treatment; C. Disease-free survival in patients treated with surgery; D. Overall survival in patients treated with surgery.