







Supplemental Figure 1. A Feature plots of three core genes. B Expression patterns of folate metabolism related genes across two clusters. C Expression patterns of folate metabolism related genes across tumor types.

Supplemental Figure 2. The mRNA level of MTHFD2 and SHMT2 in multiple PNECs cell lines and immortalized lung epithelial cell.

Supplemental Figure 3. Immune microenvironments features across tumor types. Estimation of immune cell infiltration using the xCell (A), ssGSEA (B), and CIBERSORT (C) method respectively. Expression patterns of immune suppressive (D) and active (E) checkpoints across tumor types.