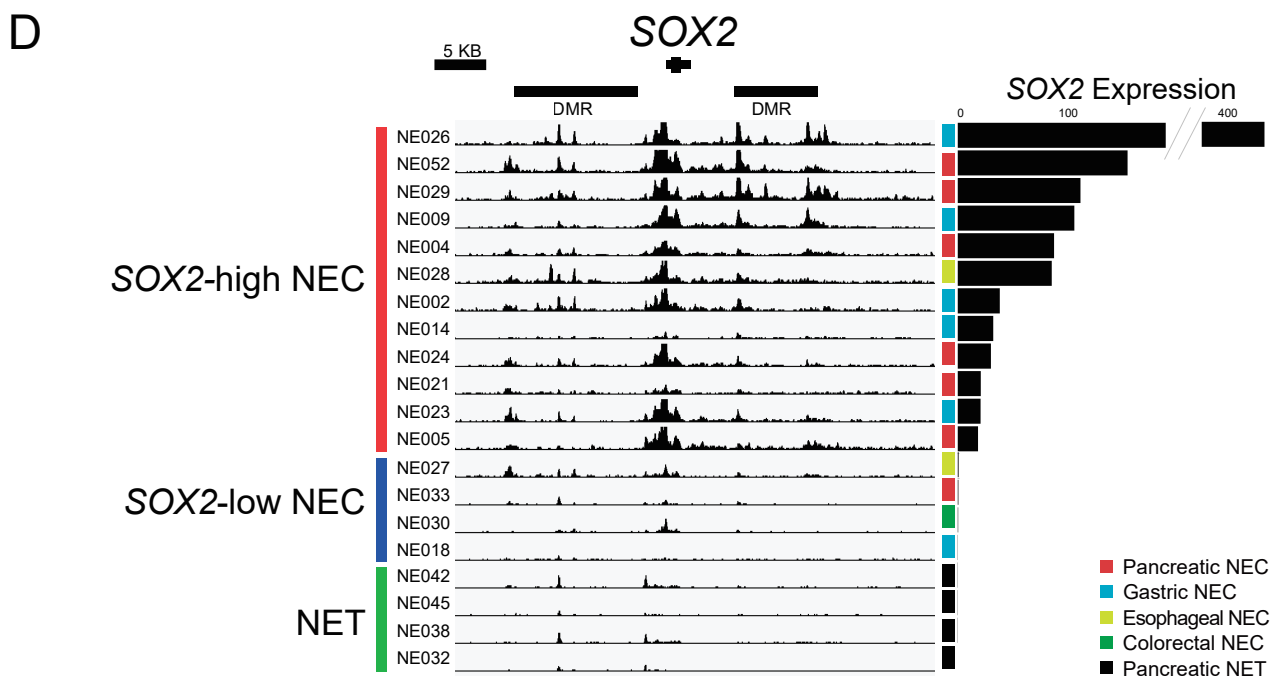
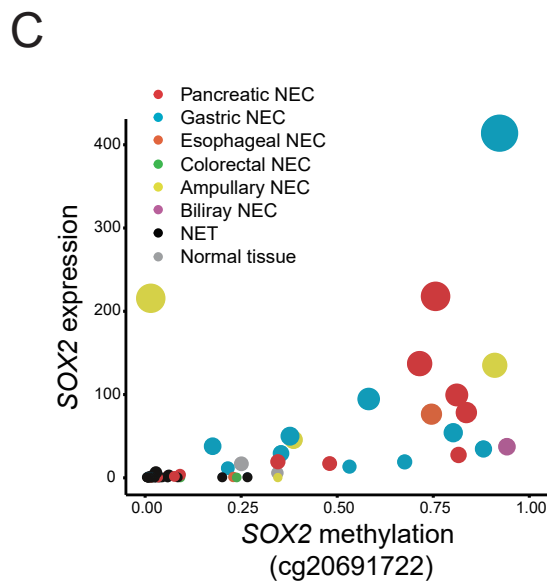
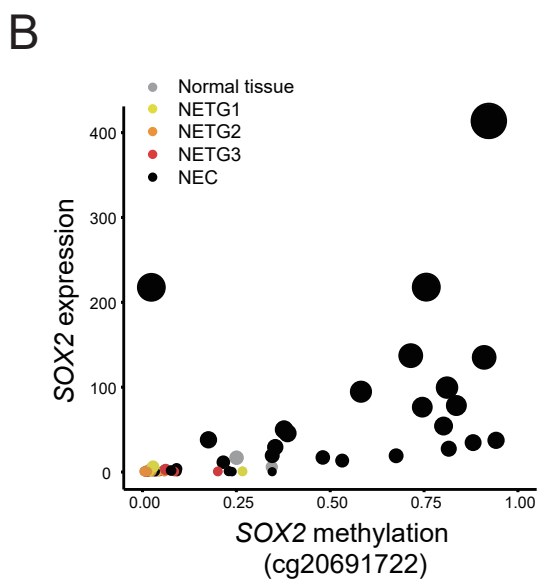
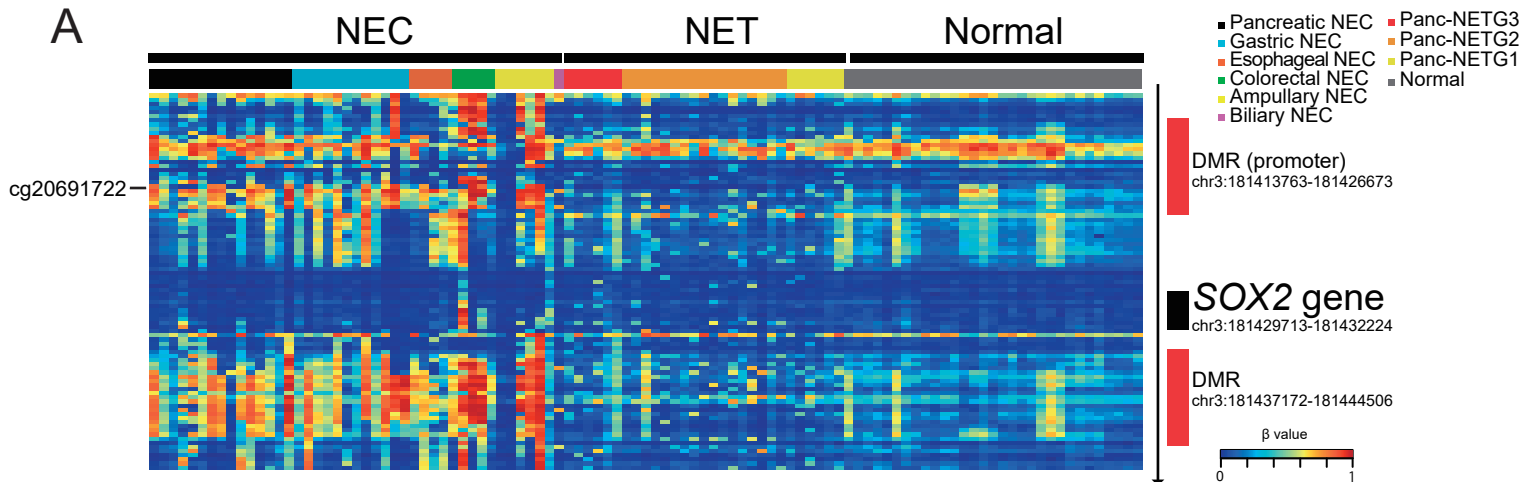


Supplementary Figure S9. Integration analysis of RNA-seq data and DNA methylation assay findings for GIS-NENs.



A, Methylation status of the genomic locus around the *SOX2* gene in GIS-NENs. **B and C**, The relationships between *SOX2* gene expression and *SOX2* methylation status are shown according to the histology for GIS-NENs (NEC, NETG1, NETG2, NETG3 and Normal tissue) and to the primary organ for GIS-NECs (Spearman rank correlation, $\rho = 0.620$, $P = 2.40 \times 10^{-8}$). **D**, ATAC-seq was performed for seven Panc-NECs, nine Nonpanc-NECs, and four Panc-NETs. The cases are arranged in descending order of *SOX2* expression. ATAC-seq open chromatin peaks are clear in the region surrounding the *SOX2* gene in cases with high expression. The right bar chart shows the level of *SOX2* gene expression. DMR, differentially methylated region.