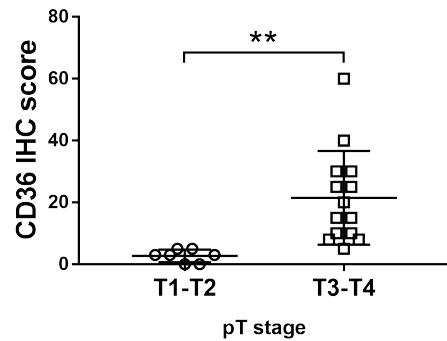
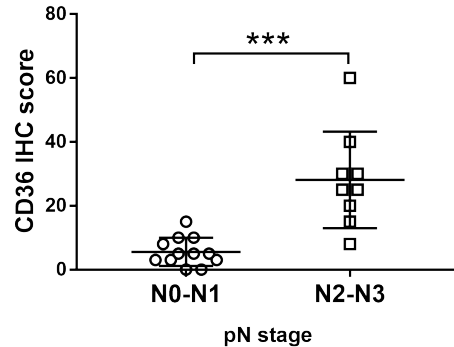


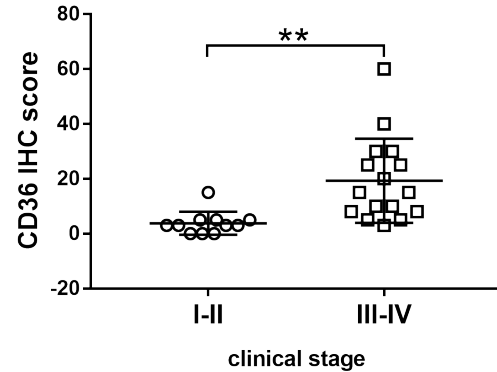
A.



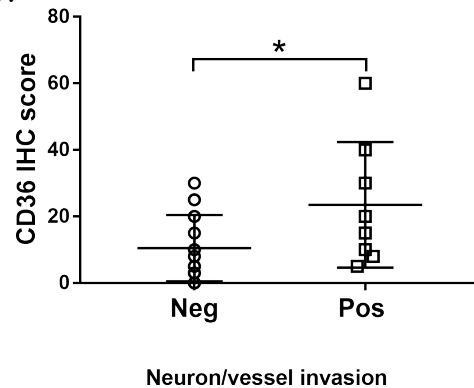
B.



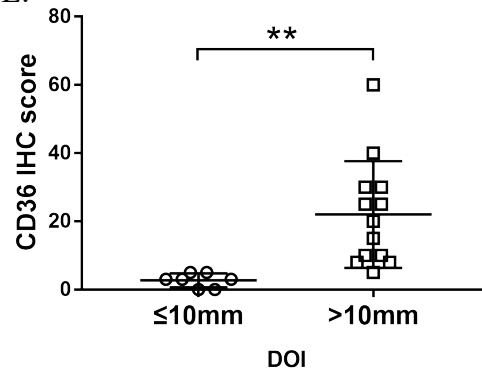
C.



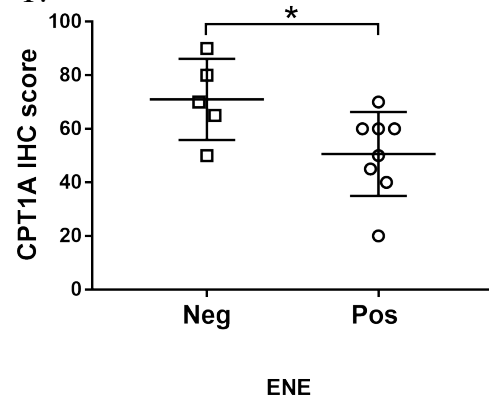
D.



E.



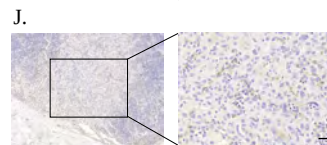
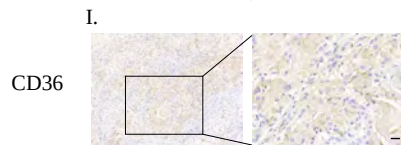
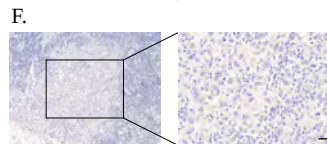
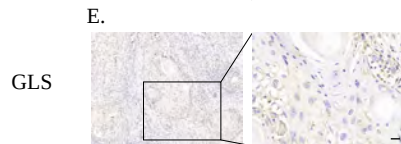
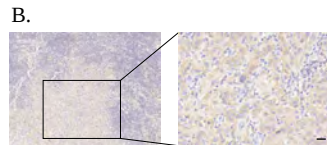
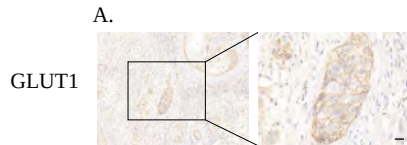
F.



False negative

Primary lesion

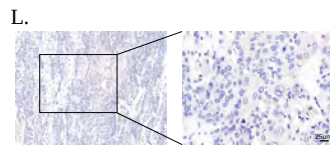
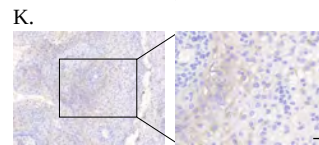
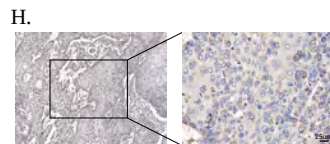
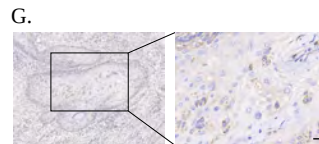
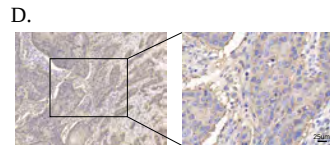
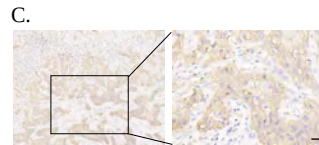
Lymph node



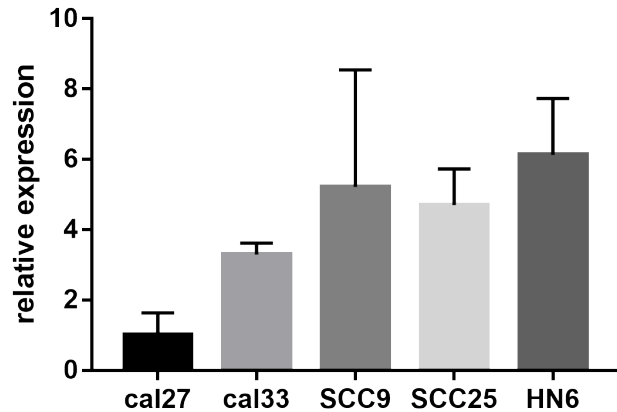
True positive

Primary lesion

Lymph node



A.



B.

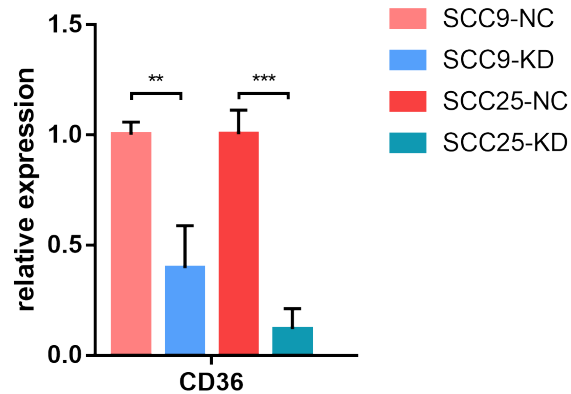


Figure S1. Association of metabolic markers with clinical factors. (A) The CD36 IHC score was higher in advanced pT stage (T3-T4 vs. T1-T2, $p=0.003$). (B) The CD36 IHC score was higher in advanced pN stage (N2-N3 vs. N0-N1, $p<0.001$). (C) The CD36 IHC score was higher in advanced clinical stage (III-IV stage vs. I-II stage, $p=0.005$). (D) The CD36 IHC score was higher in the neuron/vessel invasion-positive group (positive vs. negative, $p=0.040$). (E) The CD36 IHC score was higher in the larger DOI group (>10 mm vs. ≤ 10 mm, $p=0.006$). (F) The CPT1A IHC score was higher in the ENE-negative group (negative vs. positive, $p=0.026$).

Figure S2. Expression of GLUT1 (A-D), GLS (E-H), and CD36 (I-L) in primary lesions (A, C, E, G, J, K) and lymph nodes (B, D, F, H, J, L). Scale bar: 25 μ m.

Figure S3. (A) Expression of CD36 in different oral cancer cell lines. CD36 expression level in cal27 was used as control. (B) Quantitative real time PCR results validated that siRNA successfully knockdown CD36 expression in SCC9 and SCC25 cell lines.