

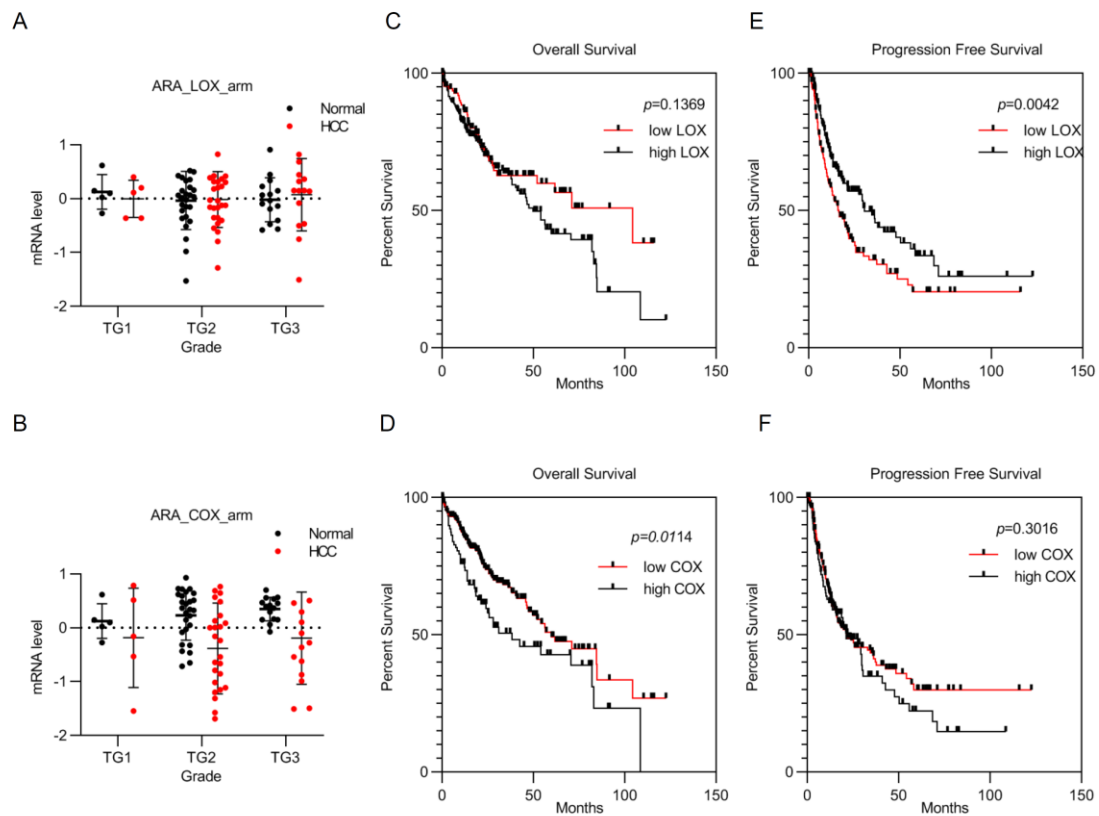
Supplementary materials:

The supplementary materials include:

Suppl. Figure 1: Expression of the COX and LOX pathway gene sets in HCC and association with patients' survival

Suppl. Figure 2: The relationship between the expression of COX and LOX pathway genes of arachidonic acid metabolism and vascular invasion.

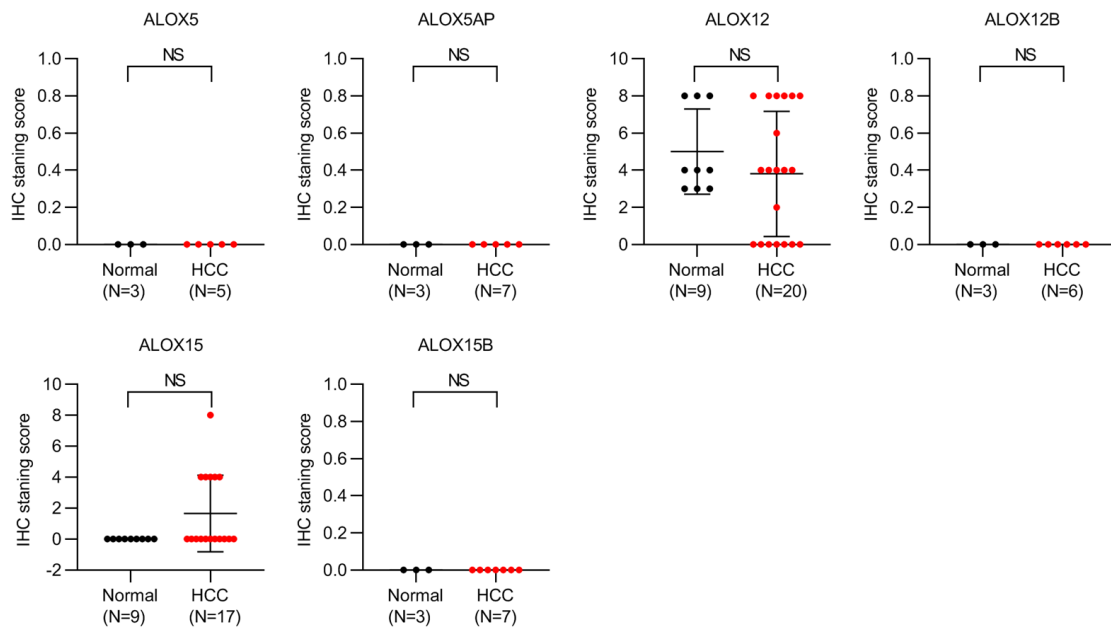
Suppl. Figure 3: The relationship between the expression of COX and LOX pathway genes of arachidonic acid metabolism and vascular invasion.



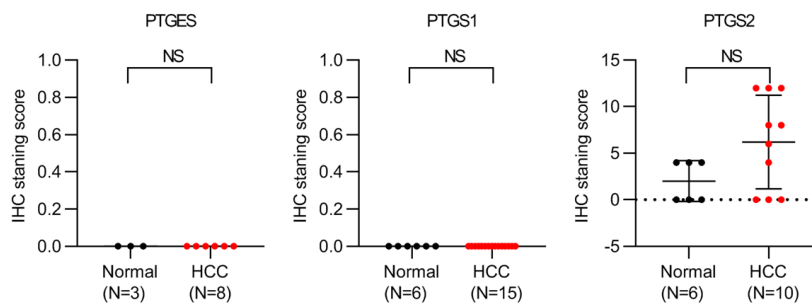
Suppl. Figure 1. Expression of the COX and LOX pathway gene sets in HCC and association with patients' survival

(A-B) The mean expression of the COX (A) or LOX (B) pathway gene set in HCC tissues of the TCGA-LIHC dataset showed no significant difference among different pathological grades. (C-F) The association of the expression of the COX or LOX pathway gene set with overall survival (C, D) and progression-free survival (E, F) of HCC patients.

A

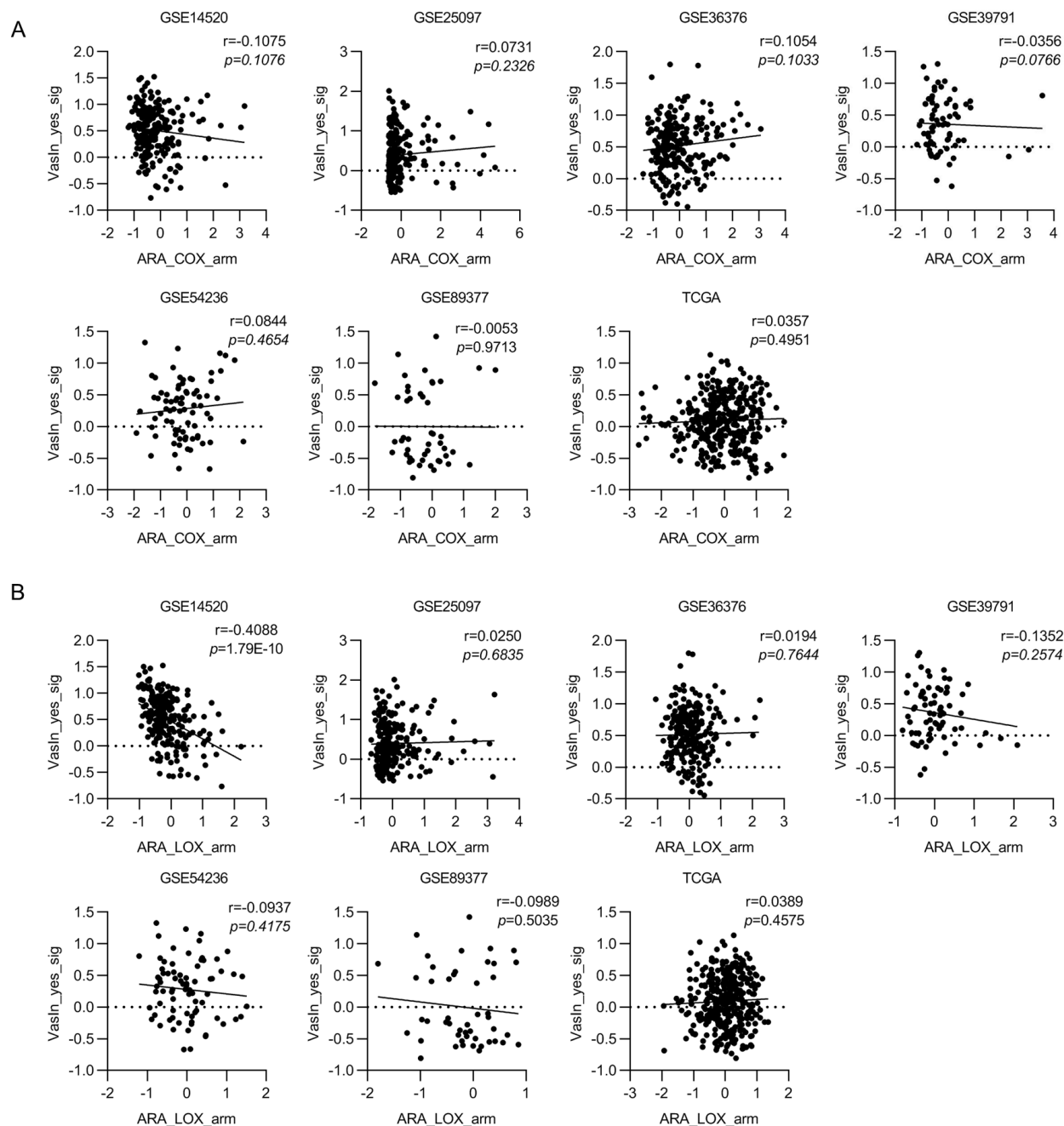


B



Suppl. Figure 2. Immunohistochemical analysis of COX and LOX branch enzymes of the arachidonic acid metabolism pathway in normal liver and HCC tissues.

The expression of the key enzymes of the COX branch (A) and LOX branch (B) of arachidonic acid metabolic pathway in normal liver (Normal) and HCC tissues were scored according to the IHC staining images deposited at the Human Protein Atlas database. Statistical analysis was performed using a two-tailed Student's t-test. NS indicates no statistical difference.



Suppl. Figure 3. The relationship between the expression of COX and LOX pathway genes of arachidonic acid metabolism and vascular invasion.

(A-B) The mean mRNA expression profiles of the COX pathway gene set (A) and the LOX pathway gene set (B) were plotted against the expression scores of a prognostic microvascular gene signature in 7 independent HCC datasets.