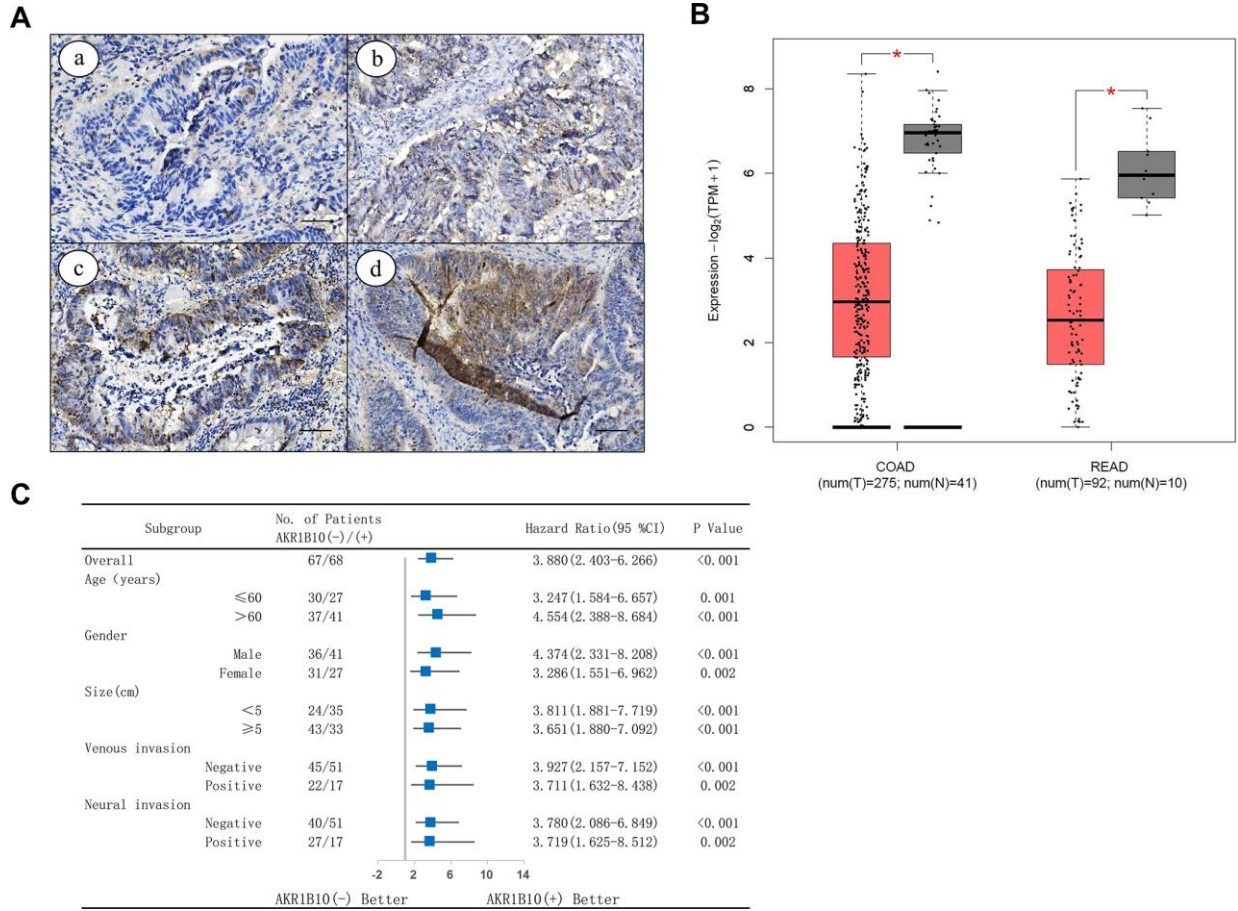
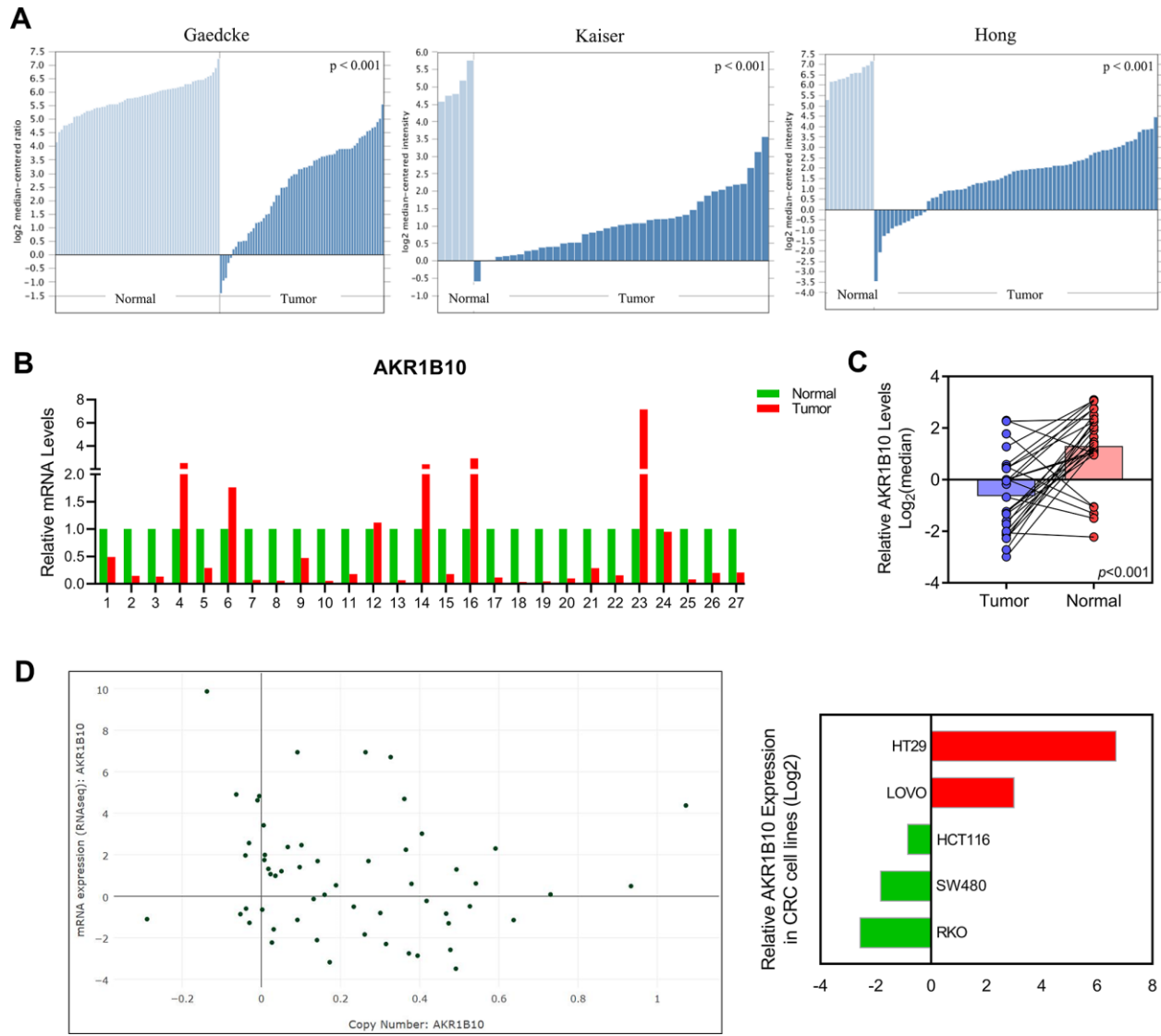


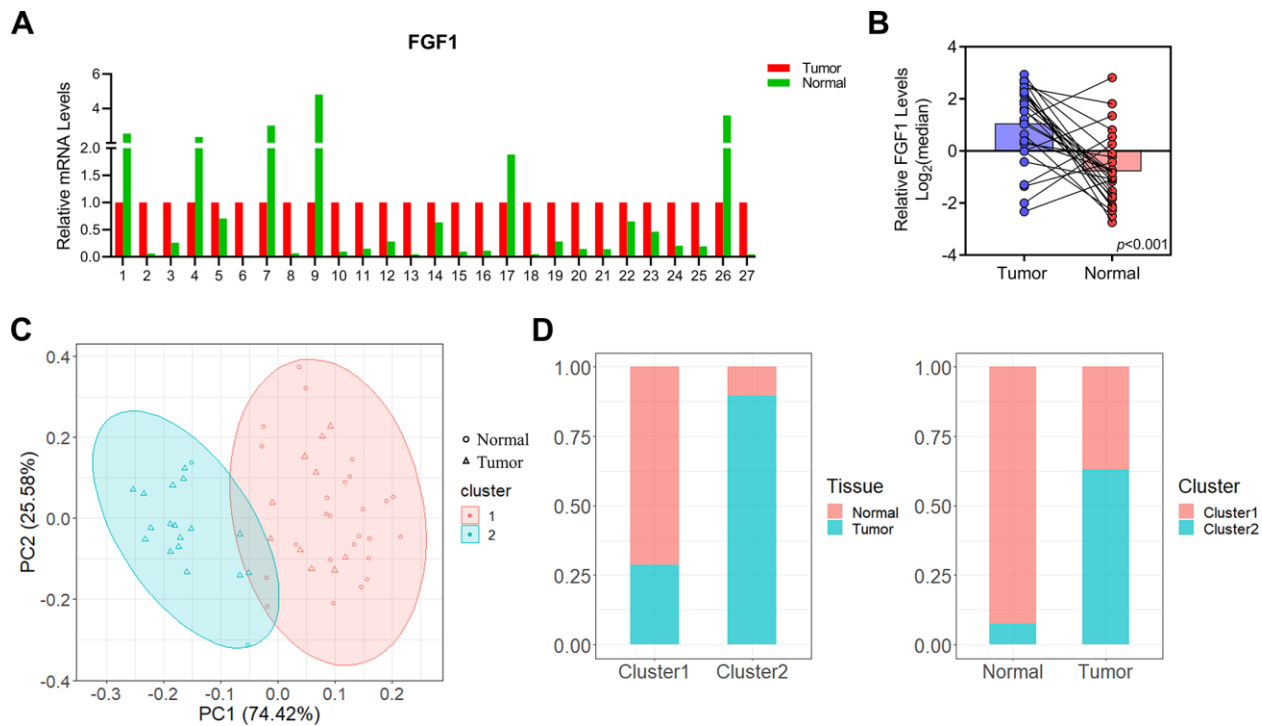
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Expression of AKR1B10 in CRC in TCGA datasets. (A) IHC images showing *in situ* AKR1B10 expression in CRC tissues (scale bar = 100µm). Negative (a), weak (b), positive (c), strong positive (d). **(B)** Comparison of AKR1B10 levels between CRC and paired normal tissues in TCGA datasets by GEPIA platform. **(C)** OS of AKR1B10^{pos} and AKR1B10^{neg} CRC patients in the subgroups of age, gender, tumor size, venous invasion and neural invasion. CRC, colorectal cancer. * $P < 0.05$.



Supplementary Figure 2. AKR1B10 expression in CRC tissues and cell lines. (A–B) AKR1B10 mRNA levels in (A) CRC and non-tumor tissues in Oncomine datasets and (B) 27 paired CRC and normal tissues. (C) Relative AKR1B10 expression in 27 paired CRC and normal tissues. (D) AKR1B10 expression in 5 CRC cell lines from the CCLE platform. CRC, colorectal cancer. CCLE, Cancer Cell Line Encyclopedia.



Supplementary Figure 3. FGF1 expression in CRC and paired normal tissues. (A) FGF1 mRNA levels in 27 paired CRC and normal tissues and (B) the relative expression levels. (C) Stratification of the 27 pairs of CRC and normal tissues into cluster 1 (red) and cluster 2 (green) according to AKR1B10 and FGF1 mRNA levels. (D) Percentage of tumor and normal samples in each cluster. CRC, colorectal cancer.