

Fig S1. The comprehensive UBE2C expression level in ESCC. a, Forest plot of UBE2C mRNA expression in ESCC based on TCGA-GTEx RNA-seq and tissue microarrays. ESCC vs. normal, random-effects model; b, sROC of UBE2C in ESCC tissues based on TCGA-GTEx RNA-seq and tissue microarrays; c, Sensitivity analysis of TCGA-GTEx RNA-seq and tissue microarrays; d, Funnel plot of TCGA-GTEx RNA-seq and tissue microarrays related to UBE2C.

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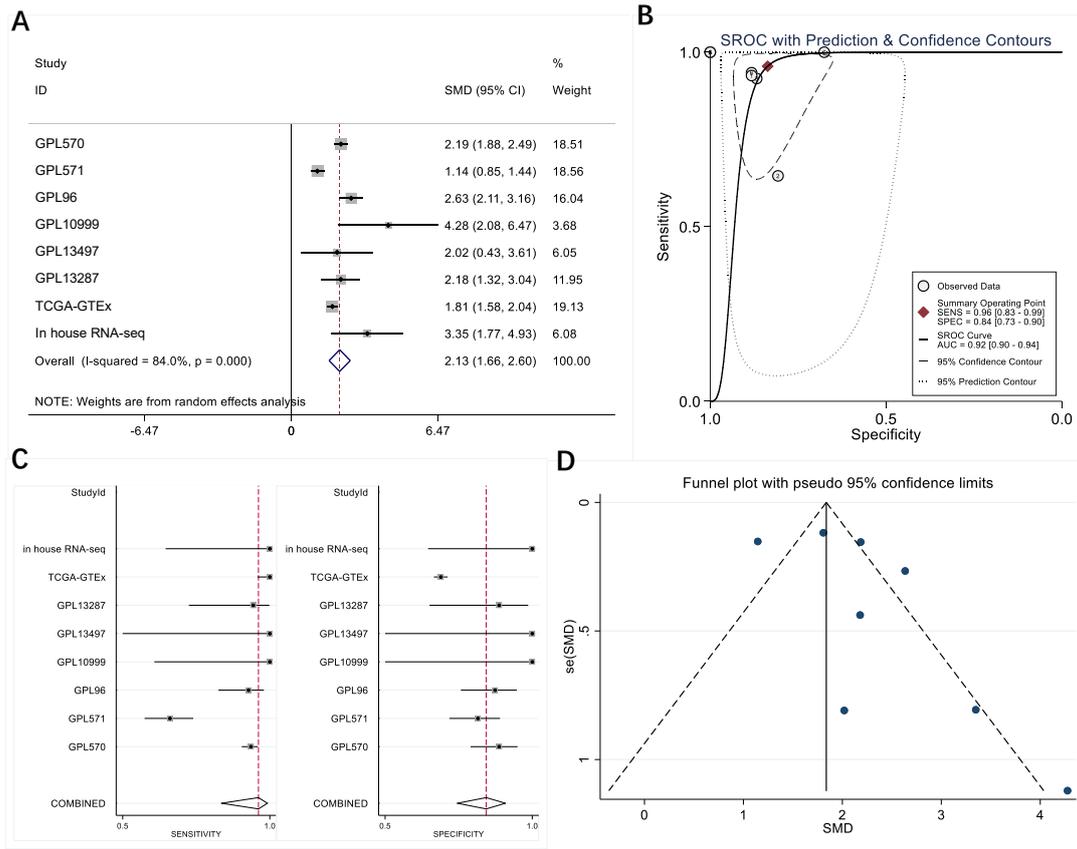


Fig S2. The comprehensive UBE2C expression level in ESCC. a, Forest plot of UBE2C mRNA expression in ESCC based on in house RNA-seq, TCGA-GTEx RNA-seq and tissue microarrays. ESCC vs. normal, random-effects model; b, sROC of UBE2C in ESCC tissues based on in house RNA-seq, TCGA-GTEx RNA-seq and tissue microarrays; c, Sensitivity analysis of in house RNA-seq, TCGA-GTEx RNA-seq and tissue microarrays; d, Funnel plot of in house RNA-seq, TCGA-GTEx RNA-seq and tissue microarrays related to UBE2C.