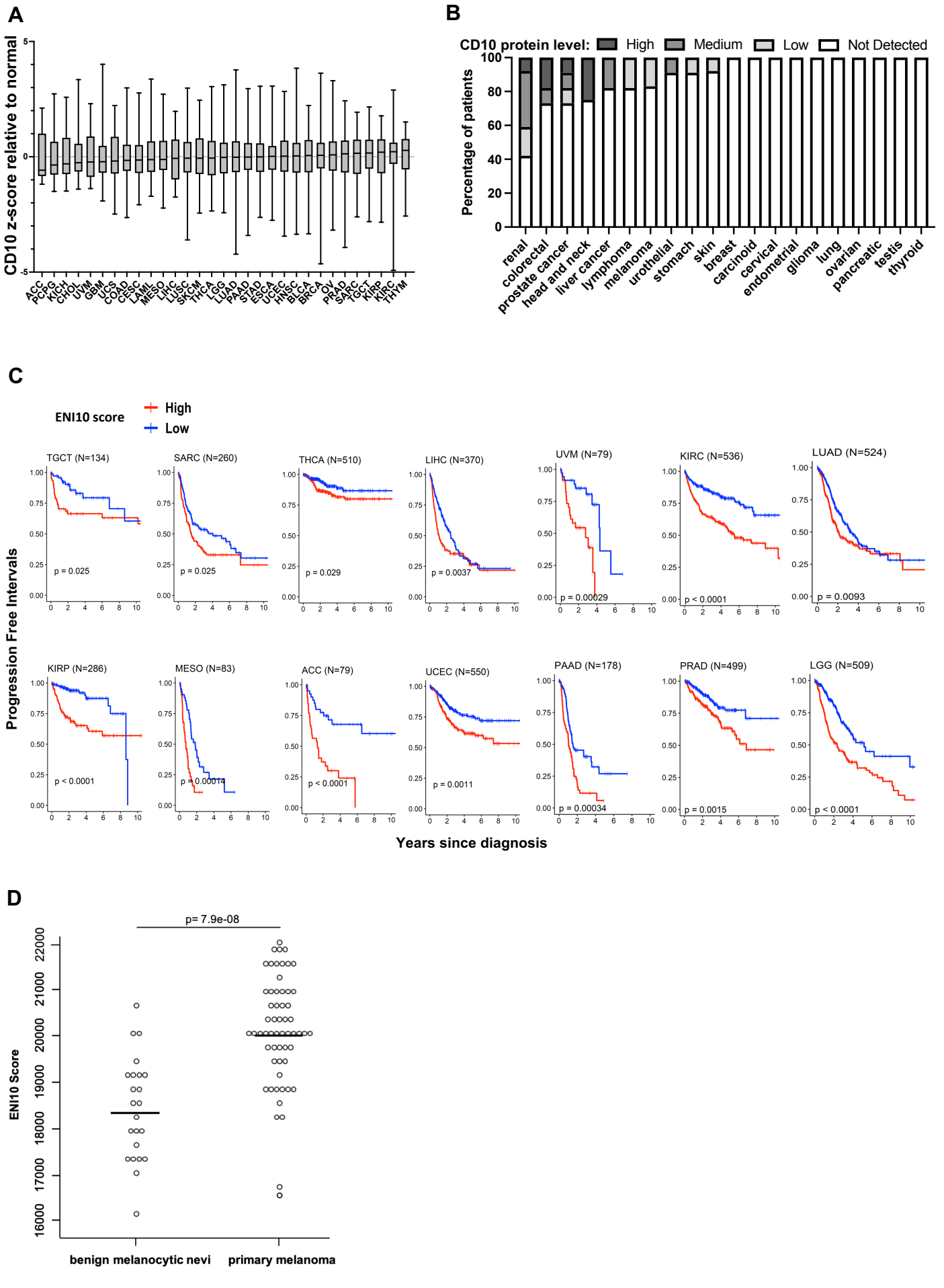
A
CD10 z-score relative to normal
ACC PCPG KICH CHOL UVM GBM UCS COAD CESC LAML MESO LIHC LUSC SKCM THCA LGG LUAD PAAD STAD ESCA UCEC HNSC BLCA BRCA OV PRAD SARC TGCT KIRP KIRC THYM
B
CD10 protein level: High Medium Low Not Detected
Percentage of patients
renal colorectal prostate cancer head and neck liver cancer lymphoma melanoma urothelial stomach skin breast carcinoid cervical endometrial glioma lung ovarian pancreatic testis thyroid
C
ENI10 score
High
Low
TGCT (N=134) p = 0.025
SARC (N=260) p = 0.025
THCA (N=510) p = 0.029
LIHC (N=370) p = 0.0037
UVM (N=79) p = 0.00029
KIRC (N=536) p < 0.0001
LUAD (N=524) p = 0.0093
KIRP (N=286) p < 0.0001
MESO (N=83) p = 0.00014
ACC (N=79) p < 0.0001
UCEC (N=550) p = 0.0011
PAAD (N=178) p = 0.00034
PRAD (N=499) p = 0.0015
LGG (N=509) p < 0.0001
Progression Free Intervals
Years since diagnosis
D
p= 7.9e-08
ENI10 Score
benign melanocytic nevi
primary melanoma

**Supplementary Figure S3**. A, CD10 transcript expression in TCGA tumor types relative to normal samples. B, CD10 protein expression in tumor types from the human protein atlas. C, Kaplan-Meier plot of various cancers patients in the TCGA cohorts divided by the median of the ENI10 score (low scores in blue and high scores in red). D, ssGSEA ENI10 score in transcriptomic data (GSE112509) from benign melanocytic nevi or primary melanoma (47). Each individual sample is indicated by an open circle and the median is shown as a bar.