

Figure S1 Densely associated blocks identified by *HALLA* software. A white dot indicates statistical significance ($P < 0.05$) of the related feature pairs.

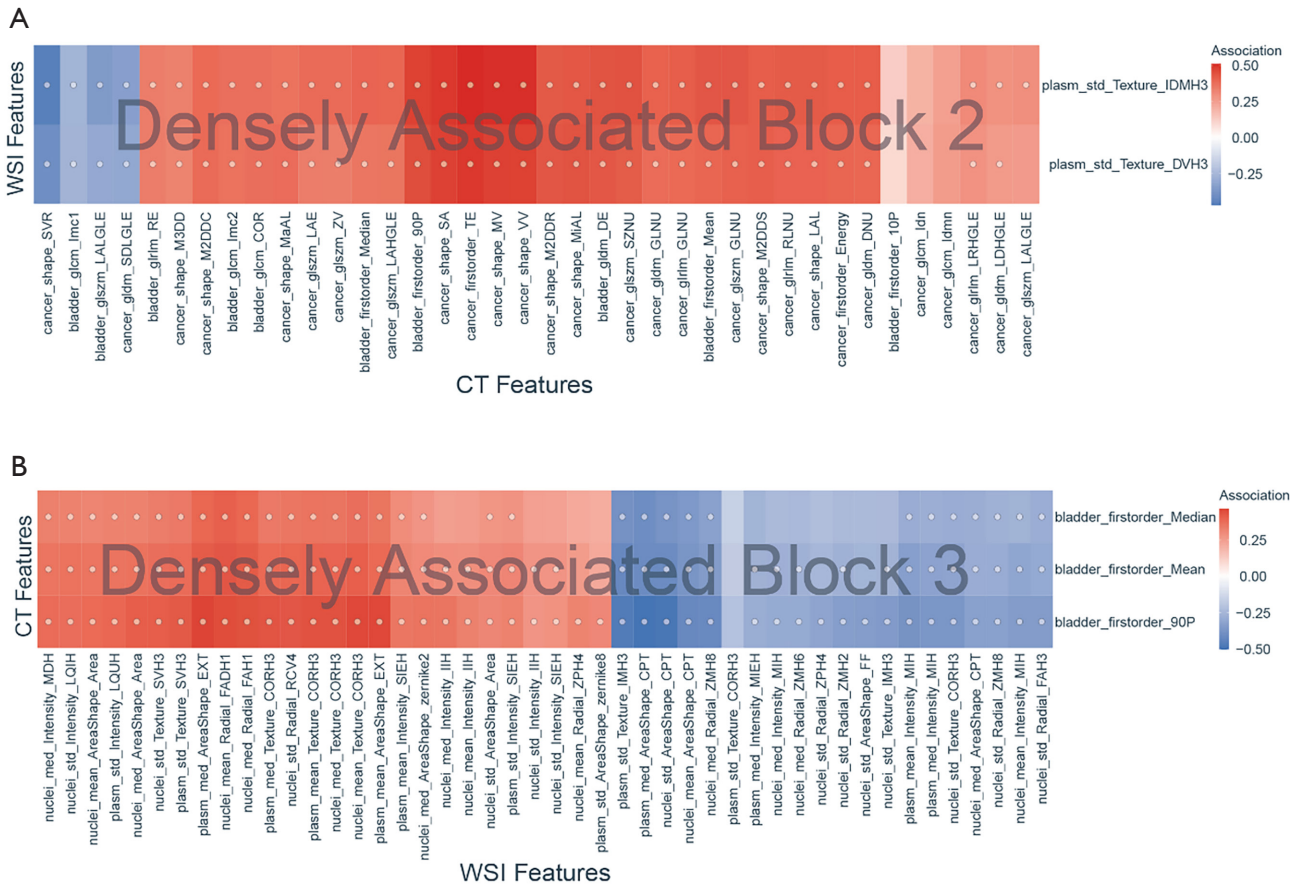


Figure S2 Heatmap of densely associated blocks 2 and 3 identified by *Halla* software. A white dot indicates statistical significance ($P < 0.05$) of the related feature pairs.

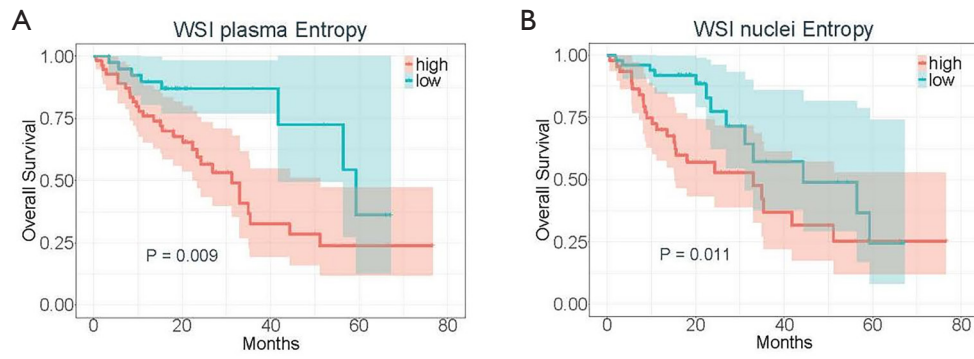


Figure S3 Survival analysis of plasmic and nucleic Shannon entropy. (A) The survival plot of plasma entropy. (B) The survival plot of nuclei entropy. WSI, whole slide imaging.

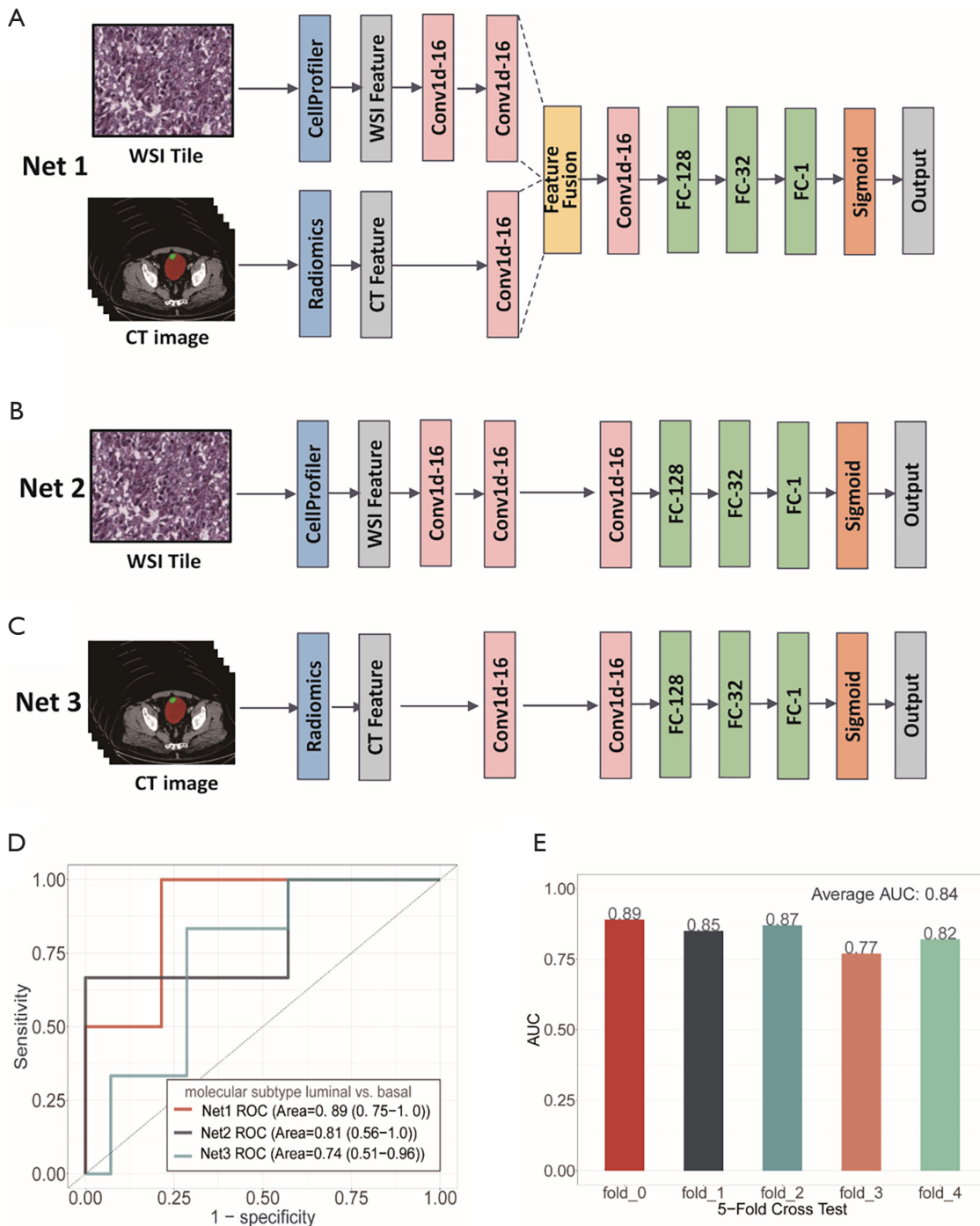


Figure S4 Comparison of three proposed neural networks in luminal/basal molecular subtype prediction. (A) Diagram of the neural network with fused features of WSI and CT. (B) Diagram of the neural network with pathological WSI features. (C) Diagram of the neural network with CT features. (D) ROC curves of the three proposed neural networks for the luminal/basal molecular subtype prediction in testing set (fold_0, 20 cases). Net1 stands for the neural network in (A), Net2 stands for the neural network in (B), and Net3 stands for the neural network in (C). The AUC was evaluated at the 95% CI. The Net1 reached the best performance among these three classification networks. (E) The AUC value was assessed with five-fold cross-validation using Net1 in the testing set. Stained with HE-staining method and magnified 40 times. WSI, whole slide imaging; CT, computed tomography; ROC, receiver operating characteristic; AUC, area under the curve.

Table S1 Clinical characteristics of each cohort

	First cohort; local hospital 1	Second cohort; local hospital 2	Third cohort; TCGA-BLCA
Basic information			
No. of participants	19	32	76
Female	0	4	17
Male	19	28	59
Pathology			
High grade	10	18	76
Low grade	9	14	0
Stage T1	16	32	0
Stage T2	3	0	26
Stage T3	0	0	31
Stage T4	0	0	9
Stage not available	0	0	10
Lymph node/distant metastasis	0	0	22
Carcinoma in situ	0	0	0
Molecular subtype			
Luminal		23	48
Basal		0	27
Not available	19	9	1