MCTI (Supplementary Material)

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Table 1: Acc and AUC performance are evaluated across four cancer datasets. Among them, the SNN using genomic profiles performs better in classification tasks. Our MCTI model also demonstrates excellent performance. The optimal results are highlighted in **bold**.

| Model	TCGA-BRCA		TCGA-ESCA		TCGA-NSCLC		TCGA-KICA	
	ACC	AUC	ACC	AUC	ACC	AUC	ACC	AUC
SNN	87.28	85.20	98.20	99.05	99.89	99.89	97.88	98.86
AvgPoool	69.40	79.25	78.31	86.54	69.05	78.88	81.22	94.56
AttnMIL	81.80	**90.45**	76.87	88.10	81.63	92.54	89.38	98.67
CLAM-SB	79.30	83.82	70.78	80.26	84.60	92.38	90.73	98.29
CLAM-MB	80.01	80.16	69.49	80.39	82.58	91.77	90.97	98.48
DSMIL	80.75	78.76	82.92	91.14	88.93	94.35	92.03	96.89
PORPOISE	**88.78**	88.57	**98.80**	**100.0**	**100.0**	**100.0**	**99.62**	99.85
M3IF	86.67	88.20	**98.80**	**100.0**	99.32	99.79	99.50	99.78
MCTI (Ours)	87.07	90.04	98.14	99.62	**100.0**	**100.0**	99.13	**99.93**
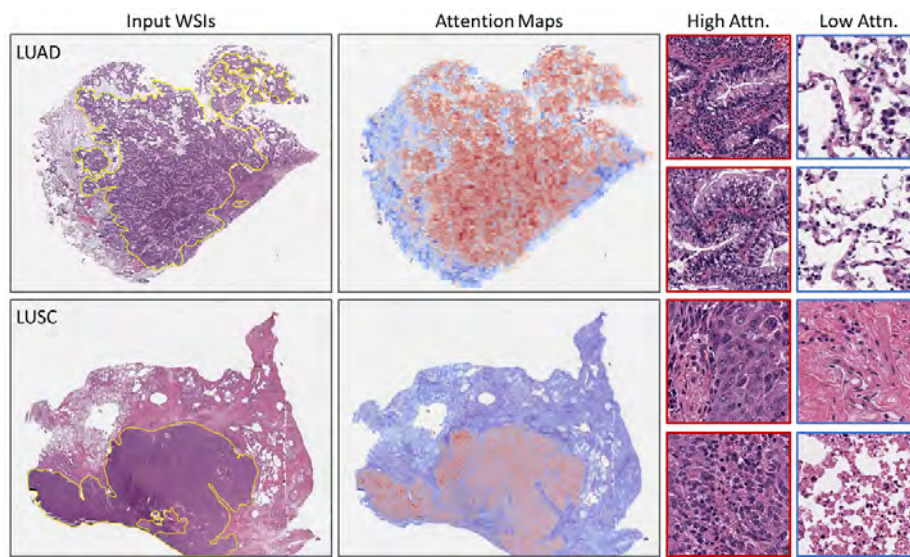
Fig. 1: Visualization of Attention maps. The yellow color in the input WSIs indicates the tumor regions. We visualize the attention scores of patches in WSI bag construction. The patch in the red box represents the high-attention region, and the patch in the blue box represents the low-attention region.