

Table S1: Predicted gene lists of our proposed model on STRING network and iRefIndex network for data of prostate cancer samples and thyroid cancer samples.

	STRING network (prostate cancer)	STRING network (thyroid cancer)	iRefIndex network (prostate cancer)	iRefIndex network (thyroid cancer)
1	AR	AKAP9	AR	AKAP9
2	BRAF	BRAF	BRAF	BRAF
3	CANT1	CCDC6	CANT1	CCDC6
4	DDX5	ERC1	DDX5	ERC1
5	ERG	GOLGA5	ERG	GOLGA5
6	ETV1	HOOK3	ETV1	HOOK3
7	ETV4	KRAS	ETV4	KRAS
8	FOXA1	NRAS	FOXA1	KTN1
9	HERPUD1	PCM1	HERPUD1	NRAS
10	KLF6	PPARG	KLF6	PCM1
11	KLK2	RET	KLK2	PPARG
12	NDRG1	TSHR	PTEN	RET
13	PTEN	A1BG	SPOP	TPM3
14	SPOP	A1CF	ZFH3	TSHR
15	TMPRSS2	A2LD1	A1BG	A1BG
16	ZFH3	A2M	A1CF	A1CF
17	A1BG	A4GALT	A2M	A2M
18	A1CF	AAAS	AAAS	AAAS
19	A2LD1	AACS	AADAT	AADAT
20	A2M	AADAC	AAGAB	AAGAB

Table S2: Functional enrichment analysis results of our proposed model on iRefIndex network. (a) Enrichment results of prostate cancer. (b) Enrichment results of thyroid cancer.

a	Function term	p-value
1	GO:0033148: positive regulation of intracellular estrogen receptor signaling pathway	5.43E-05
2	GO:0019899: enzyme binding	2.89E-04
3	GO:0043565: sequence-specific DNA binding	1.52E-03
4	GO:0001077: transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	1.59E-03
5	GO:0003700: transcription factor activity, sequence-specific DNA binding	2.06E-03
6	hsa05202:Transcriptional misregulation in cancer	3.36E-03
7	GO:0005654: nucleoplasm	4.56E-03
8	GO:0060740: prostate gland epithelium morphogenesis	7.90E-03
9	GO:0060736: prostate gland growth	9.02E-03
10	GO:0005634: nucleus	9.72E-03

b	Function term	p-value
1	hsa05216:Thyroid cancer	1.47E-12
2	hsa05200:Pathways in cancer	1.21E-05
3	GO:0000165: MAPK cascade	1.87E-04
4	GO:0005801: cis-Golgi network	8.65E-04
5	GO:0015031: protein transport	8.83E-04
6	hsa05219:Bladder cancer	1.84E-03
7	hsa05213:Endometrial cancer	2.95E-03
8	hsa05221:Acute myeloid leukemia	3.42E-03
9	hsa05223:Non-small cell lung cancer	3.42E-03
10	hsa04730:Long-term depression	3.91E-03

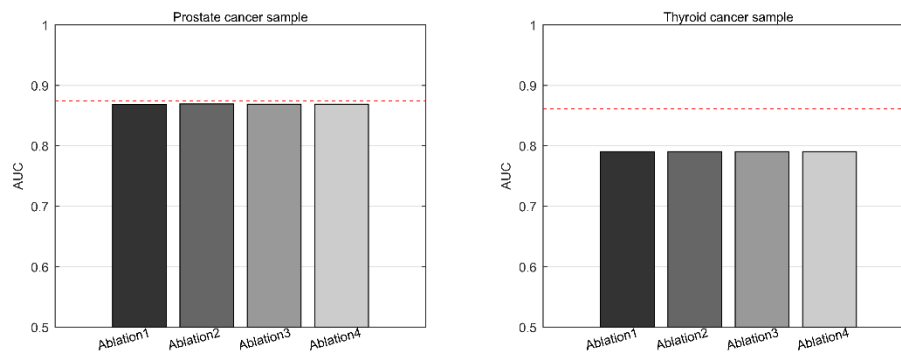


Figure S1: Ablation study on modules in our model for STRING network. The red dash lines represent the AUCs for cases of all modules, and the four bars denote the AUCs for cases of random ablation of three fourths of modules. (a) Prostate cancer samples; (b) Thyroid cancer samples.

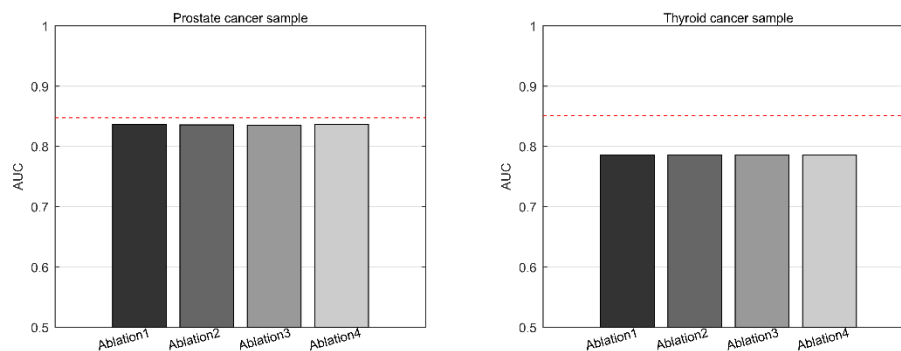


Figure S2: Ablation study on modules in our model for iRefIndex network. The red dash lines represent the AUCs for cases of all modules, and the four bars denote the AUCs for cases of random ablation of three fourths of modules. (a) Prostate cancer samples; (b) Thyroid cancer samples.

Supplementary Text:

Hyperparameter settings

In the selection of hyperparameters, there are totally three hyperparameter in our model, i.e. λ_X , λ_H , and λ_ϵ . When the degree of freedom of hyperparameters is large, the hyperparameters selection is much more difficult through grid search. Here we incorporate the design that matrix \mathbf{H}_ϵ is served as residual in the fusion of the two types of features \mathbf{H} and $\tilde{\mathbf{H}}$. Considering that the scale of residuals is much smaller than that of the primary matrix, we enforce the value of hyperparameter λ_ϵ being 2~3 magnitude greater than that of hyperparameter λ_H . This setting can ensure the scale dominant of matrix \mathbf{H} in comparison of residual matrix \mathbf{H}_ϵ . Based on the consideration above, there are only two free hyperparameter λ_X and λ_H , which are then determined by grid search strategy.