

Supplementary Table 1: Data Statistics of all datasets used for evaluation in this work.

No.	Application	Task	Dataset	Train	Val	Test	Total	Evaluation	Internal	Level
1	Pathological Diagnosis	Pathological Subtyping	BRCA-PathSubtype	656	95	234	985	Held-out	-	Slide
2	Pathological Diagnosis	Pathological Subtyping	GBMLGG_PathSubtype	839	200	237	1276	Held-out	-	Slide
3	Pathological Diagnosis	Pathological Subtyping	HANCOCK_PathSubtype	470	68	134	672	Independent	-	Slide
4	Pathological Diagnosis	Pathological Subtyping	TCGA-NSCLC	664	100	289	1053	Held-out	-	Slide
5	Pathological Diagnosis	Pathological Subtyping	EBrains_PathSubtype	-	-	732	732	External	GBMLGG_PathSubtype	Slide
6	Pathological Diagnosis	Pathological Subtyping	NFGC_Lauren	-	-	388	388	External	TCGA-STAD_Lauren	Slide
7	Pathological Diagnosis	Pathological Subtyping	NFGC_PathSubtype	-	-	385	385	External	TCGA-STAD_PathSubtype	Slide
8	Pathological Diagnosis	Pathological Subtyping	YN1_PathSubtype	-	-	254	254	External	TCGA-STAD_PathSubtype	Slide
9	Pathological Diagnosis	Pathological Subtyping	YN3_Lauren	-	-	319	319	External	TCGA-STAD_Lauren	Slide
10	Pathological Diagnosis	Pathological Subtyping	YN3_PathSubtype	-	-	315	315	External	TCGA-STAD_PathSubtype	Slide
11	Pathological Diagnosis	Metastasis Detection	CAMELYON	629	90	179	898	Independent	-	Slide
12	Pathological Diagnosis	Metastasis Detection	NF_Metastatic	493	70	142	705	Independent	-	Patient
13	Pathological Diagnosis	Metastasis Detection	NF_Metastatic_Fine	493	70	142	705	Independent	-	Patient
14	Pathological Diagnosis	Metastasis Detection	QFS_Metastatic	-	-	430	430	External	NF_Metastatic	Patient
15	Pathological Diagnosis	Metastasis Detection	QFS_Metastatic_Fine	-	-	430	430	External	NF_Metastatic_Fine	Patient
16	Pathological Diagnosis	Morphology Prediction	NFGC_Perineural	277	39	80	396	Independent	-	Patient
17	Pathological Diagnosis	Morphology Prediction	NFGC_Vascular	276	39	80	395	Independent	-	Patient
18	Pathological Diagnosis	Morphology Prediction	YN3_Perineural	-	-	319	319	External	NFGC_Perineural	Patient
19	Pathological Diagnosis	Morphology Prediction	YN3_Vascular	-	-	319	319	External	NFGC_Vascular	Patient
20	Pathological Diagnosis	Pathological Grading	PANDA	7143	1019	2040	10202	Independent	-	Slide
21	Pathological Diagnosis	Pathological Staging	HANCOCK-TStage	496	67	142	705	Independent	-	Patient
22	Molecular Prediction	Mutation Prediction	BRCA-GATA3	438	68	128	634	Held-out	-	Patient
23	Molecular Prediction	Mutation Prediction	BRCA-PIK3CA	438	68	128	634	Held-out	-	Patient
24	Molecular Prediction	Mutation Prediction	BRCA-TP53	438	68	128	634	Held-out	-	Patient
25	Molecular Prediction	Mutation Prediction	BRCA-TTN	438	68	128	634	Held-out	-	Patient
26	Molecular Prediction	Mutation Prediction	CRC-APC	243	36	67	346	Held-out	-	Patient
27	Molecular Prediction	Mutation Prediction	GBM-EGFR	112	19	35	166	Held-out	-	Patient
28	Molecular Prediction	Mutation Prediction	GBM-TP53	112	19	35	166	Held-out	-	Patient
29	Molecular Prediction	Mutation Prediction	HNSC-TP53	294	43	86	423	Held-out	-	Patient
30	Molecular Prediction	Mutation Prediction	LGG-CIC	313	38	88	439	Held-out	-	Patient
31	Molecular Prediction	Mutation Prediction	LUAD-EGFR	313	44	91	448	Held-out	-	Patient
32	Molecular Prediction	Mutation Prediction	LUAD-KRAS	313	44	91	448	Held-out	-	Patient
33	Molecular Prediction	Mutation Prediction	LUSC-TP53	302	43	87	432	Held-out	-	Patient
34	Molecular Prediction	Mutation Prediction	NSCLC-TMB	589	83	163	835	Held-out	-	Patient
35	Molecular Prediction	Mutation Prediction	SKCM-BRAF	287	41	84	412	Held-out	-	Patient
36	Molecular Prediction	Mutation Prediction	SKCM-DNAH5	287	41	84	412	Held-out	-	Patient
37	Molecular Prediction	Mutation Prediction	UCEC-ARID1A	277	37	83	397	Held-out	-	Patient
38	Molecular Prediction	Mutation Prediction	UCEC-PTEN	277	37	83	397	Held-out	-	Patient
39	Molecular Prediction	Mutation Prediction	UCEC-TTN	277	37	83	397	Held-out	-	Patient
40	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_PIK3CA	-	-	116	116	External	BRCA_PIK3CA	Patient
41	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_TP53	-	-	116	116	External	BRCA_TP53	Patient
42	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_TTN	-	-	120	120	External	BRCA_TTN	Patient
43	Molecular Prediction	Mutation Prediction	CPTAC_LUAD_KRAS	-	-	175	175	External	LUAD_KRAS	Patient
44	Molecular Prediction	Mutation Prediction	CPTAC_LUAD_EGFR	-	-	175	175	External	LUAD_EGFR	Patient
45	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_ER	667	94	188	949	Held-out	-	Patient
46	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_HER2	447	67	132	646	Held-out	-	Patient
47	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_PR	666	94	188	948	Held-out	-	Patient
48	Molecular Prediction	IHC Biomarker Prediction	IHC_NF1_CK7	293	42	84	419	Independent	-	Patient
49	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_HER2_Level	940	134	270	1344	Independent	-	Patient
50	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_CK5	672	96	193	961	Independent	-	Patient
51	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_ER_Level	1083	154	311	1548	Independent	-	Patient
52	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_HER2	-	-	1344	1344	External	TCGA_BRCA_ER	Patient
53	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_PR	-	-	1556	1556	External	TCGA_BRCA_HER2	Patient
54	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_ER	-	-	1548	1548	External	TCGA_BRCA_PR	Patient
55	Molecular Prediction	Molecular Subtyping	BRCA_MolSubtype	323	53	129	505	Held-out	-	Patient
56	Molecular Prediction	Molecular Subtyping	CRC_MolSubtype	325	49	118	492	Held-out	-	Patient
57	Molecular Prediction	Molecular Subtyping	GBMLGG_MolSubtype	401	64	87	552	Held-out	-	Patient
58	Molecular Prediction	Molecular Subtyping	TCGA_HNSC_HPV	284	39	82	405	Held-out	-	Patient
59	Molecular Prediction	Molecular Subtyping	EBrains_MolSubtype	-	-	428	428	External	GBMLGG_MolSubtype	Patient
60	Molecular Prediction	Molecular Subtyping	HANCOCK_HPV	-	-	332	332	External	TCGA_HNSC_HPV	Patient
61	Molecular Prediction	Molecular Subtyping	ZJ1_Breast_MolSubtype	-	-	2045	2045	External	BRCA_MolSubtype	Patient
62	Survival Prediction	Overall Survival	OS_BRCA	716	102	205	1023	Held-out	-	Patient
63	Survival Prediction	Overall Survival	OS_CRC	405	58	116	579	Held-out	-	Patient
64	Survival Prediction	Overall Survival	OS_GBMLGG	581	83	166	830	Held-out	-	Patient
65	Survival Prediction	Overall Survival	OS_HNSC	308	44	89	441	Held-out	-	Patient
66	Survival Prediction	Overall Survival	OS_KIRC	348	50	100	498	Held-out	-	Patient
67	Survival Prediction	Overall Survival	OS_LUAD	318	45	92	455	Held-out	-	Patient
68	Survival Prediction	Overall Survival	OS_LUSC	316	45	91	452	Held-out	-	Patient
69	Survival Prediction	Overall Survival	OS_SKCM	290	41	84	415	Held-out	-	Patient
70	Survival Prediction	Overall Survival	OS_UCEC	346	49	100	495	Held-out	-	Patient
71	Survival Prediction	Disease-Free Survival	DFS_BRCA	619	84	175	878	Held-out	-	Patient
72	Survival Prediction	Overall Survival	OS_HANCOCK	-	-	747	747	External	OS_HNSC	Patient
73	Survival Prediction	Overall Survival	OS_ZJ1	-	-	454	454	External	OS_BRCA	Patient
74	Survival Prediction	Disease-Free Survival	DFS_YN1	-	-	260	260	External	DFS_STAD	Patient
75	Survival Prediction	Disease-Free Survival	DFS_ZJ1	-	-	454	454	External	DFS_BRCA	Patient
76	Survival Prediction	Overall Survival	OS_NFCRC	-	-	-	294	Independent (5fold)	-	Patient
77	Survival Prediction	Recurrence-Free Survival	RFS_HANCOCK	-	-	-	747	Independent (5fold)	-	Patient

Supplementary Table 1: (Continuous Table) Data Statistics of all datasets used for evaluation in this work.

No.	Application	Task	Dataset	Train	Val	Test	Total	Evaluation	Internal	Level
78	Multimodal Fusion	Overall Survival	OS.BRCA	705	101	201	1007	Held-out	-	Patient
79	Multimodal Fusion	Overall Survival	OS.CRC	377	56	108	541	Held-out	-	Patient
80	Multimodal Fusion	Overall Survival	OS.GBMLGG	383	55	112	550	Held-out	-	Patient
81	Multimodal Fusion	Overall Survival	OS.HNSC	302	40	88	430	Held-out	-	Patient
82	Multimodal Fusion	Overall Survival	OS.KIRC	330	49	94	473	Held-out	-	Patient
83	Multimodal Fusion	Overall Survival	OS.LUAD	312	42	90	444	Held-out	-	Patient
84	Multimodal Fusion	Overall Survival	OS.LUSC	306	43	85	434	Held-out	-	Patient
85	Multimodal Fusion	Overall Survival	OS.SKCM	269	40	80	389	Held-out	-	Patient
86	Multimodal Fusion	Overall Survival	OS.UCEC	335	47	96	478	Held-out	-	Patient
87	Vision-Language	Zero-shot Slide Classification	CAMELYON	-	-	898	898	Zero-shot	-	Slide
88	Vision-Language	Zero-shot Slide Classification	PANDA	-	-	10202	10202	Zero-shot	-	Patient
89	Vision-Language	Zero-shot Slide Classification	UBC-OCEAN	-	-	527	527	Zero-shot	-	Slide
90	Vision-Language	Zero-shot Slide Classification	BCNB-ER	-	-	1038	1038	Zero-shot	-	Patient
91	Vision-Language	Zero-shot Slide Classification	BCNB-PR	-	-	1038	1038	Zero-shot	-	Patient
92	Vision-Language	Zero-shot Slide Classification	BCNB-HER2	-	-	1038	1038	Zero-shot	-	Patient
93	Vision-Language	Zero-shot Slide Retrieval	TCGA	-	-	934	934	Zero-shot	-	Patient
94	Vision-Language	Zero-shot Slide Retrieval	Breast&Lung	-	-	500	500	Zero-shot	-	Patient
95	Vision-Language	Report Generation	TCGA	7073	452	934	934	Held-out	-	Patient
96	Vision-Language	Report Generation	Nanfeng	-	-	250	250	External	TCGA	Patient
97	Vision-Language	Report Generation	ZJ-First	-	-	250	250	External	TCGA	Patient

Supplementary Table 2: Average Performance of 15 types of oncological tasks. *P-value* for every group of experiments is given through one-sided Wilcoxon signed-rank test with 1000 bootstrap replicates between mSTAR and the second-best FM for data analysis. * represents $P < 0.05$, ** means $P < 0.01$ and *** indicates $P < 0.001$.

Task	Metric	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
Pathological Subtyping***	Macro-AUC	0.6807±0.154	0.7555±0.149	0.7686±0.174	0.7761±0.161	0.7648±0.156	0.7659±0.177	0.7930±0.152
Metastasis Detection***	Macro-AUC	0.8205±0.109	0.8824±0.085	0.9511±0.029	0.9482±0.025	0.9285±0.041	0.9187±0.058	0.9652±0.027
Morphology Prediction***	Macro-AUC	0.6785±0.109	0.7502±0.092	0.7888±0.114	0.8101±0.099	0.7629±0.120	0.7802±0.101	0.8164±0.097
Pathological Grading	Macro-AUC	0.8872±0.008	0.9046±0.008	0.9220±0.008	0.9457±0.006	0.9291±0.007	0.9221±0.007	0.9409±0.006
Pathological Staging***	Macro-AUC	0.7527±0.062	0.7184±0.055	0.7617±0.055	0.7645±0.052	0.7450±0.056	0.7508±0.061	0.7786±0.054
Mutation Prediction***	Macro-AUC	0.5473±0.132	0.6122±0.140	0.6331±0.139	0.6711±0.143	0.6399±0.120	0.6331±0.131	0.6973±0.129
IHC Biomarker Prediction***	Macro-AUC	0.6108±0.124	0.7039±0.112	0.7215±0.131	0.7455±0.136	0.7334±0.127	0.7174±0.138	0.7631±0.134
Molecular Subtyping***	Macro-AUC	0.7265±0.114	0.8208±0.111	0.8634±0.084	0.8687±0.075	0.8672±0.075	0.8231±0.108	0.8865±0.079
Report Generation	BLEU 1	0.2154±0.034	0.2087±0.080	0.2414±0.021	0.2854±0.051	0.2591±0.044	0.2760±0.060	0.3178±0.033
Disease-Free Survival**	C-Index	0.5366±0.023	0.5712±0.047	0.5672±0.064	0.5993±0.050	0.5691±0.060	0.5533±0.057	0.6132±0.038
Overall Survival**	C-Index	0.6151±0.078	0.6356±0.084	0.6674±0.077	0.6784±0.066	0.6553±0.091	0.6482±0.076	0.6863±0.068
Recurrence-Free Survival**	C-Index	0.5791±0.029	0.6210±0.042	0.6590±0.059	0.6514±0.070	0.6429±0.059	0.6082±0.056	0.6632±0.067
Multimodal Fusion***	C-Index	0.6821±0.083	0.6755±0.084	0.6782±0.085	0.6903±0.082	0.6822±0.083	0.6840±0.081	0.7083±0.078
Zero-shot Slide Classification***	Recall@50	-	0.5912±0.084	0.5180±0.083	-	-	-	0.6297±0.129
Zero-shot Slide Retrieval	Recall@50	-	0.1550±0.019	0.1090±0.010	-	-	-	0.2200±0.016

Supplementary Table 3: Ablation study on different combinational modalities (Pathology, Reports and RNASeq) for survival analysis. Average C-Index and its std across 9 TCGA survival datasets are reported.

Aggregator (TransMIL)	Pretrained Data			Avg C-Index
	Pathology	Reports	RNASeq	
w/o pretraining	✓			0.666±0.068
w/ pretraining	✓	✓		0.679±0.057
	✓		✓	0.679±0.059
	✓	✓	✓	0.689±0.055

E. BREAST, RIGHT, MASTECTOMY.
 - TWO FOCI OF INVASIVE DUCTAL CARCINOMA,
 - SBR GRADE 3, MEASURING 1.1-CM
 - SBR GRADE 2, MEASURING 0.6-CM
 - INTERMEDIATE NUCLEAR GRADE: DUCTAL CARCINOMA IN SITU, SOLID AND CRIBRIFORM TYPES
 - SURGICAL RESECTION MARGINS NEGATIVE FOR TUMOR
 - BIOPSY SITE CHANGES WITH FIBROSIS
 - FIBROADENOMA AND SCLEROSING ADENOSIS
 - SEE SYNOPTIC REPORT AND SEE NOTE

NOTE: Left axillary sentinel lymph node #2 touch preparation is negative. Therefore, the false- negativity is due to sampling error. The morphology of metastatic tumor is similar to the larger grade 3 tumor (see below).

In the left mastectomy specimen, 2 nodules are grossly identified, larger nodule located in UOQ measuring 1.6 and is of grade 3, and a smaller nodule, located in posterior UIQ, measuring 0.5-cm and is of grade 1. Breast biomarkers on both nodules are pending.

In the right mastectomy specimen, 4 nodules are grossly identified, one is fibroadenoma, one is sclerosing adenosis, and the other two are separate foci of invasive ductal carcinoma. The largest invasive tumor measures 1.1-cm and it is of grade 3. Breast biomarkers are as follows, ER negative, PR negative and HER-2/neu equivocal (2+, FISH pending). The smaller nodule measures 0.5-cm and it is of grade 2. The breast biomarkers are as follows ER positive, PR positive and HER-2/neu equivocal (2+, FISH pending).

Also, the morphology of grade 3 tumors (right and left) is different. It seems that there are 4 different primary tumors, 2 in each breast.

SYNOPTIC REPORT - BREAST, ER/PR RESULTS
 Specimens Involved
 Specimens: E: RIGHT BREAST
 Specimen: Surgical Excision
 Block Number: E5, larger tumor

ER: Negative Allred Score: 0 = Proportion Score 0 + Intensity Score 0
 PR: Negative Allred Score: 0 = Proportion Score 0 + Intensity Score 0

COMMENT:
 The Allred score for estrogen and progesterone receptors is calculated by adding the sum of the proportion score (0 = no staining, 1 = <1% of cells staining, 2 = 1-10% of cells staining, 3 = 11-30% of cells staining, 4 = 31-60% of cells staining, 5 = >60% of cells staining) to the intensity score (1 = weak intensity of staining, 2 = intermediate intensity of staining, 3 = strong intensity of staining), with a scoring range from 0 to 8.
 ER/PR positive is defined as an Allred score of >2 and ER/PR negative is defined as an Allred score of less than or equal to 2.

METHODOLOGY:
 Tissue was fixed in 10% neutral buffered formalin for no less than 8 and no longer than 24 hours.
 Immunohistochemistry was performed using the mouse anti-human ER (ER 1D5, 1:100) and PR (PGR 136, 1:100) provided by Dako following the manufacturer's instructions. This assay was not modified.
 Interpretation of the ER/PR immunohistochemical stain is guided by published results in the medical literature, information provided by the reagent manufacturer and by internal review of staining performance.

PathVysion HER-2 DNA Probe Kit
 Case No
 Analytical Interpretation of Results: HER-2 NOT AMPLIFIED
 Clinical Interpretation of results
 Amplification of the HER-2 gene was evaluated with interphase fluorescence in-situ hybridization (FISH) on formalin-fixed paraffin embedded tissue sections using a chromosome 17 centromeric probe and a HER-2 probe that spans the entire HER-2 gene in the by Dr. A majority of tumors cells displayed 2 chromosome 17 signals and 2 HER-2 signals, with a HER-2/CEP 17 Ratio <=2.0, consistent with no amplification of the HER2/neu gene.
 Block used E5 Source of case:
 Tissue fixation formalin-fixed tissue Outside Case No: NA
 Tissue source breast Results interpreted: yes
 HER2/CEP17 ratio: 1.03
 This ratio is derived by dividing the total number of LSI HER-2/neu signals by the total number of CEP17 signals in at least 20 interphase nuclei with nonoverlapping nuclei in the neoplastic mammary epithelial cells. Cells with no signals or with signals of only one color are disregarded.
 Method of ratio enumeration: manual count

COMMENT
 This case was initially signed out as a provisional report on [REDACTED], and has been amended to include results of immunohistochemical stains. The diagnoses have not changed from the original report.

The lymph nodes resected in the case (specimen 1-8) show diffuse involvement with well-formed non-necrotizing granulomatous inflammation. Occasional mixed dust nodules with central hyalinization and focal central necrosis are also present. Special stains for fungal elements and acid-fast organisms are negative. There is no evidence of metastatic carcinoma in any of the lymph nodes examined.

Sections of the tumor in specimen 8 show predominately moderately differentiated squamous cell carcinoma (90%), with a small component (10%) of a poorly differentiated spindle cell carcinoma that demonstrates shows multiple mitoses and severe cytologic atypia. There is no malignant cartilage, bone, or skeletal muscle identified in the spindle cell component. Immunohistochemistry shows the squamous cell component of the tumor to be positive for multiple cytokeratins (HMWCK, CK5/6, AE1/AE3) and p63. The spindle component shows weak positive staining for CK5/6 and p63, with very focal positive staining for CK7. The EGFR shows strong membranous staining in approximately 90% of both the moderately differentiated component and the spindle component. Both components are negative for p53 and TTF-1. The findings are consistent with a pleomorphic carcinoma composed of predominantly squamous cell carcinoma (moderately differentiated, 90%) and pleomorphic spindle-cell carcinoma (poorly differentiated, 10%), pT2N0.

The residual lung parenchyma in both specimen 1 ("wedge resection right middle lobe") and specimen 8 ("right lower lobe") shows patchy interstitial fibrosis that appears accentuated in a subpleural distribution, with focal areas of architectural remodeling and cyst formation (microscopic honeycomb change). There is mild chronic interstitial inflammation associated with areas of fibrosis. Fibroblastic foci are readily identified. The blood vessels show focal fibrointimal thickening, likely secondary to the background inflammatory process, but no diagnostic evidence of active vasculitis. Granulomas are noted within an intraparenchymal lymph node (specimen 1), but are not identified in the lung parenchyma itself.

The overall findings in the lung tissue are in keeping with pulmonary

Status: corrected Page: 3 of 6

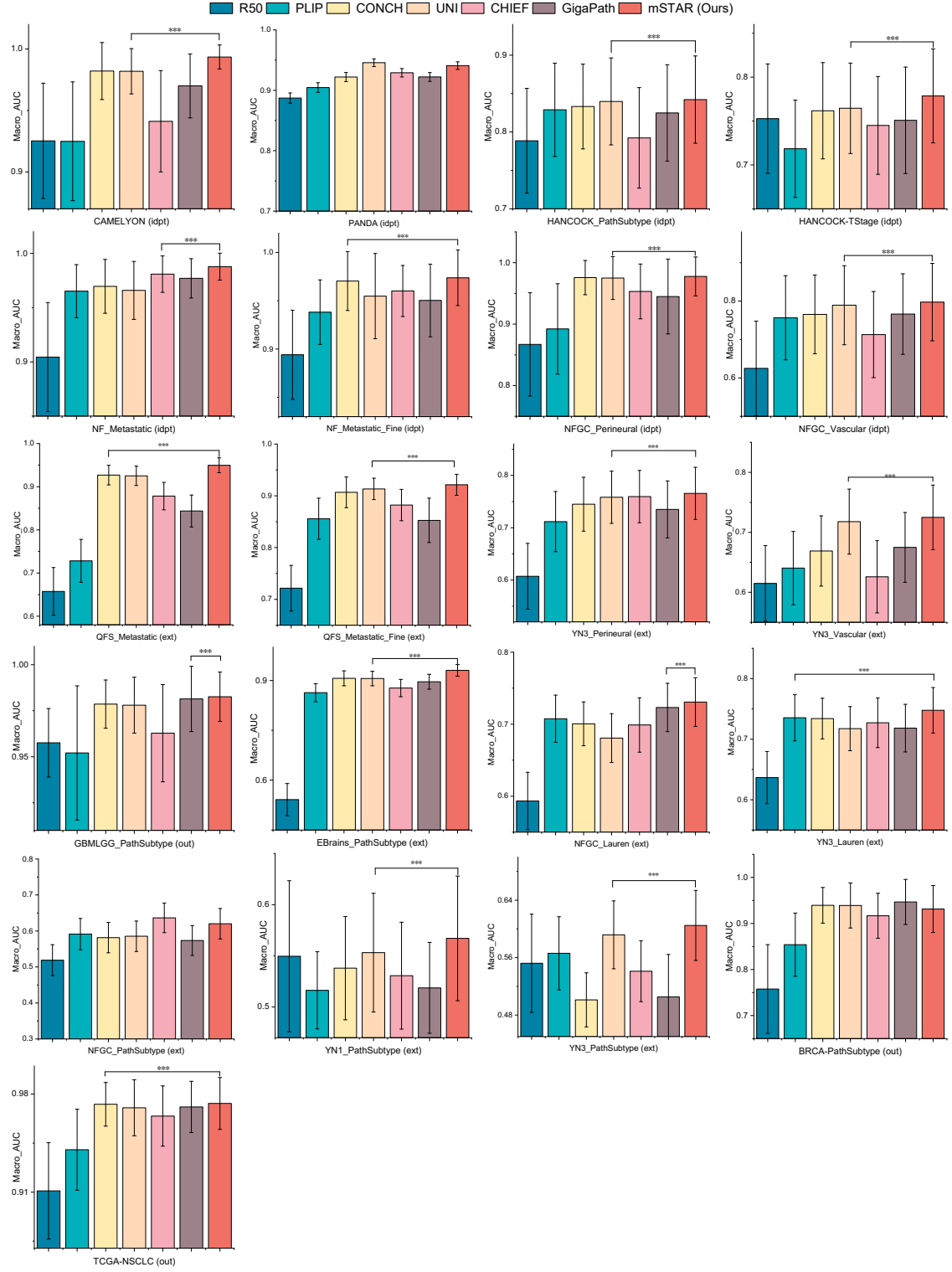
(a) TCGA-E2-A158 from TCGA-BRCA

(b) TCGA-18-4086 from TCGA-LUSC

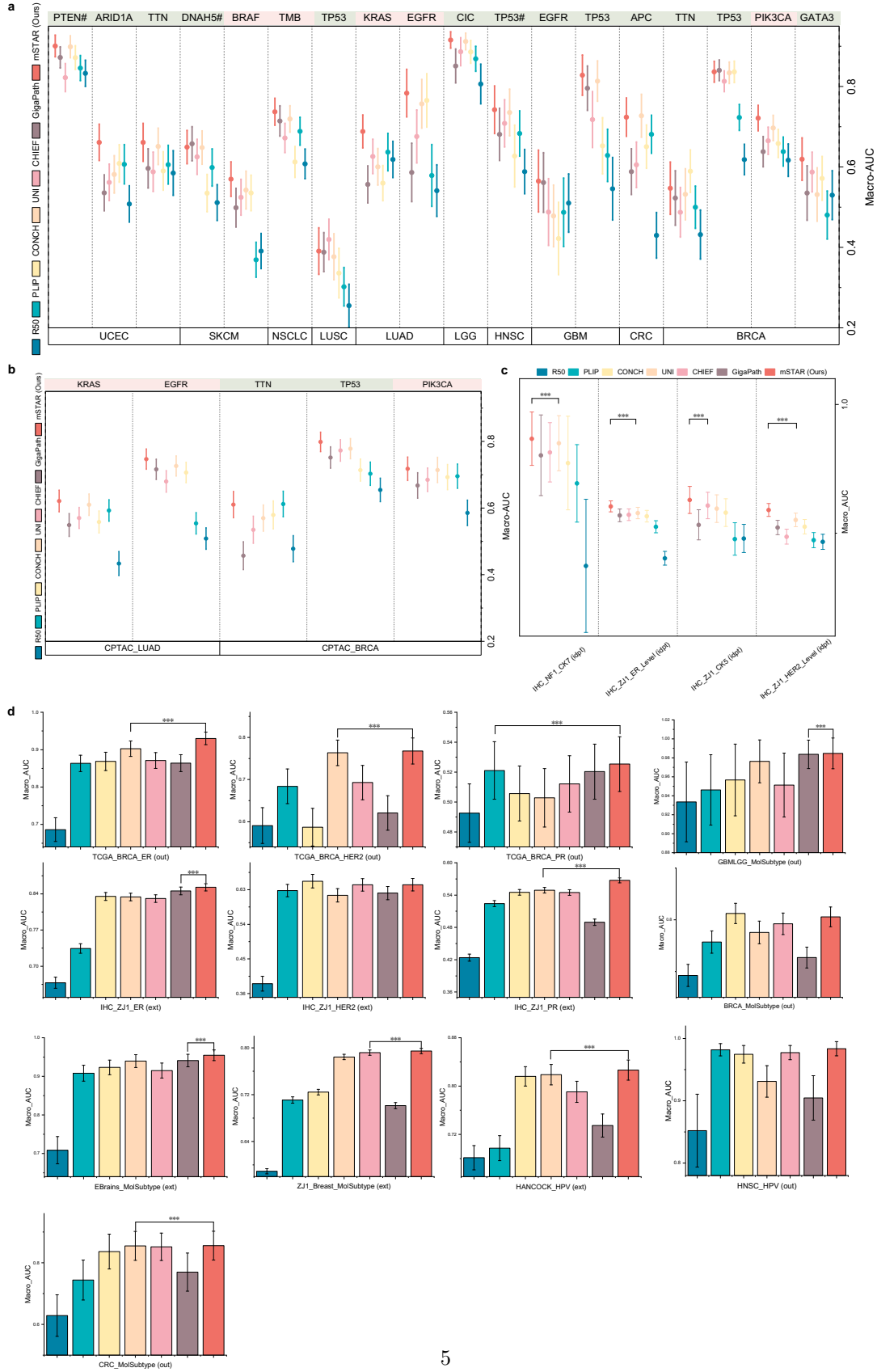
Supplementary Figure 1: Examples of pathology reports. (a) from breast cancer and (b) from lung cancer, where the text highlighted in the red box demonstrates the connection between pathology reports and gene expression profiles, and the one in the green box showcases the morphological descriptions in pathology reports.

Supplementary Table 4: Ablation study on different pretraining loss (Inter-modal and Inter-cancer Contrastive Losses) for survival analysis. Average C-Index and its std across 9 TCGA survival datasets are reported.

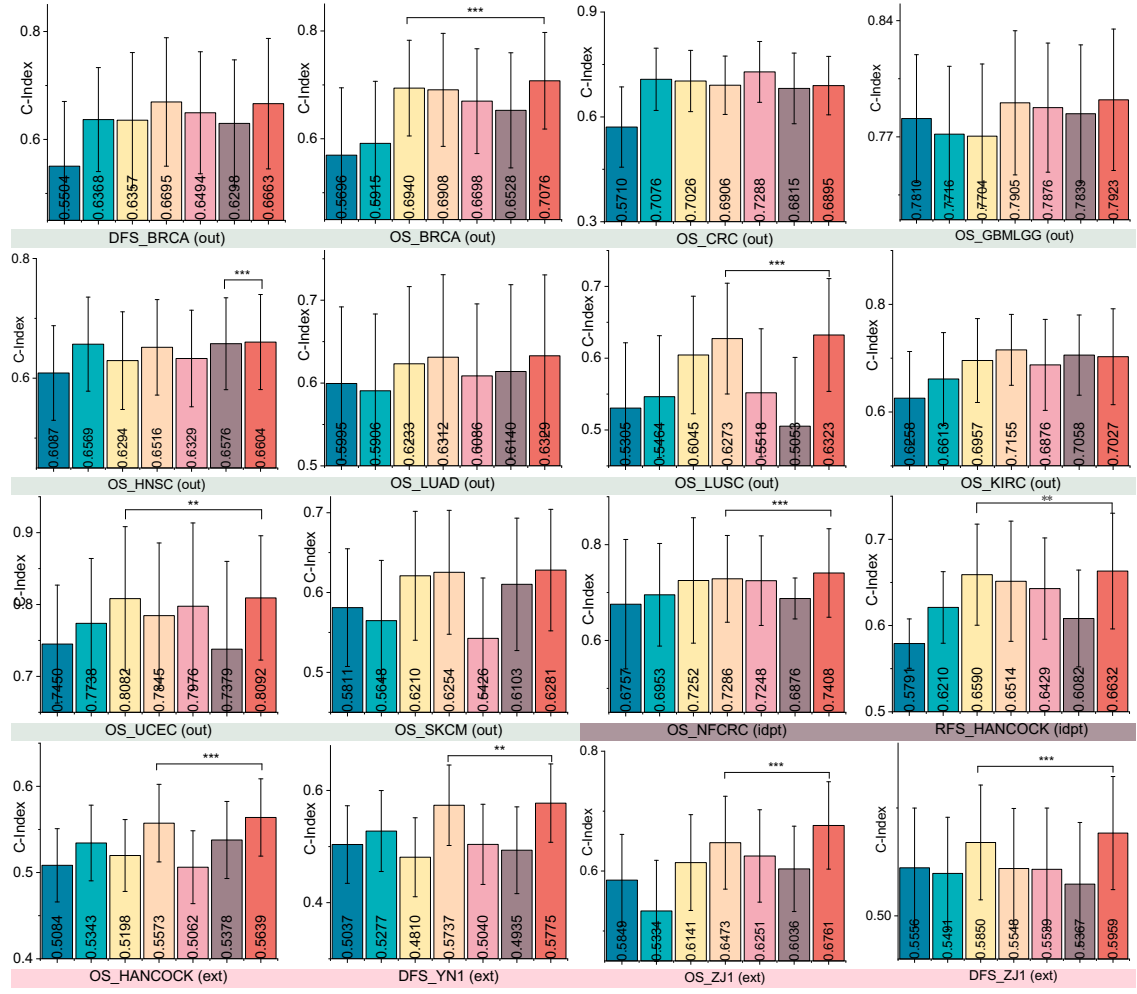
Loss		Avg C-Index
Inter-modality	Inter-cancer	
	✓	0.6788±0.0731
✓		0.6724±0.0536
✓	✓	0.6812±0.0666



Supplementary Figure 2: Performance of Pathological Diagnosis. * represents $P < 0.05$, ** means $P < 0.01$ and *** indicates $P < 0.001$. ‘out’ refers to held-out datasets. ‘idpt’ means independent datasets. ‘ext’ represents external datasets.



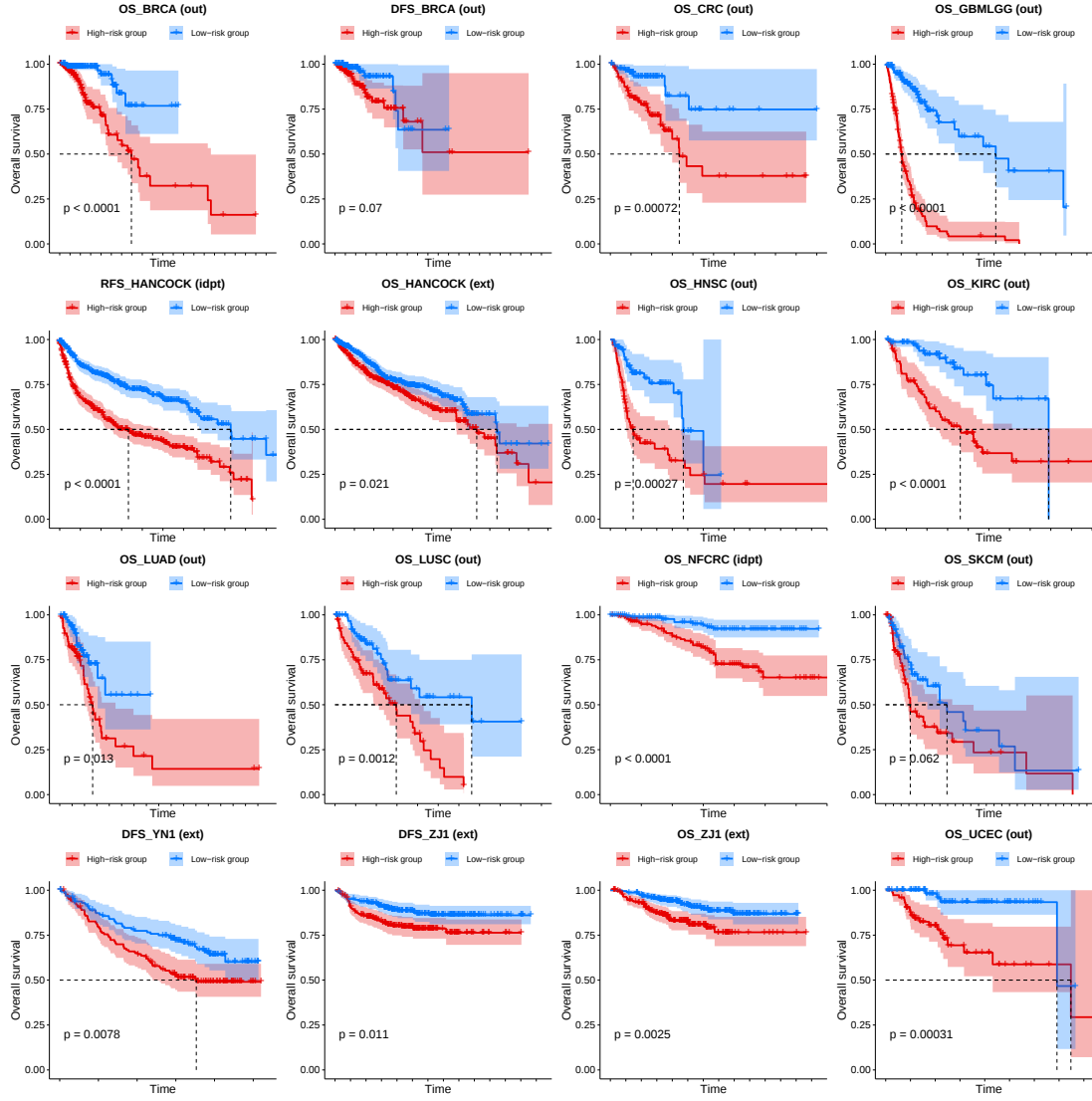
Supplementary Figure 3: Performance of Molecular Prediction. **a**, Mutation Prediction. Among the genes where mSTAR performed the best, results showed a statistically significant difference compared to the second-best FM, except for the genes marked with '#'. **b**, Performance of Mutation Prediction on external cohorts. **c**, Independent IHC Biomarker Prediction. **d**, Held-out and External IHC Biomarker Prediction, and Held-out Molecular Subtyping. * represents $P < 0.05$, ** means $P < 0.01$ and *** indicates $P < 0.001$. 'out' refers to held-out datasets. 'idpt' means independent datasets. 'ext' represents external datasets. High-frequency mutations are highlighted in green and genes related to FDA-approved therapies are highlighted in red.



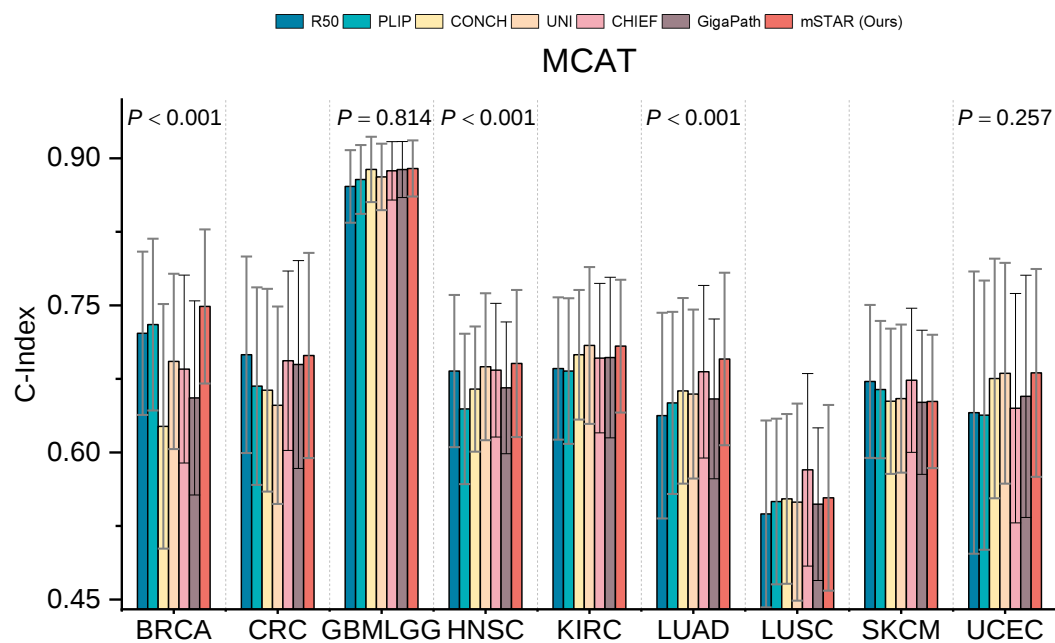
Supplementary Figure 4: Performance of Survival Prediction. * represents $P < 0.05$, ** means $P < 0.01$ and *** indicates $P < 0.001$. ‘out’ refers to held-out datasets. ‘idpt’ means independent datasets. ‘ext’ represents external datasets.

Supplementary Table 5: Resources Comparison between scaling slides only (Virchow) v.s. scaling modalities (mSTAR) for pretraining, with UNI as a baseline. * means that the pretraining GPU hours are coarsely estimated based on that of UNI, since it didn’t report such pretraining details.

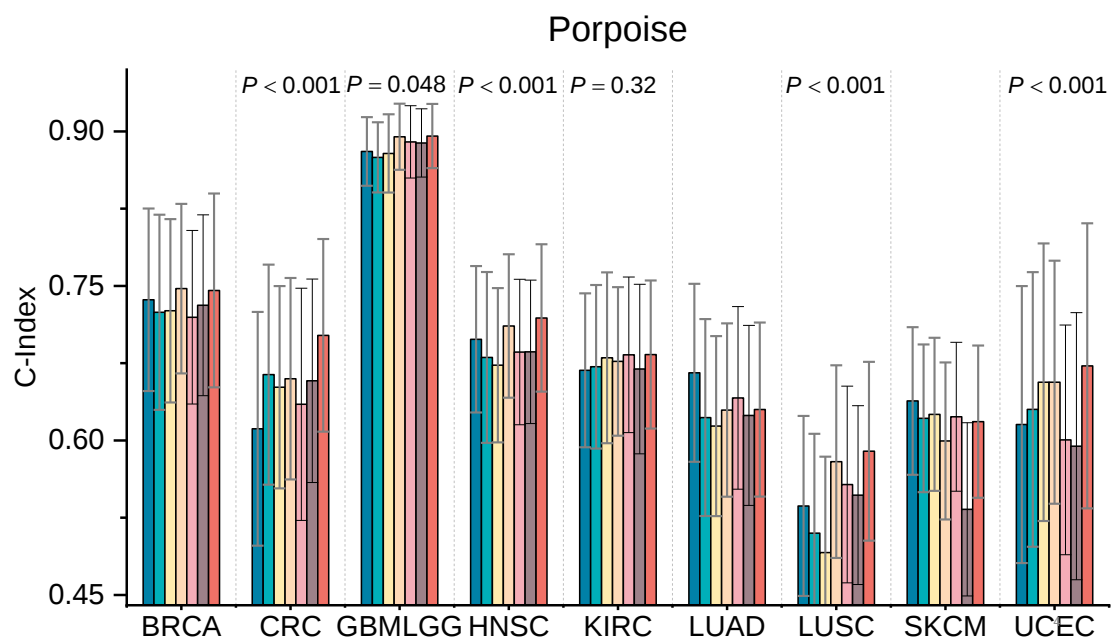
Models	#Params	# Pretraining Slide-level Data	# Pretraining GPU hours
UNI	303M	100,426	1,024 80G A100 GPU hours
Virchow	631M	1,488,550	1,024 × 2 × 15 80G A100 GPU hours*
mSTAR (all)	415M	100,426 + 22,127	672 80G H800 GPU hours



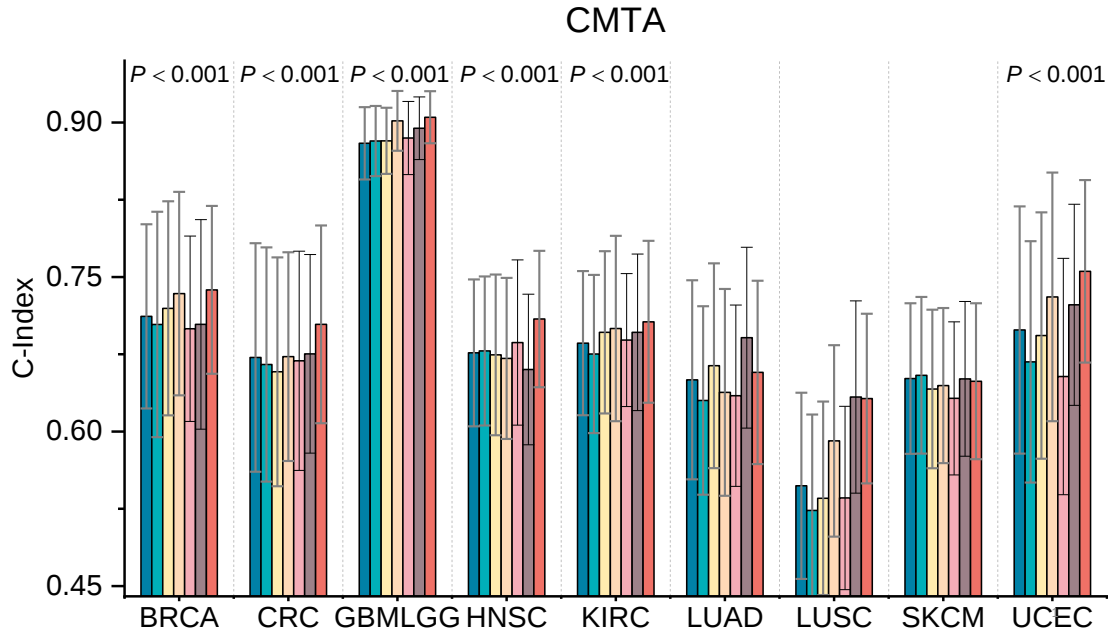
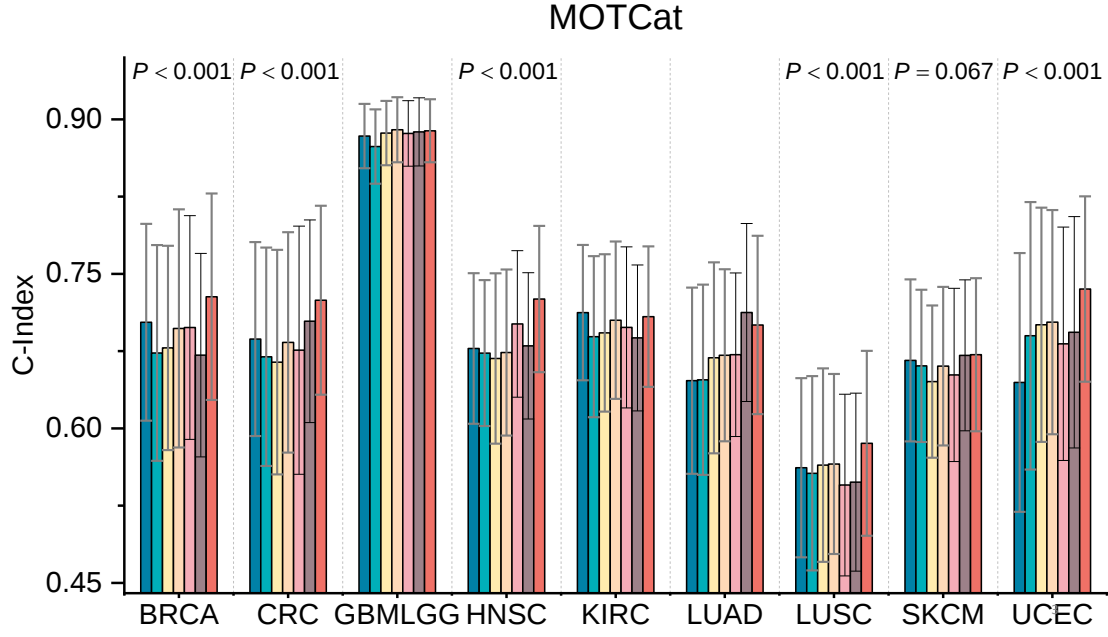
Supplementary Figure 5: Kaplan-Meier curves of mSTAR on every survival prediction task. P -value is given by Logrank Test [42].



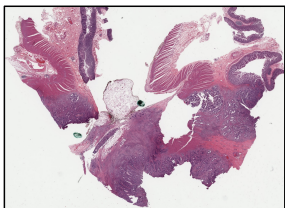
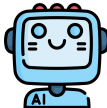
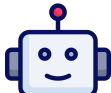
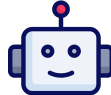
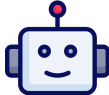
(a)



(b)

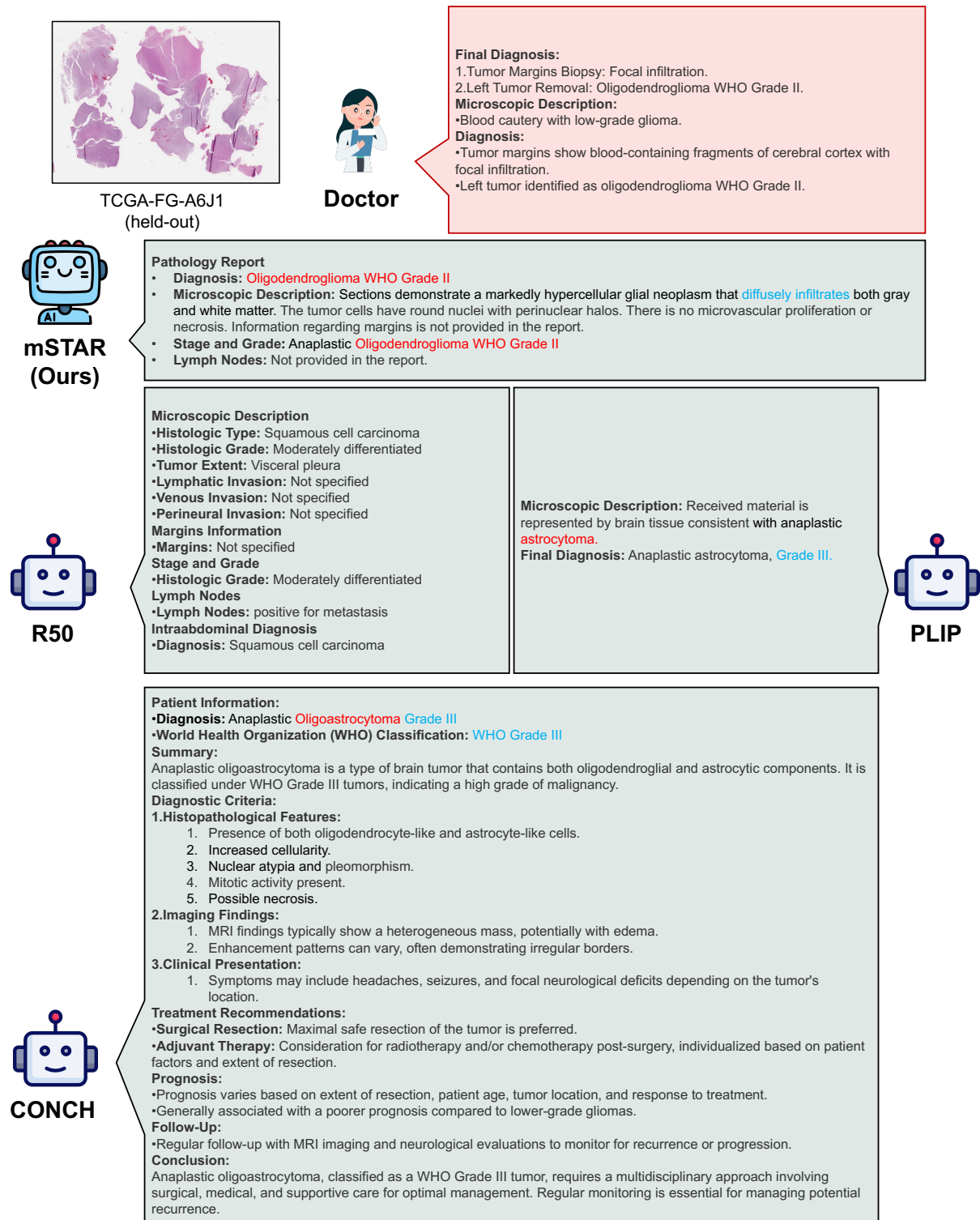


Supplementary Figure 6: Performance (C-Index and 95% CI) of Multimodal Fusion from 4 multimodal fusion models across 9 multimodal held-out datasets on Overall Survival consisting of pathological slides and RNASeq data: (a) MCAT, (b) Porpoise, (c) MOTCat and (d) CMTA. If the performance of mSTAR is the best one compared against the compared FMs, P-value would be given through one-sided Wilcoxon signed-rank test between mSTAR and the second-best FM. The colors of legends are shared across all sub-figures.

 TCGA-AZ-6605 (held-out)		 Doctor	Final Diagnosis: 1. Colon Right Hemicolectomy: - A. Moderately differentiated adenocarcinoma of the ascending colon, invasive into subserosa with perforation of the visceral peritoneum. - B. Proximal terminal ileal and distal colonic margins are free of tumor. - C. Metastatic adenocarcinoma in one of twenty-two lymph nodes. 2. Pathologic Stage: - PT4b N1 MX. 3. Margins: - Proximal margin uninvolved by invasive carcinoma. - Distal margin uninvolved by invasive carcinoma. - Mesenteric margin uninvolved by invasive carcinoma.	
 mSTAR (Ours)	Microscopic Description: - Histologic Type: Adenocarcinoma - Histologic Grade: Moderately Differentiated - Primary Tumor: - Tumor invades through the muscularis propria into pericolic fat (pT3) - Margins Information: - Proximal Margin: Negative for tumor - Distal Margin: Negative for tumor - Circumferential Radial Margin: Negative for tumor - Vascular Invasion: Not identified - Regional Lymph Nodes: - Metastatic carcinoma in one of thirteen lymph nodes (pN1) - Non-Lymph Node Pericolic Tumor: Not identified - Distant Metastasis: Cannot be assessed (pM cannot be assessed)			
 R50	Microscopic Description • Histologic Type: Squamous Cell Carcinoma • Histologic Grade: Moderately Differentiated • Tumor Extent: Visceral Pleura • Lymphatic Invasion: Not Specified • Venous Invasion: Not Specified • Perineural Invasion: Not Specified Margins Information • Margins: Not Specified Stage and Grade • Histologic Grade: Moderately Differentiated Lymph Nodes • Lymph Nodes: Positive for Metastasis Intraabdominal Diagnosis • Diagnosis: Squamous Cell Carcinoma	•Microscopic Description: • Histologic Type: Adenocarcinoma • Histologic Grade: Poorly differentiated • Tumor Features: Ulcerated •Tumor Extent: • Adjacent Structures: Lesser omentum • Margins Information: Margins uninvolved •Stage and Grade: • Histologic Grade: Poorly differentiated •Lymph Nodes: • Lymph Nodes: Positive for metastasis •Intraabdominal Diagnosis: • Diagnosis: Adenocarcinoma of the stomach	 PLIP	
 CONCH	•Microscopic Description • Adenocarcinoma tubulare G2 • Infiltratio carcinomatosa telae adiposae pericolicae • Intestine ends free of neoplastic lesions • Lymphonodulitis reactiva no •Margins Information • Incision lines free of neoplastic lesions •Stage and Grade • Dukes B • Astler-Coller C2 • PT3 • PNO •Lymph Nodes • Lymphonodulitis reactiva no VIII •Diagnosis • Adenocarcinoma tubulopapillare coli • Tubulopapillar adenocarcinoma of the colon	•Microscopic Description • Histologic Type: Adenocarcinoma • Histologic Grade: Moderately differentiated • Primary Tumor (PT): Tumor invades through the muscularis propria into pericolic fat (PT3) •Margins Information • Proximal Margin: Negative • Distal Margin: Negative • Circumferential Radial Margin: Negative (noted twice) •Vascular and Lymph Node Invasion • Vascular Invasion: Negative • Regional Lymph Nodes (PN): pN0 • Distant Metastasis (PM): Cannot be assessed •Additional Notes • Distance of Tumor from Closest Margin: (Information not provided)	 UNI	
 CHIEF	Microscopic Description: • Adenocarcinoma tubulopapillare partim mucinosum G3. • Infiltratio carcinomatosa tunicae muscularis propriae et telae adiposae pericolicae. • Intestine ends free of neoplastic lesions. Margins Information: • Incision lines free of neoplastic lesions. Stage and Grade: • Dukes B • Astler-Coller B2 • pT3 pNo Lymph Nodes: • Lymphonodulitis reactiva no Diagnosis: • Adenocarcinoma tubulopapillare coli. • Tubulopapillar adenocarcinoma of the colon.	•Microscopic Description • Histologic Type: Colonic Adenocarcinoma • Histologic Grade: Moderately Differentiated • Primary Tumor: • PT: Tumor invades through muscularis propria into subserosal fat (PT3) • Margins Information: • Proximal Margin: Negative • Distal Margin: Negative • Circumferential Radial Margin: Negative (noted twice) • Vascular Invasion: Negative • Regional Lymph Nodes: PN (pNO) • Non-Lymph Node Pericolic Tumor: Not identified (noted twice) • Distant Metastasis: PM cannot be assessed	 GigaPath	

10

(a) Ground truth of reports from doctors and the generated text from various models for case TCGA-AZ-6605 (held-out).



(b) Ground truth of reports from doctors and the generated text from various models for case TCGA-FG-A6J1 (part1, held-out).



Report: Diagnosis of Glioblastoma Multiforme

Patient Information

- **Patient ID:** [Enter Patient ID]
- **Patient Name:** [Enter Patient Name]
- **Date of Birth:** [Enter Date of Birth]
- **Date of Report:** [Enter Date of Report]
- **Referring Physician:** [Enter Referring Physician Name]

Clinical Summary

- **Chief Complaint:** [Enter Chief Complaint]
- **Presenting Symptoms:**
 - Headaches
 - Seizures
 - Cognitive changes
 - Focal neurological signs

Diagnostic Imaging

- **Techniques Used:** MRI or CT scan
- **Findings:**
 - Presence of a mass lesion
 - Characteristics (e.g., enhancing lesions, edema)
 - Location of the tumor (e.g., frontal lobe, temporal lobe)

Histopathological Findings

- **Biopsy Results:**
 - Tumor type: Glioblastoma Multiforme (GBM)
 - Grade: IV
 - Key characteristics: pleomorphic cells, necrosis, microvascular proliferation

Treatment Plan

- **Recommended Treatment:**
 - Surgery: Resection or biopsy
 - Adjuvant therapy: Radiation therapy, chemotherapy (Temozolomide)
- **Prognosis:** [Enter Prognosis Information]

Follow-Up

- **Next Steps:**
 - Schedule follow-up MRI
 - Monitor for treatment side effects
 - Refer to oncology for further management

Notes

- [Any additional notes or considerations]

Signature: [Enter Physician's Signature] **Title:** [Enter Physician's Title] **Contact Information:** [Enter Contact Information]



Diagnosis: Anaplastic **Oligodendroglioma**, **WHO Grade III**

Microscopic Description:

- Sections demonstrate a **diffusely infiltrating** glial neoplasm that diffusely infiltrates both gray and white matter.
- The neoplastic cells exhibit:
 - Round to oval nuclei with prominent perinuclear halos.
 - Prominent nucleoli.
- **Mitoses are noted.**

Margins: Information not specified.

Stage and Grade: **WHO Grade III.**

Lymph Nodes Included in Biopsy: Not specified.

Pathology Report

Microscopic Description: The received material is represented by brain tissue consistent with anaplastic **oligodendroglioma**.

Final Diagnosis: Anaplastic **oligodendroglioma**, **Grade III.**

Margins Information: Not specified.

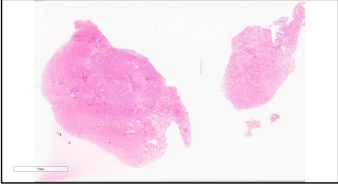
Stage and Grade: Anaplastic **oligodendroglioma**, **WHO Grade III.**

Lymph Nodes Included in Biopsy: Not specified.

Diagnosis: Anaplastic oligodendroglioma, WHO Grade III.



(c) Ground truth of reports from doctors and the generated text from various models for case TCGA-FG-A6J1 (part2, held-out).





Doctor

Nanfang-NO.14739
(external)

Pathology Report

Microscopic Description:

- Location: Right upper lung nodule
- Nodules: 2 sites

Node 1:

- Classification: Infiltrating adenocarcinoma
- Maximum Diameter: Approximately 13 mm

Histological Types:

- Acinar type: Approximately 60%
- Papillary type: Approximately 30%
- Lepidic type: Approximately 10%

Node 2:

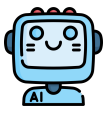
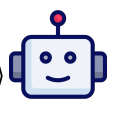
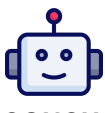
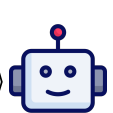
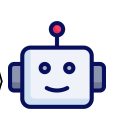
- Classification: Infiltrating adenocarcinoma
- Maximum Diameter: Approximately 5 mm

Histological Types:

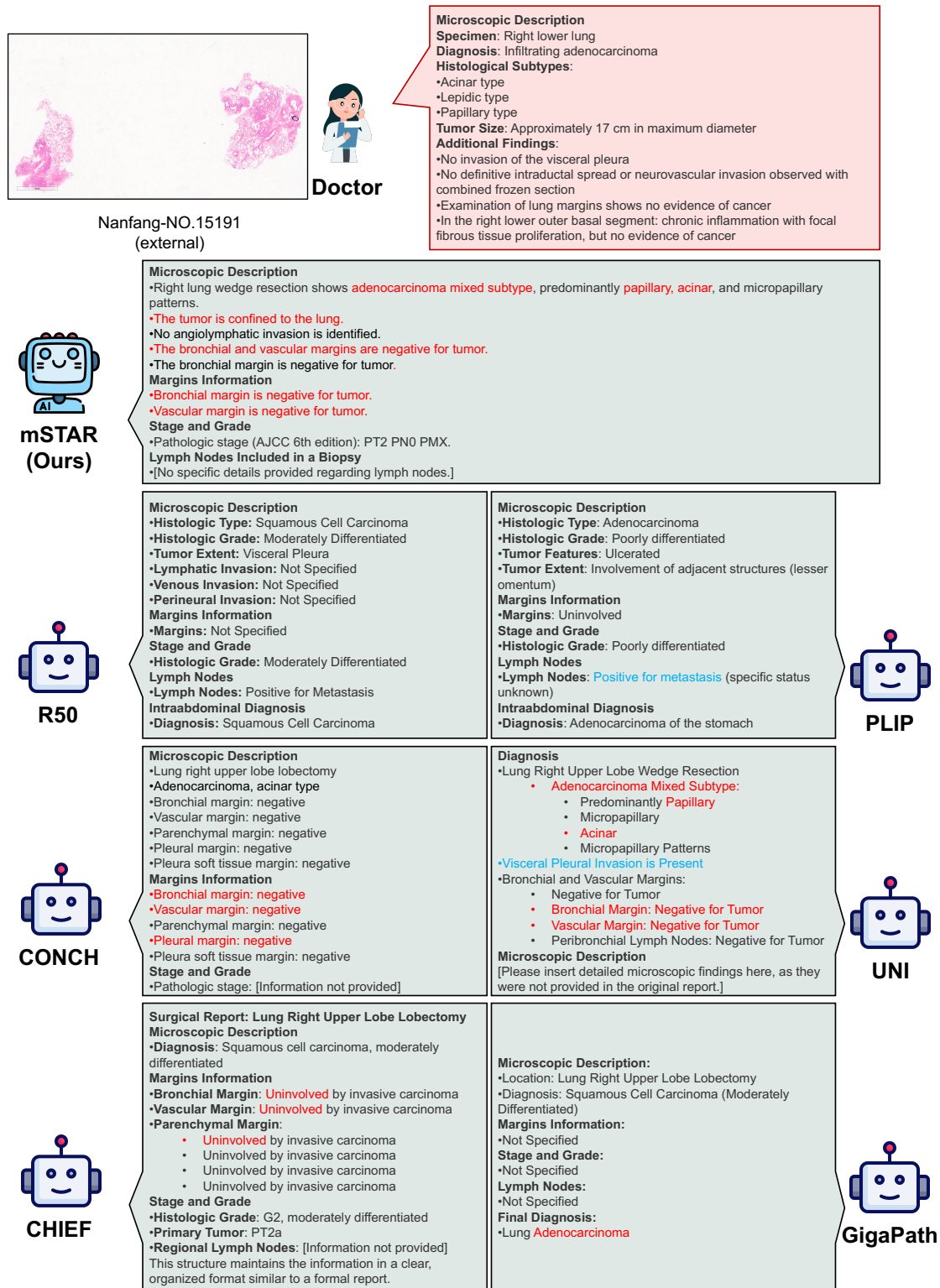
- Papillary type: Approximately 60%
- Acinar type: Approximately 40%

Additional Findings:

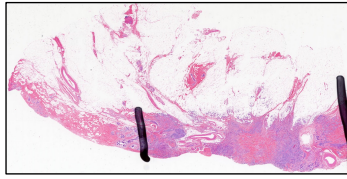
- No evidence of cancer cell dissemination along alveolar spaces.
- No invasion of the elastic layer noted.
- No definite vascular invasion or nerve infiltration observed.

 mSTAR (Ours)	Microscopic Description •Right lung wedge resection: • Adenocarcinoma, mixed subtype predominantly showing papillary and acinar patterns. • The tumor is confined to the lung. • The bronchial margins are negative for tumor. • The vascular margins are negative for tumor. Margins Information •Bronchial margin: Negative for tumor. •Vascular margin: Negative for tumor.	
 R50	Microscopic Description •Histologic Type: Squamous Cell Carcinoma •Histologic Grade: Moderately Differentiated •Tumor Extent: Visceral Pleura •Lymphatic Invasion: Not Specified •Venous Invasion: Not Specified •Perineural Invasion: Not Specified Margins Information •Margins: Not Specified Stage and Grade •Histologic Grade: Moderately Differentiated Lymph Nodes •Lymph Nodes: Positive for Metastasis Intraabdominal Diagnosis •Diagnosis: Squamous Cell Carcinoma	 PLIP
 CONCH	Microscopic Description •Specimen: Lung (Right Upper Lobe Lobectomy) •Diagnosis: Squamous Cell Carcinoma (Moderately Differentiated) Lymph Node Evaluation •Lymph Nodes Included in Biopsy: • 4R Lymph Node: Negative for metastasis Margins Information •Bronchial Margin: Negative for tumor •Vascular Margin: Negative for tumor •Pleural Margin: Negative for tumor •Parenchymal Margin: Negative for tumor Stage and Grade •Histologic Grade: Moderately Differentiated •Primary Tumor (PT): PT2a	 UNI
 CHIEF	Microscopic Description: •Lung right upper lobe lobectomy •Squamous cell carcinoma, moderately differentiated Margins Information: •Bronchial margin: uninvolved by invasive carcinoma •Vascular margin: uninvolved by invasive carcinoma •Parenchymal margin: uninvolved by invasive carcinoma Stage and Grade: •Histologic Grade: G2 (moderately differentiated) •Pathologic Staging: PTNM • Primary Tumor (PT): PT2 (tumor more than 4 cm but not more than) (Note: The description ends abruptly; please fill in the remaining details for clarity if available.)	 GigaPath

(d) Ground truth of reports from doctors and the generated text from various models for case Nanfang-NO.14739 (external).



(e) Ground truth of reports from doctors and the generated text from various models for case Nanfang-NO.15191 (external).



ZJ-First_1151
(external)



Doctor

Microscopic Description: The tumor cells show a nest-like and glandular arrangement with invasive growth. The tumor cells exhibit nuclear atypia with visible mitotic figures, and large areas of ductal carcinoma are observed in the surrounding tissue.

Margins Information:

- Upper: Negative for cancer cells
- Lower: Negative for cancer cells
- Inner: Negative for cancer cells
- Outer: Negative for cancer cells
- Basal: Negative for cancer cells
- Surface: Negative for cancer cells

Lymph Nodes: No cancer metastasis observed in 3 sentinel lymph nodes.

Stage and Grade: Invasive ductal carcinoma of the breast, WHO grade II.

Diagnosis: Invasive ductal carcinoma, right breast mass excision specimen.



mSTAR
(Ours)

Microscopic Description:

- Invasive ductal carcinoma, SBR grade.
- Ductal carcinoma in situ, intermediate nuclear grade.

Margins Information:

- Surgical margins are free of tumor.

Stage and Grade:

- Pathologic Staging (PTNM):
 - Primary Tumor (PT): PT2 - tumor more than 2 cm but not more than 5 cm in greatest dimension, limited to the breast.
 - Regional Lymph Nodes (PN): PNO - no regional lymph node metastasis.
 - Distant Metastasis (PMX): cannot be assessed.

Lymph Nodes Included in Biopsy:

- Sentinel lymph node #1, right axilla - biopsy one lymph node negative for tumor.

Diagnosis:

- Invasive ductal carcinoma with ductal carcinoma in situ.



R50

Microscopic Description

- Histologic Type: Squamous Cell Carcinoma
- Histologic Grade: Moderately Differentiated
- Tumor Extent: Visceral Pleura
- Lymphatic Invasion: Not Specified
- Venous Invasion: Not Specified
- Perineural Invasion: Not Specified

Margins Information

- Margins: Not Specified

Stage and Grade

- Histologic Grade: Moderately Differentiated

Lymph Nodes

- Lymph Nodes: Positive for Metastasis

Intraabdominal Diagnosis

- Diagnosis: Squamous Cell Carcinoma

Microscopic Description:

- Histologic Type: Infiltrating Ductal Carcinoma
- Histologic Grade: Moderately Differentiated

Margins Information:

- Margins: Not Specified

Stage and Grade:

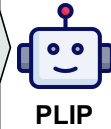
- Histologic Grade: Moderately Differentiated

Lymph Nodes:

- Lymph Nodes: positive for metastasis
- Axillary: 010

Diagnosis:

- Infiltrating Ductal Carcinoma



PLIP



CONCH

Microscopic Description:

- Infiltrating ductal carcinoma, Nottingham grade III
 - Tubules: 33
 - Nuclei: 23
 - Mitoses: 23
 - Nottingham score: 89
- Ductal carcinoma in situ (DCIS), high nuclear grade, solid type with comedo necrosis and calcifications
- Angiolymphatic invasion: Absent
- Non-neoplastic breast parenchyma shows nonproliferative fibrocystic changes

Margins Information:

- All surgical resection margins are negative for tumor.

Stage and Grade:

- Nottingham grade III of III

Lymph Nodes:

- Right axillary sentinel lymph node #1: Negative for metastatic carcinoma
- Right axillary sentinel lymph node #2: Negative for metastatic carcinoma

Final Diagnosis:

- Breast: Right mastectomy
 - Infiltrating Ductal Carcinoma: Nottingham Grade II of III
 - Tubules: 33
 - Nuclei: 23
 - Mitoses: 23
 - Nottingham Score: 89
 - Ductal Carcinoma in Situ: Intermediate nuclear grade, solid and cribriform types with comedo necrosis and microcalcifications

Margins Information:

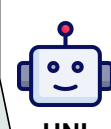
- Surgical margins are negative for tumor.

Stage and Grade:

- Nottingham Score: 89

Lymph Nodes:

- Sentinel Lymph Node #1: Right axilla biopsy
 - One lymph node negative for tumor.
- Sentinel Lymph Node #2: Left axilla biopsy
 - One lymph node negative for tumor.
- Sentinel Lymph Node #2: Right axilla (details not provided).



UNI



CHIEF

Diagnosis: Breast Cancer

Microscopic Description: Infiltrative Ductal Carcinoma

Margins Information: Not specified

Stage and Grade:

- Grade: 2
- T Stage: 2
- N Stage: 0
- M Stage: 0

Lymph Nodes: Not specified

Microscopic Description:

- Infiltrating ductal carcinoma, Nottingham Grade III of III.
- Ductal carcinoma in situ (DCIS), high nuclear grade, solid type with comedo necrosis and microcalcifications.

Margins Information:

- Surgical margins are free of tumor.

Stage and Grade:

- Nottingham Grade III of III.

Lymph Nodes:

- No lymph nodes identified in the biopsy.

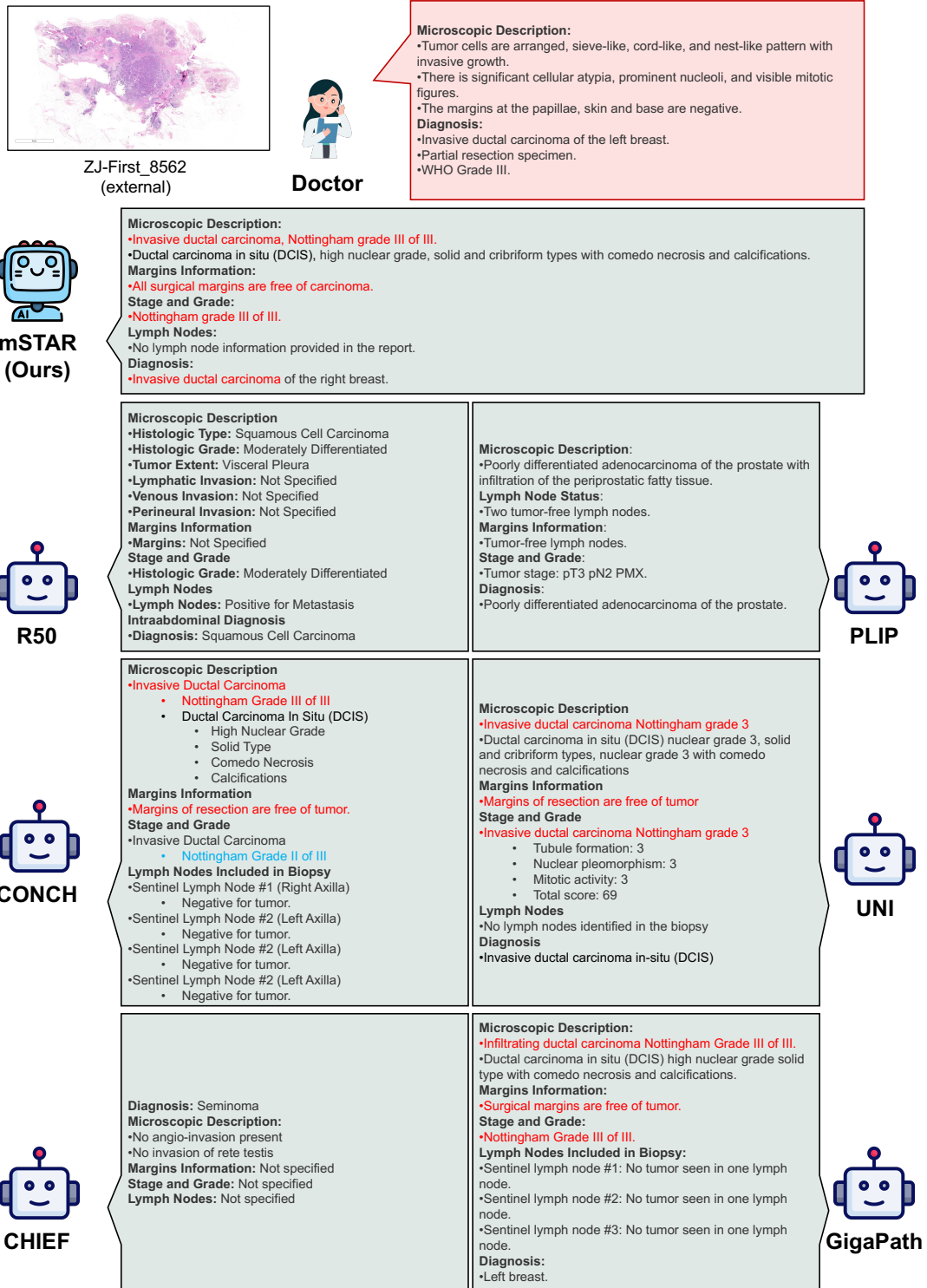
Diagnosis:

- Infiltrating ductal carcinoma, Nottingham Grade II of III.



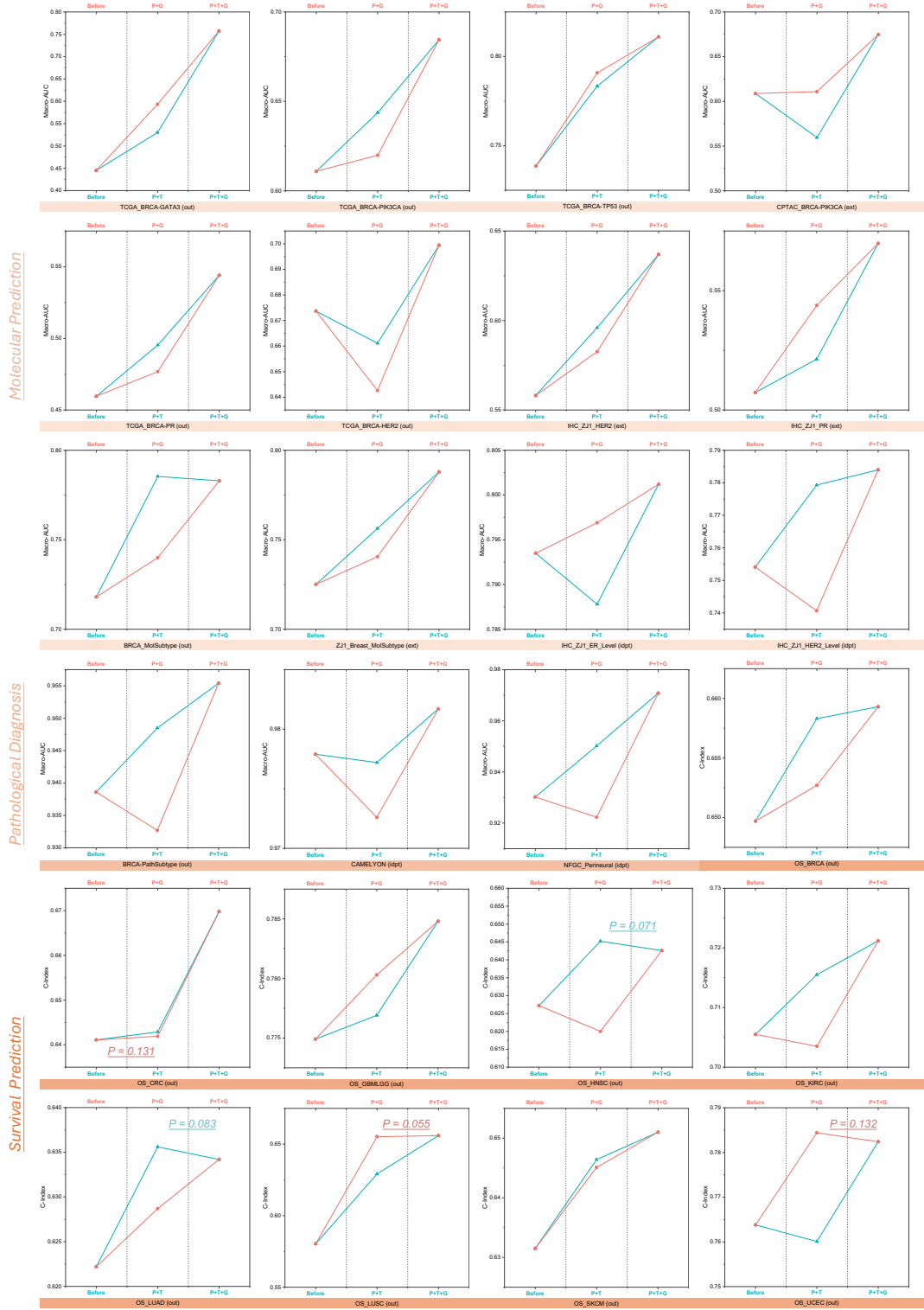
GigaPath

(f) Ground truth of reports from doctors and the generated text from various models for case ZJ-First_1151 (external).



(g) Ground truth of reports from doctors and the generated text from various models for case ZJ-First_8562 (external).

Supplementary Figure 7: Pathology Reports Generation for several cases. The words highlighted in **red** are matched with the ground-truth report, while the ones highlighted in **blue** are contradicted to the ground-truth report. All logos are designed by Freepik [freepik.com](https://www.freepik.com).



Supplementary Figure 8: Performance on each dataset in ablation studies (24 datasets), where the red curve indicates the trajectory of ‘before pretraining → + genes → + text’, while the green one represents the trajectory of ‘before pretraining → + text → + genes’. One-sided Wilcoxon signed-rank tests were conducted for every pairwise comparisons along the trajectory. Unless otherwise specified, reported differences are statistically significant ($P < 0.001$).

Supplementary Table 6: Performance Comparison between scaling slides only (Virchow) v.s. scaling modalities (mSTAR) for pretraining, with UNI as a baseline. The best-performing model for each metric is bolded. Std is given by bootstrapping with 1,000 bootstraps. Both Virchow and mSTAR underwent one-sided Wilcoxon signed-rank tests against the baseline UNI. For results outperforming the baseline, all unmarked (*) ones exhibited statistically significant differences at $P < 0.001$.

Task	Dataset	UNI	Virchow	mSTAR
Pathological Diagnosis	CAMELYON (idpt)	0.9819±0.0184	0.9683±0.0248	0.9935±0.0098
Pathological Diagnosis	NFGC_Perineural (idpt)	0.9750±0.0349	0.9270±0.0685	0.9776±0.0316
Pathological Diagnosis	BRCA-PathSubtype (out)	0.9391±0.0489	0.9449±0.0526	0.9314±0.0510
Molecular Prediction	BRCA_PIK3CA (out)	0.6969±0.0315	0.6669±0.0492	0.7215±0.0318
Molecular Prediction	TCGA_BRCA_HER2 (out)	0.7636±0.0305	0.7287±0.0506	0.7679±0.0310
Molecular Prediction	TCGA_BRCA_PR (out)	0.5028±0.0195	0.5080±0.0258*	0.5254±0.0183
Molecular Prediction	BRCA_MolSubtype (out)	0.7756±0.0219	0.7659±0.0301	0.8057±0.0191
Molecular Prediction	IHC.ZJ1_HER2_Level (idpt)	0.7758±0.0132	0.7628±0.0196	0.7951±0.0125
Molecular Prediction	IHC.ZJ1_ER_Level (idpt)	0.7892±0.0111	0.7960±0.0152	0.8020±0.0107
Molecular Prediction	IHC.ZJ1_HER2 (ext)	0.6153±0.0173	0.6558±0.0226	0.6429±0.0162
Molecular Prediction	IHC.ZJ1_PR (ext)	0.5490±0.0052	0.5733±0.0063	0.5673±0.0047
Molecular Prediction	ZJ1_Breast_MolSubtype (ext)	0.7844±0.0046	0.7582±0.0066	0.7946±0.0045
Survival Prediction	OS_BRCA (out)	0.6908±0.1048	0.6525±0.0506	0.7076±0.0896
Survival Prediction	OS_CRC (out)	0.6906±0.0835	0.6140±0.0577	0.6895±0.0836
Survival Prediction	OS_GBMLGG (out)	0.7905±0.0434	0.7790±0.0206	0.7923±0.0426*
Survival Prediction	OS_HNSC (out)	0.6516±0.0798	0.6000±0.0381	0.6604±0.0794
Survival Prediction	OS_KIRC (out)	0.7155±0.0659	0.6967±0.0395	0.7027±0.0890
Survival Prediction	OS_LUAD (out)	0.6312±0.0996	0.6194±0.0457	0.6329±0.0976*
Survival Prediction	OS_LUSC (out)	0.6273±0.0771	0.5382±0.0463	0.6323±0.0785
Survival Prediction	OS_SKCM (out)	0.6254±0.0776	0.6207±0.0423	0.6281±0.0761*
Survival Prediction	OS_UCEC (out)	0.7845±0.1012	0.7477±0.0556	0.8092±0.0865

Supplementary Table 7: Macro-AUC of Pathological Diagnosis on 21 datasets, including 10 external datasets, 8 independent datasets and 3 held-out datasets. The best-performing model for each metric is bolded. Std is given by bootstrapping with 1,000 bootstraps.

Task	dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
Pathological Subtyping	BRCA_PathSubtype	0.7577±0.0963	0.8540±0.0686	0.9395±0.0387	0.9391±0.0489	0.9167±0.0489	0.9467±0.0489	0.9314±0.0510	Held-out
	EBrains_PathSubtype	0.5415±0.0186	0.8632±0.0364	0.9065±0.0131	0.9059±0.0152	0.8772±0.0264	0.8962±0.0177	0.9304±0.0134	External
	GBMLGG_PathSubtype	0.9576±0.0682	0.9521±0.0607	0.9786±0.0552	0.9780±0.0566	0.9628±0.0654	0.9814±0.0627	0.9826±0.0568	Held-out
	HANCOCK_PathSubtype	0.7886±0.0430	0.8289±0.0435	0.8332±0.0423	0.8398±0.0423	0.7923±0.0411	0.8248±0.0414	0.8422±0.0424	Independent
	NFGC_Lauren	0.5933±0.0344	0.7076±0.0289	0.7005±0.0156	0.6807±0.0200	0.6989±0.0215	0.7232±0.0183	0.7307±0.0185	External
	NFGC_PathSubtype	0.5190±0.0738	0.5915±0.0377	0.5816±0.0505	0.5854±0.0580	0.6366±0.0522	0.5737±0.0444	0.6202±0.0609	External
	TCGA-NSCLC	0.9109±0.0840	0.9403±0.0735	0.9727±0.0278	0.9702±0.0349	0.9643±0.0446	0.9708±0.0609	0.9733±0.0316	Held-out
	YN1_PathSubtype	0.5496±0.1232	0.5163±0.1096	0.5380±0.1024	0.5531±0.1029	0.5306±0.1120	0.5187±0.1049	0.5671±0.1008	External
	YN3_Lauren	0.6366±0.0630	0.7354±0.0574	0.7340±0.0514	0.7174±0.0499	0.7271±0.0500	0.7183±0.0545	0.7477±0.0497	External
	YN3_PathSubtype	0.5522±0.0629	0.5661±0.0610	0.5012±0.0585	0.5918±0.0542	0.5411±0.0602	0.5054±0.0582	0.6048±0.0538	External
Metastasis Detection	CAMELYON	0.9253±0.0484	0.9249±0.0270	0.9821±0.0224	0.9819±0.0218	0.9412±0.0260	0.9700±0.0224	0.9935±0.0174	Independent
	NF_Metastatic	0.9044±0.0469	0.9652±0.0483	0.9696±0.0232	0.9659±0.0184	0.9809±0.0412	0.9770±0.0260	0.9873±0.0098	Independent
	NF_Metastatic_Fine	0.8941±0.0503	0.9382±0.0244	0.9704±0.0248	0.9548±0.0267	0.9601±0.0168	0.9503±0.0181	0.9738±0.0124	Independent
	QFS_Metastatic	0.6574±0.0553	0.7282±0.0497	0.9269±0.0227	0.9253±0.0224	0.8783±0.0318	0.8438±0.0370	0.9497±0.0172	External
	QFS_Metastatic_Fine	0.7215±0.0441	0.8557±0.0398	0.9067±0.0296	0.9133±0.0207	0.8821±0.0303	0.8526±0.0428	0.9213±0.0202	External
Morphology Prediction	NFGC_Perineural	0.8670±0.0430	0.8922±0.0381	0.9757±0.0336	0.9750±0.0364	0.9532±0.0410	0.9449±0.0393	0.9776±0.0376	Independent
	NFGC_Vascular	0.6247±0.0684	0.7566±0.0509	0.7654±0.0377	0.7892±0.0473	0.7128±0.0424	0.7661±0.0590	0.7973±0.0488	Independent
	YN3_Perineural	0.6072±0.0084	0.7117±0.0080	0.7450±0.0075	0.7583±0.0064	0.7596±0.0070	0.7350±0.0073	0.7657±0.0063	External
	YN3_Vascular	0.6149±0.0623	0.6404±0.0554	0.6689±0.0548	0.7178±0.0515	0.6259±0.0557	0.6749±0.0606	0.7249±0.0535	External
Pathological Grading	PANDA	0.8872±0.0461	0.9046±0.0334	0.9220±0.0305	0.9457±0.0441	0.9291±0.0264	0.9221±0.0376	0.9409±0.0288	Independent
Pathological Staging	HANCOCK-TStage	0.7527±0.0398	0.7184±0.0328	0.7617±0.0305	0.7645±0.0339	0.7450±0.0378	0.7508±0.0336	0.7786±0.0338	Independent
Avg Macro-AUC		0.7268±0.1455	0.7901±0.1330	0.8229±0.1527	0.8311±0.1412	0.8103±0.1425	0.8117±0.1491	0.8448±0.1360	

Supplementary Table 8: Macro-AUC of Mutation Prediction on 18 datasets. The best-performing model for each metric is bolded. 95% CI is included in parentheses.

	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA.GATA3	0.5299 (0.4690, 0.5908)	0.4805 (0.4206, 0.5404)	0.5715 (0.5169, 0.6261)	0.5314 (0.4649, 0.5979)	0.5874 (0.5379, 0.6369)	0.5352 (0.4673, 0.6031)	0.6194 (0.5665, 0.6723)
BRCA.PIK3CA	0.6168 (0.5763, 0.6573)	0.6382 (0.6020, 0.6744)	0.6584 (0.6234, 0.6934)	0.6969 (0.6654, 0.7284)	0.6651 (0.6311, 0.6991)	0.6380 (0.6003, 0.6757)	0.7215 (0.6897, 0.7533)
BRCA.TP53	0.6184 (0.5804, 0.6564)	0.7231 (0.6907, 0.7555)	0.8364 (0.8097, 0.8631)	0.8341 (0.8075, 0.8607)	0.8130 (0.7871, 0.8389)	0.8403 (0.8144, 0.8662)	0.8366 (0.8105, 0.8627)
BRCA.TTN	0.4319 (0.3709, 0.4929)	0.4999 (0.4473, 0.5525)	0.5895 (0.5366, 0.6424)	0.5320 (0.4684, 0.5956)	0.4873 (0.4256, 0.5490)	0.5228 (0.4549, 0.5907)	0.5471 (0.4819, 0.6123)
CRC.APC	0.4300 (0.3732, 0.4868)	0.6812 (0.6338, 0.7286)	0.6505 (0.5966, 0.7044)	0.7273 (0.6739, 0.7807)	0.6053 (0.5486, 0.6620)	0.5884 (0.5314, 0.6454)	0.7238 (0.6760, 0.7716)
GBM.EGFR	0.5102 (0.4376, 0.5828)	0.4872 (0.4020, 0.5724)	0.4221 (0.3321, 0.5121)	0.4782 (0.4014, 0.5550)	0.4879 (0.4047, 0.5711)	0.5612 (0.4869, 0.6355)	0.5649 (0.4879, 0.6419)
GBM.TP53	0.5458 (0.4680, 0.6236)	0.6287 (0.5636, 0.6938)	0.6526 (0.5826, 0.7226)	0.8135 (0.7632, 0.8638)	0.7179 (0.6483, 0.7875)	0.7958 (0.7405, 0.8511)	0.8282 (0.7780, 0.8784)
HNSC.TP53	0.5884 (0.5333, 0.6435)	0.6832 (0.6268, 0.7396)	0.6271 (0.5502, 0.7040)	0.7354 (0.6773, 0.7935)	0.7084 (0.6496, 0.7672)	0.6810 (0.6160, 0.7460)	0.7423 (0.6830, 0.8016)
LGG.CIC	0.8063 (0.7569, 0.8557)	0.8689 (0.8377, 0.9001)	0.8861 (0.8577, 0.9145)	0.9121 (0.8913, 0.9329)	0.8865 (0.8516, 0.9214)	0.8511 (0.8089, 0.8933)	0.9157 (0.8952, 0.9362)
LUAD.EGFR	0.5411 (0.4768, 0.6054)	0.5788 (0.5019, 0.6557)	0.7655 (0.6991, 0.8319)	0.7570 (0.6964, 0.8176)	0.6758 (0.6098, 0.7418)	0.5864 (0.5136, 0.6592)	0.7836 (0.7244, 0.8428)
LUAD.KRAS	0.6186 (0.5735, 0.6637)	0.6369 (0.5903, 0.6835)	0.5598 (0.5160, 0.6036)	0.6004 (0.5549, 0.6459)	0.6261 (0.5832, 0.6690)	0.5566 (0.5105, 0.6027)	0.6883 (0.6473, 0.7293)
NSCLC.TP53	0.2552 (0.2019, 0.3085)	0.3021 (0.2541, 0.3501)	0.3361 (0.2743, 0.3979)	0.3768 (0.3195, 0.4341)	0.4198 (0.3694, 0.4702)	0.3882 (0.3396, 0.4368)	0.3908 (0.3328, 0.4488)
NSCLC.TMB	0.6077 (0.5707, 0.6447)	0.6887 (0.6539, 0.7235)	0.6124 (0.5739, 0.6509)	0.7193 (0.6864, 0.7522)	0.6720 (0.6355, 0.7085)	0.7143 (0.6766, 0.7520)	0.7372 (0.7036, 0.7708)
SKCM.BRAF	0.3909 (0.3472, 0.4346)	0.3692 (0.3256, 0.4128)	0.5354 (0.4911, 0.5797)	0.5425 (0.4954, 0.5896)	0.5246 (0.4800, 0.5692)	0.4987 (0.4506, 0.5468)	0.5698 (0.5267, 0.6129)
SKCM.DNAH5	0.5114 (0.4667, 0.5561)	0.5987 (0.5523, 0.6451)	0.5349 (0.4884, 0.5814)	0.6482 (0.6068, 0.6896)	0.6251 (0.5813, 0.6689)	0.6576 (0.6150, 0.7002)	0.6494 (0.6079, 0.6909)
UCEC.ARID1A	0.5080 (0.4628, 0.5532)	0.6066 (0.5576, 0.6556)	0.6088 (0.5621, 0.6555)	0.5815 (0.5349, 0.6281)	0.5617 (0.5163, 0.6071)	0.5357 (0.4909, 0.5805)	0.6611 (0.6159, 0.7063)
UCEC.PTEN	0.8328 (0.8001, 0.8655)	0.8458 (0.8145, 0.8771)	0.8719 (0.8424, 0.9014)	0.8988 (0.8714, 0.9262)	0.8221 (0.7872, 0.8570)	0.8723 (0.8459, 0.8987)	0.9008 (0.8737, 0.9279)
UCEC.TTN	0.5849 (0.5293, 0.6405)	0.6056 (0.5574, 0.6538)	0.5901 (0.5423, 0.6379)	0.6512 (0.6059, 0.6965)	0.5880 (0.5390, 0.6370)	0.5965 (0.5476, 0.6454)	0.6611 (0.6138, 0.7084)
Average	0.5516±0.1353	0.6069±0.1438	0.6283±0.1428	0.6687±0.1470	0.6374±0.1234	0.6345±0.1349	0.6968±0.1327

Supplementary Table 9: Macro-AUC of Mutation Prediction on 5 external datasets. The best-performing model for each metric is bolded. 95% CI is included in parentheses.

Task	dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
Mutation Prediction	CPTAC_BRCA.PIK3CA	0.5856±0.0382	0.6957±0.0366	0.6929±0.0379	0.7143±0.0380	0.6849±0.0355	0.6678±0.0383	0.7180±0.0353	External
	CPTAC_BRCA.TP53	0.6545±0.0353	0.7031±0.0350	0.7140±0.0333	0.7782±0.0303	0.7729±0.0324	0.7517±0.0321	0.7986±0.0293	External
	CPTAC_BRCA.TTN	0.4780±0.0393	0.6122±0.0385	0.5794±0.0421	0.5699±0.0394	0.5349±0.0408	0.4571±0.0419	0.6104±0.0395	External
	CPTAC_LUAD.EGFR	0.5085±0.0323	0.5542±0.0322	0.7066±0.0307	0.7264±0.0303	0.6799±0.0324	0.7163±0.0305	0.7470±0.0304	External
	CPTAC_LUAD.KRAS	0.4336±0.0360	0.5928±0.0323	0.5583±0.0331	0.6101±0.0323	0.5703±0.0316	0.5491±0.0343	0.6212±0.0326	External
Overall Macro-AUC		0.5320±0.0788	0.6316±0.0585	0.6502±0.0671	0.6798±0.0774	0.6486±0.0858	0.6284±0.1096	0.6990±0.0728	

Supplementary Table 10: Macro-AUC of IHC Biomarker Prediction on 10 datasets. The best-performing model for each metric is bolded. Std is given by bootstrapping with 1,000 bootstraps.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
IHC.ZJ1_ER (ext)	0.6683±0.0107	0.7345±0.0093	0.8350±0.0076	0.8339±0.0074	0.8309±0.0073	0.8457±0.0074	0.8526±0.0071	External
IHC.ZJ1_HER2 (ext)	0.3857±0.0194	0.6278±0.0160	0.6521±0.0175	0.6153±0.0173	0.6427±0.0162	0.6212±0.0171	0.6429±0.0162	External
IHC.ZJ1_PR (ext)	0.4238±0.0065	0.5241±0.0056	0.5451±0.0051	0.5490±0.0052	0.5449±0.0052	0.4896±0.0059	0.5673±0.0047	External
TCGA_BRCA_ER (out)	0.6863±0.0318	0.8635±0.0219	0.8685±0.0245	0.9026±0.0205	0.8710±0.0211	0.8638±0.0226	0.9300±0.0168	Held-out
TCGA_BRCA_HER2 (out)	0.5907±0.0424	0.6840±0.0413	0.5867±0.0448	0.7636±0.0305	0.6929±0.0407	0.6208±0.0411	0.7679±0.0310	Held-out
TCGA_BRCA_PR (out)	0.4926±0.0195	0.5211±0.0192	0.5057±0.0184	0.5028±0.0195	0.5121±0.0188	0.5203±0.0184	0.5254±0.0183	Held-out
IHC_NF1_CK7 (idpt)	0.6865±0.1294	0.8467±0.0752	0.8862±0.0909	0.9247±0.0535	0.9070±0.0576	0.9012±0.0783	0.9335±0.0519	Independent
IHC.ZJ1_CK5 (idpt)	0.7397±0.0274	0.7387±0.0315	0.7900±0.0269	0.7977±0.0268	0.8037±0.0257	0.7662±0.0293	0.8146±0.0263	Independent
IHC.ZJ1_ER_Level (idpt)	0.7013±0.0134	0.7625±0.0117	0.7830±0.0113	0.7892±0.0111	0.7858±0.0113	0.7846±0.0124	0.8020±0.0107	Independent
IHC.ZJ1_HER2_Level (idpt)	0.7332±0.0147	0.7365±0.0146	0.7626±0.0141	0.7758±0.0132	0.7432±0.0145	0.7610±0.0139	0.7951±0.0125	Independent
Avg	0.6108±0.1243	0.7039±0.1116	0.7215±0.1313	0.7455±0.1360	0.7334±0.1268	0.7174±0.1378	0.7631±0.1339	

Supplementary Table 11: Macro-AUC of Molecular Subtyping on 7 datasets. The best-performing model for each metric is bolded. Std is given by bootstrapping with 1,000 bootstraps.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
EBrains_MolSubtype (ext)	0.7086±0.0353	0.9081±0.0206	0.9232±0.0189	0.9396±0.0166	0.9150±0.0194	0.9410±0.0162	0.9546±0.0138	External
HANCOCK_HP V (ext)	0.6814±0.0201	0.6972±0.0207	0.8161±0.0160	0.8189±0.0169	0.7905±0.0175	0.7347±0.0191	0.8265±0.0166	External
ZJ1_Breast_MolSubtype (ext)	0.5891±0.0044	0.7109±0.0054	0.7244±0.0048	0.7844±0.0046	0.7918±0.0045	0.7013±0.0052	0.7946±0.0045	External
BRCA_MolSubtype (out)	0.6924±0.0213	0.7570±0.0215	0.8123±0.0196	0.7756±0.0219	0.7923±0.0208	0.7270±0.0202	0.8057±0.0191	Held-out
CRC_MolSubtype (out)	0.6286±0.0676	0.7440±0.0648	0.8365±0.0565	0.8549±0.0470	0.8520±0.0445	0.7697±0.0619	0.8556±0.0468	Held-out
GBMLGG_MolSubtype (out)	0.9335±0.0420	0.9462±0.0371	0.9567±0.0378	0.9763±0.0226	0.9513±0.0337	0.9837±0.0150	0.9847±0.0162	Held-out
TCGA_HNSC_HP V (out)	0.8521±0.0585	0.9819±0.0098	0.9746±0.0141	0.9311±0.0253	0.9773±0.0114	0.9046±0.0357	0.9836±0.0114	Held-out
Avg	0.7265±0.1138	0.8208±0.1112	0.8634±0.0841	0.8687±0.0746	0.8672±0.0745	0.8231±0.1076	0.8865±0.0786	

Supplementary Table 12: Positive Rates of mutation for every gene. The gene marked with * refers to the one related to FDA-approved drugs.

Source	Datasets	Positive Rate
TCGA	BRCA_GATA3	12.5%
	BRCA_PIK3CA*	36.0%
	BRCA_TP53	32.6%
	BRCA_TTN	17.5%
	CRC_APC	77.2%
	GBM_EGFR	22.9%
	GBM_TP53	31.3%
	HNSC_TP53	74.2%
	LGG_CIC	21.0%
	LUAD_EGFR*	12.5%
	LUAD_KRAS*	29.7%
	LUSC_TP53	50.9%
	NSCLC_TMB*	22.2%
	SKCM_BRAF*	53.4%
	SKCM_DNAH5	52.2%
	UCEC_ARID1A	43.3%
CPTAC	UCEC_PTEN	64.7%
	UCEC_TTN	39.5%
	BRCA_PIK3CA*	36.2%
	BRCA_TP53	32.8%
	BRCA_TTN	30.0%
	LUAD_KRAS*	32.6%
	LUAD_EGFR*	30.3%

Supplementary Table 13: Label Distribution of IHC Biomarker Prediction for binary classification.

Dataset	Negative	Positive	Sum
TCGA_BRCA_ER	214	735	949
TCGA_BRCA_HER2	404	142	546
TCGA_BRCA_PR	307	641	948
IHC_ZJ1_ER	499	1049	1548
IHC_ZJ1_PR	623	933	1556
IHC_ZJ1_HER2	164	1180	1344
IHC_ZJ1_CK5	753	208	961

Supplementary Table 14: Label Distribution of IHC Biomarker Expression Level Prediction.

Dataset	Level 0	Level 1	Level 2	Level 3	Sum
IHC_ZJ1_ER_Level	499	268	421	360	1548
IHC_ZJ1_HER2_Level	164	347	424	409	1344
IHC_NF1_CK7	224	24	171	-	419

Supplementary Table 15: Macro-AUC of Zero-shot Slide Classification on 6 datasets. Best performing model for each metric is in bold. 95% CI is included in parentheses.

dataset	PLIP	CONCH	mSTAR(Ours)
CAMELYON	0.622 (0.534,0.710)	0.638 (0.550,0.726)	0.742 (0.668,0.817)
PANDA	0.561 (0.547,0.575)	0.582 (0.566,0.598)	0.462 (0.446,0.478)
UBC-OCEAN	0.762 (0.691,0.833)	0.370 (0.307,0.433)	0.692 (0.621,0.763)
BCNB-ER	0.563 (0.473,0.653)	0.500 (0.500,0.500)	0.725 (0.641,0.809)
BCNB-PR	0.523 (0.435,0.611)	0.500 (0.500,0.500)	0.722 (0.644,0.800)
BCNB-HER2	0.516 (0.430,0.602)	0.518 (0.428,0.608)	0.435 (0.345,0.525)
Avg Macro-AUC	0.5912	0.518	0.6297

Supplementary Table 16: Performance (Macro-AUC) of Zero-shot Retrieval for Image-to-Text and Text-to-Image tasks on one held-out dataset and one external dataset.

dataset	model	Image2Text			Text2Image		
		@5	@10	@50	@5	@10	@50
TCGA-Report (held-out)	PLIP	0.0119	0.0321	0.1536	0.0202	0.0393	0.1774
TCGA-Report (held-out)	CONCH	0.0083	0.0167	0.0655	0.0107	0.0190	0.0810
TCGA-Report (held-out)	mSTAR (Ours)	0.0643	0.1274	0.5262	0.0667	0.1298	0.5405
Breast&Lung (external)	PLIP	0.0200	0.0400	0.1880	0.0260	0.0340	0.1220
Breast&Lung (external)	CONCH	0.0060	0.0120	0.1040	0.0080	0.0220	0.1140
Breast&Lung (external)	mSTAR (Ours)	0.0360	0.0520	0.2240	0.0340	0.0600	0.2160

Supplementary Table 17: Performance of Pathological Report Generation on one held-out dataset and two external datasets. Best performing model for each metric is in bold. 6 metrics are reported.

Source	Metric	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
TCGA	BLEU.1	0.2541	0.3124	0.2447	0.3552	0.3087	0.3545	0.3624	held-out
	BLEU.2	0.1501	0.2078	0.1590	0.2403	0.2028	0.2388	0.2474	
	BLEU.3	0.0942	0.1457	0.1092	0.1716	0.1399	0.1694	0.1775	
	BLEU.4	0.0558	0.1057	0.0765	0.1274	0.0994	0.1253	0.1329	
	METEOR	0.1291	0.1348	0.1177	0.1489	0.1343	0.1491	0.1518	
	ROUGE.L	0.2185	0.2638	0.2372	0.2931	0.2623	0.2921	0.3012	
Nanfang	BLEU.1	0.1705	0.1186	0.2136	0.2361	0.2017	0.2097	0.3052	external
	BLEU.2	0.0906	0.0693	0.0950	0.0964	0.1025	0.1035	0.1389	
	BLEU.3	0.0494	0.0423	0.0464	0.0462	0.0585	0.0584	0.0730	
	BLEU.4	0.0222	0.0239	0.0214	0.0229	0.0334	0.0330	0.0392	
	METEOR	0.0910	0.0668	0.0753	0.0814	0.0751	0.0768	0.1027	
	ROUGE.L	0.1535	0.1527	0.1670	0.1672	0.1505	0.1621	0.2133	
ZJ_First	BLEU.1	0.2215	0.1951	0.2658	0.2650	0.2668	0.2639	0.2858	external
	BLEU.2	0.1220	0.1270	0.1527	0.1440	0.1604	0.1501	0.1645	
	BLEU.3	0.0544	0.0761	0.0908	0.0881	0.0989	0.0874	0.1023	
	BLEU.4	0.0157	0.0421	0.0544	0.0539	0.0615	0.0507	0.0632	
	METEOR	0.1230	0.1087	0.1140	0.1109	0.1210	0.1158	0.1199	
	ROUGE.L	0.1970	0.2281	0.1917	0.1880	0.2252	0.1966	0.2140	

Supplementary Table 18: C-Index of Survival Prediction on 16 datasets, including 10 held-out datasets, 4 external datasets and 2 independent datasets.

Task	dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)	Evaluation
Disease-Free Survival	DFS_BRCA	0.5504±0.1201	0.6368±0.0964	0.6357±0.1254	0.6695±0.119	0.6494±0.1131	0.6298±0.1177	0.6663±0.1209	Held-out
	DFS_YN1	0.5037±0.0691	0.5277±0.0722	0.4810±0.0704	0.5737±0.0717	0.5040±0.0715	0.4935±0.0774	0.5775±0.0698	External
	DFS_ZJ1	0.5556±0.0693	0.5491±0.0651	0.5850±0.0665	0.5548±0.0696	0.5539±0.0710	0.5367±0.0715	0.5959±0.0655	External
	OS_BRCA	0.5696±0.1250	0.5915±0.1151	0.6940±0.0888	0.6908±0.1048	0.6698±0.0972	0.6528±0.1067	0.7076±0.0896	Held-out
Overall Survival	OS_CRC	0.5710±0.1148	0.7076±0.0890	0.7026±0.0877	0.6906±0.0835	0.7288±0.0870	0.6815±0.1011	0.6895±0.0836	Held-out
	OS_GBMLGG	0.7810±0.0385	0.7716±0.0409	0.7704±0.0435	0.7905±0.0434	0.7876±0.0389	0.7839±0.0415	0.7923±0.0426	Held-out
	OS_HANCOCK	0.5084±0.0425	0.5343±0.0439	0.5198±0.0417	0.5573±0.0450	0.5062±0.0423	0.5378±0.0447	0.5639±0.0448	External
	OS_HNSC	0.6087±0.0790	0.6569±0.0786	0.6294±0.0816	0.6516±0.0798	0.6329±0.0807	0.6576±0.0768	0.6604±0.0794	Held-out
	OS_KIRC	0.6258±0.0866	0.6613±0.0862	0.6957±0.0779	0.7155±0.0659	0.6876±0.0845	0.7058±0.0745	0.7027±0.0890	Held-out
	OS_LUAD	0.5995±0.0924	0.5906±0.0928	0.6233±0.0931	0.6312±0.0996	0.6086±0.0869	0.6140±0.1047	0.6329±0.0976	Held-out
	OS_LUSC	0.5305±0.0910	0.5464±0.0850	0.6045±0.0819	0.6273±0.0771	0.5518±0.0892	0.5053±0.0958	0.6323±0.0785	Held-out
	OS_NFRC	0.6757±0.1350	0.6953±0.1071	0.7252±0.1309	0.7286±0.0906	0.7248±0.0935	0.6876±0.0427	0.7408±0.0923	Independent
	OS_SKCM	0.5811±0.0737	0.5648±0.0755	0.6210±0.0807	0.6254±0.0776	0.5426±0.0756	0.6103±0.0829	0.6281±0.0761	Held-out
	OS_UCEC	0.7450±0.0820	0.7738±0.0903	0.8082±0.1002	0.7845±0.1012	0.7976±0.1159	0.7379±0.1221	0.8092±0.0865	Held-out
	OS_ZJ1	0.5849±0.0762	0.5334±0.0845	0.6141±0.0799	0.6473±0.0775	0.6251±0.0771	0.6036±0.0712	0.6761±0.0729	External
Recurrence-Free Survival	RFS_HANCOCK	0.5791±0.0286	0.6210±0.0415	0.6590±0.0586	0.6514±0.0697	0.6429±0.0587	0.6082±0.0561	0.6632±0.0532	Independent
Overall C-Index		0.5981±0.0750	0.6226±0.0797	0.6481±0.0819	0.6619±0.0683	0.6384±0.0892	0.6279±0.0796	0.6711±0.0672	

Supplementary Table 19: C-Index of Multimodal Survival Analysis on average across 4 multi-modal fusion approaches on 9 TCGA held-out datasets. Best performing model for each metric is bolded.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA	0.7182±0.0125	0.7080±0.0224	0.6876±0.0397	0.7178±0.0234	0.7006±0.0124	0.6905±0.0293	0.7400±0.0081
CRC	0.6674±0.0338	0.6665±0.0022	0.6594±0.0051	0.6661±0.0133	0.6683±0.0212	0.6818±0.0171	0.7073±0.0100
GBMLGG	0.8789±0.0046	0.8772±0.0033	0.8840±0.0039	0.8918±0.0075	0.8871±0.0018	0.8899±0.0026	0.8948±0.0065
HNSC	0.6838±0.0087	0.6691±0.0145	0.6700±0.0039	0.6858±0.0159	0.6894±0.0070	0.6731±0.0104	0.7111±0.0131
KIRC	0.6880±0.0158	0.6797±0.0068	0.6922±0.0073	0.6977±0.0125	0.6915±0.0060	0.6876±0.0111	0.7017±0.0106
LUAD	0.6499±0.0102	0.6375±0.0117	0.6523±0.0223	0.6495±0.0165	0.6575±0.0199	0.6706±0.0338	0.6708±0.0288
LUSC	0.5457±0.0102	0.5349±0.0190	0.5358±0.0278	0.5713±0.0156	0.5550±0.0175	0.5689±0.0373	0.5902±0.0278
SKCM	0.6570±0.0132	0.6502±0.0169	0.6411±0.0099	0.6399±0.0240	0.6452±0.0195	0.6266±0.0546	0.6476±0.0191
UCEC	0.6498±0.0303	0.6564±0.0239	0.6814±0.0171	0.6928±0.0274	0.6453±0.0293	0.6670±0.0479	0.7111±0.0352
Avg	0.6821±0.0827	0.6755±0.0844	0.6782±0.0853	0.6903±0.0819	0.6822±0.0831	0.6840±0.0814	0.7083±0.0781

Supplementary Table 20: C-Index of Multimodal Survival Analysis with MCAT on 9 TCGA held-out datasets. Best performing model for each metric is bolded. 95% CI is included in parentheses.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA	0.7215 (0.6382, 0.8048)	0.7304 (0.6428, 0.8180)	0.6266 (0.5019, 0.7513)	0.6928 (0.6034, 0.7822)	0.6850 (0.5892, 0.7808)	0.6556 (0.5566, 0.7546)	0.7489 (0.6703, 0.8275)
CRC	0.6996 (0.5994, 0.7998)	0.6676 (0.5669, 0.7683)	0.6635 (0.5601, 0.7669)	0.6481 (0.5474, 0.7488)	0.6935 (0.6020, 0.7850)	0.6897 (0.5837, 0.7957)	0.6989 (0.5943, 0.8035)
GBMLGG	0.8713 (0.8343, 0.9083)	0.8784 (0.8433, 0.9135)	0.8886 (0.8553, 0.9219)	0.8810 (0.8471, 0.9149)	0.8872 (0.8574, 0.9170)	0.8885 (0.8599, 0.9171)	0.8896 (0.8610, 0.9182)
HNSC	0.6830 (0.6054, 0.7606)	0.6444 (0.5677, 0.7211)	0.6646 (0.6008, 0.7284)	0.6874 (0.6125, 0.7623)	0.6839 (0.6157, 0.7521)	0.6659 (0.5987, 0.7331)	0.6907 (0.6157, 0.7657)
KIRC	0.6856 (0.6130, 0.7582)	0.6830 (0.6088, 0.7572)	0.6996 (0.6335, 0.7657)	0.7091 (0.6291, 0.7891)	0.6962 (0.6200, 0.7724)	0.6968 (0.6149, 0.7787)	0.7084 (0.6407, 0.7761)
LUAD	0.6375 (0.5326, 0.7424)	0.6505 (0.5576, 0.7434)	0.6628 (0.5681, 0.7575)	0.6595 (0.5733, 0.7457)	0.6823 (0.5943, 0.7703)	0.6546 (0.5731, 0.7361)	0.6953 (0.6073, 0.7833)
LUSC	0.5373 (0.4420, 0.6326)	0.5499 (0.4654, 0.6344)	0.5526 (0.4660, 0.6392)	0.5493 (0.4488, 0.6498)	0.5823 (0.4841, 0.6805)	0.5472 (0.4694, 0.6250)	0.5537 (0.4590, 0.6484)
SKCM	0.6724 (0.5944, 0.7504)	0.6641 (0.5941, 0.7341)	0.6522 (0.5781, 0.7263)	0.6549 (0.5794, 0.7304)	0.6736 (0.6001, 0.7471)	0.6511 (0.5776, 0.7246)	0.6520 (0.5840, 0.7200)
UCEC	0.6406 (0.4967, 0.7845)	0.6380 (0.5007, 0.7753)	0.6754 (0.5532, 0.7976)	0.6807 (0.5681, 0.7933)	0.6451 (0.5281, 0.7621)	0.6572 (0.5337, 0.7807)	0.6811 (0.5751, 0.7871)
Avg	0.6832	0.6785	0.6762	0.6848	0.6921	0.6785	0.7021

Supplementary Table 21: C-Index of Multimodal Survival Analysis with Porpoise on 9 TCGA held-out datasets. Best performing model for each metric is bolded. 95% CI is included in parentheses.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA	0.7366 (0.6480, 0.8252)	0.7244 (0.6297, 0.8191)	0.7259 (0.6369, 0.8149)	0.7474 (0.6651, 0.8297)	0.7196 (0.6353, 0.8039)	0.7312 (0.6434, 0.8190)	0.7456 (0.6515, 0.8397)
CRC	0.6113 (0.4978, 0.7248)	0.6639 (0.5571, 0.7707)	0.6517 (0.5535, 0.7499)	0.6599 (0.5621, 0.7567)	0.6351 (0.5224, 0.7478)	0.6579 (0.5591, 0.7567)	0.7020 (0.6085, 0.7955)
GBMLGG	0.8805 (0.8472, 0.9138)	0.8748 (0.8407, 0.9089)	0.8786 (0.8406, 0.9166)	0.8948 (0.8627, 0.9269)	0.8898 (0.8547, 0.9249)	0.8888 (0.8557, 0.9219)	0.8955 (0.8643, 0.9267)
HNSC	0.6982 (0.6271, 0.7693)	0.6806 (0.5977, 0.7635)	0.6730 (0.5981, 0.7479)	0.7111 (0.6415, 0.7807)	0.6858 (0.6152, 0.7564)	0.6860 (0.6164, 0.7556)	0.7189 (0.6474, 0.7904)
KIRC	0.6681 (0.5934, 0.7428)	0.6715 (0.5921, 0.7509)	0.6802 (0.5973, 0.7631)	0.6767 (0.6046, 0.7488)	0.6831 (0.6076, 0.7586)	0.6693 (0.5870, 0.7516)	0.6834 (0.6115, 0.7553)
LUAD	0.6656 (0.5792, 0.7520)	0.6222 (0.5266, 0.7178)	0.6139 (0.5265, 0.7013)	0.6295 (0.5454, 0.7136)	0.6413 (0.5527, 0.7299)	0.6243 (0.5369, 0.7117)	0.6300 (0.5455, 0.7145)
LUSC	0.5364 (0.4490, 0.6238)	0.5100 (0.4136, 0.6064)	0.4911 (0.3980, 0.5842)	0.5794 (0.4859, 0.6729)	0.5572 (0.4617, 0.6527)	0.5469 (0.4601, 0.6337)	0.5895 (0.5027, 0.6763)
SKCM	0.6383 (0.5666, 0.7100)	0.6215 (0.5498, 0.6932)	0.6253 (0.5510, 0.6996)	0.5995 (0.5233, 0.6757)	0.6230 (0.5507, 0.6953)	0.5331 (0.4490, 0.6172)	0.6182 (0.5443, 0.6921)
UCEC	0.6154 (0.4809, 0.7499)	0.6301 (0.4968, 0.7634)	0.6565 (0.5218, 0.7912)	0.6565 (0.5385, 0.7745)	0.6005 (0.4890, 0.7120)	0.5944 (0.4648, 0.7240)	0.6724 (0.5340, 0.8108)
Avg	0.6723	0.6666	0.6662	0.6839	0.6706	0.6591	0.6951

Supplementary Table 22: C-Index of Multimodal Survival Analysis with MOTCat on 9 TCGA held-out datasets. Best performing model for each metric is bolded. 95% CI is included in parentheses.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA	0.7030 (0.6075, 0.7985)	0.6732 (0.5685, 0.7779)	0.6781 (0.5789, 0.7773)	0.6970 (0.5814, 0.8126)	0.6979 (0.5893, 0.8065)	0.6711 (0.5723, 0.7699)	0.7278 (0.6276, 0.8280)
CRC	0.6867 (0.5926, 0.7808)	0.6695 (0.5635, 0.7755)	0.6643 (0.5553, 0.7733)	0.6835 (0.5765, 0.7905)	0.6759 (0.5554, 0.7964)	0.7040 (0.6056, 0.8024)	0.7244 (0.6327, 0.8161)
GBMLGG	0.8838 (0.8526, 0.9150)	0.8736 (0.8375, 0.9097)	0.8867 (0.8555, 0.9179)	0.8899 (0.8583, 0.9215)	0.8863 (0.8545, 0.9181)	0.8878 (0.8547, 0.9209)	0.8889 (0.8583, 0.9195)
HNSC	0.6776 (0.6045, 0.7507)	0.6731 (0.6023, 0.7439)	0.6679 (0.5852, 0.7506)	0.6736 (0.5930, 0.7542)	0.7014 (0.6303, 0.7725)	0.6801 (0.6091, 0.7511)	0.7256 (0.6546, 0.7966)
KIRC	0.7124 (0.6467, 0.7781)	0.6890 (0.6108, 0.7672)	0.6927 (0.6163, 0.7691)	0.7050 (0.6286, 0.7814)	0.6980 (0.6198, 0.7762)	0.6878 (0.6170, 0.7586)	0.7085 (0.6403, 0.7767)
LUAD	0.6463 (0.5559, 0.7367)	0.6472 (0.5549, 0.7395)	0.6685 (0.5758, 0.7612)	0.6710 (0.5875, 0.7545)	0.6715 (0.5921, 0.7509)	0.7125 (0.6261, 0.7989)	0.7004 (0.6138, 0.7870)
LUSC	0.5618 (0.4748, 0.6488)	0.5564 (0.4621, 0.6507)	0.5643 (0.4704, 0.6582)	0.5654 (0.4780, 0.6528)	0.5450 (0.4568, 0.6332)	0.5478 (0.4614, 0.6342)	0.5855 (0.4957, 0.6753)
SKCM	0.6660 (0.5874, 0.7446)	0.6607 (0.5868, 0.7346)	0.6454 (0.5715, 0.7193)	0.6604 (0.5834, 0.7374)	0.6519 (0.5678, 0.7360)	0.6709 (0.5976, 0.7442)	0.6715 (0.5972, 0.7458)
UCEC	0.6446 (0.5190, 0.7702)	0.6899 (0.5601, 0.8197)	0.7006 (0.5869, 0.8143)	0.7031 (0.5943, 0.8119)	0.6821 (0.5688, 0.7954)	0.6933 (0.5810, 0.8056)	0.7353 (0.6453, 0.8253)
Avg	0.6869	0.6814	0.6854	0.6943	0.6900	0.6950	0.7187

Supplementary Table 23: C-Index of Multimodal Survival Analysis with CMTA on 9 TCGA held-out datasets. Best performing model for each metric is bolded. 95% CI is included in parentheses.

dataset	R50	PLIP	CONCH	UNI	CHIEF	GigaPath	mSTAR (Ours)
BRCA	0.7118 (0.6224, 0.8012)	0.7039 (0.5945, 0.8133)	0.7196 (0.6157, 0.8235)	0.7339 (0.6351, 0.8327)	0.6998 (0.6098, 0.7898)	0.7040 (0.6023, 0.8057)	0.7375 (0.6560, 0.8190)
CRC	0.6719 (0.5610, 0.7828)	0.6651 (0.5514, 0.7788)	0.6580 (0.5469, 0.7691)	0.6727 (0.5714, 0.7740)	0.6687 (0.5623, 0.7751)	0.6754 (0.5790, 0.7718)	0.7040 (0.6080, 0.8000)
GBMLGG	0.8798 (0.8447, 0.9149)	0.8820 (0.8479, 0.9161)	0.8822 (0.8501, 0.9143)	0.9016 (0.8726, 0.9306)	0.8849 (0.8494, 0.9204)	0.8944 (0.8640, 0.9248)	0.9051 (0.8798, 0.9304)
HNSC	0.6764 (0.6051, 0.7477)	0.6782 (0.6059, 0.7505)	0.6744 (0.5964, 0.7524)	0.6710 (0.5928, 0.7492)	0.6864 (0.6062, 0.7666)	0.6602 (0.5871, 0.7333)	0.7092 (0.6430, 0.7754)
KIRC	0.6858 (0.6158, 0.7558)	0.6752 (0.5984, 0.7520)	0.6963 (0.6175, 0.7751)	0.7000 (0.6100, 0.7900)	0.6888 (0.6243, 0.7533)	0.6963 (0.6203, 0.7723)	0.7065 (0.6279, 0.7851)
LUAD	0.6502 (0.5536, 0.7468)	0.6301 (0.5386, 0.7216)	0.6639 (0.5645, 0.7633)	0.6380 (0.5376, 0.7384)	0.6348 (0.5468, 0.7228)	0.6911 (0.6033, 0.7789)	0.6574 (0.5684, 0.7464)
LUSC	0.5473 (0.4569, 0.6377)	0.5234 (0.4303, 0.6165)	0.5352 (0.4413, 0.6291)	0.5909 (0.4980, 0.6838)	0.5355 (0.4465, 0.6245)	0.6335 (0.5402, 0.7268)	0.6320 (0.5497, 0.7143)
SKCM	0.6514 (0.5783, 0.7245)	0.6546 (0.5786, 0.7306)	0.6413 (0.5643, 0.7183)	0.6446 (0.5693, 0.7199)	0.6322 (0.5579, 0.7065)	0.6511 (0.5760, 0.7262)	0.6488 (0.5731, 0.7245)
UCEC	0.6986 (0.5786, 0.8186)	0.6676 (0.5504, 0.7848)	0.6932 (0.5736, 0.8128)	0.7307 (0.6100, 0.8514)	0.6534 (0.5387, 0.7681)	0.7230 (0.6254, 0.8206)	0.7555 (0.6669, 0.8441)
Avg	0.6859	0.6756	0.6849	0.6982	0.6761	0.7032	0.7173

Supplementary Table 24: Data splits (cases) of 9 cancer datasets on TCGA. CRC=COAD+READ and GBMLGG=GBM+LGG. Apart from these specific cancer types, other TCGA datasets were used for pretraining without data partitioning.

Cancer Type	Train	Validation	Test	Total
BRCA	716	102	307	1023
CRC	405	58	116	579
GBMLGG	581	83	166	830
HNSC	308	44	89	441
KIRC	348	50	100	498
LUAD	318	45	92	455
LUSC	316	45	91	452
SKCM	290	41	84	415
UCEC	346	49	100	495

Supplementary Notes 25: Prompts used in GPT-4 for cleaning pathology reports.

Helping me to check the formatting and spelling of the supplied text, including some incorrect use of punctuation like mis-using of 'X' and 'x' and capitalization and deletion of some words of unknown meaning as well.

Supplementary Notes 26: Prompts used in GPT-4o-mini to filter out information unseen under microscopic examination from pathology reports for the task of report generation.

I need you to be a professional pathologist and help me organize the contents of the pathology report. The report I give may be a chaos in organization and have information I don't need. You need to remove the following contents: 1. patient's information like patient's id. Only keep the following contents if available: 1. Microscopic description: a detailed description of what the pathologist sees during microscopic exam of the specimen 2. Margins Information: The margins are an area of normal cells around a tumor. 3. stage and grade 4. Lymph nodes included in a biopsy 5. Diagnosis

Supplementary Table 27: Hyperparameters of ABMIL used for Slide-level Prediction. A single 80GB NVIDIA H800 GPU was used for training.

Hyperparameter	Value
Input dim	512/1024
Hidden dim	512
Dropout	0.25
Batch size	1
Epochs	30
Optimizer	Adam
Learning rate	2e-4
Scheduler	Cosine
Weight decay	1e-5

Supplementary Table 28: Architecture Hyperparameters of Porpoise used for Multimodal Survival Analysis. A single 80GB NVIDIA H800 GPU was used for training. D is the number of genes, varying across different datasets.

Hyperparameter	WSI	RNASeq
Input dim	512/1024	D
Hidden dim	$512 \rightarrow 256$	256
Dropout	0.1	0.1
Feature dim after fusion	256	

Supplementary Table 29: Architecture Hyperparameters of MCAT and MOTCat used for Multimodal Survival Analysis. A single 80GB NVIDIA H800 GPU was used for training. D is the number of genes, varying across different unique functional categories and different datasets. $256 \times 2 \rightarrow 256$ refers to 256-dimensional features from two modalities were fused into a 256-dimensional slide-level feature.

Hyperparameter	WSI	RNASeq
Input dim	512/1024	$6 \times D$
Hidden dim	256	6×256
Dropout	0.25	0.25
Feature dim after fusion	$256 \times 2 \rightarrow 256$	

Supplementary Table 30: Architecture Hyperparameters of CMTA used for Multimodal Survival Analysis. A single 80GB NVIDIA H800 GPU was used for training. D is the number of genes, varying across different datasets. $256 \times 2 \rightarrow 256$ refers to 256-dimensional features from two modalities were fused into a 256-dimensional slide-level feature.

Hyperparameter	WSI	RNASeq
Input dim	512/1024	$6 \times D$
Hidden dim	256	$6 \times (1024 \rightarrow 256)$
Dropout	0.25	0.25
Feature dim after fusion	$256 \times 2 \rightarrow 256$	

Supplementary Table 31: Training Hyperparameters used in Multimodal Survival Analysis. A single 80GB NVIDIA H800 GPU was used for training.

Hyperparameter	Value
Batch size	1
Epochs	30
Optimizer	Adam
Learning rate	$2e-4$
Scheduler	Cosine
Weight decay	$1e-5$

Supplementary Table 32: Architecture Hyperparameters of HistGen used for Pathology Report Generation. A single 80GB NVIDIA H800 GPU was used for training. D is the feature dimension of pathological patch, varying across different FMs.

Hyperparameter	Value
Input dim	D
Hidden dim	512
Layers of decoder	3 (8 heads)
Dimension of cross-modal context	512×2048
Optimizer	Adam
Learning rate	$1e-4$
Beam size	3

Supplementary Table 33: Prompt templates for all tasks that required prompts. In these templates, the placeholder "CLASSNAME" was replaced with the actual name of the class. The class prompts of CLASSNAME for each task are presented in [34-39](#).

#	Prompt
1	CLASSNAME.
2	a photomicrograph showing CLASSNAME.
3	a photomicrograph of CLASSNAME.
4	an image of CLASSNAME.
5	an image showing CLASSNAME.
6	an example of CLASSNAME.
7	CLASSNAME is shown.
8	this is CLASSNAME.
9	there is CLASSNAME.
10	a histopathological image showing CLASSNAME.
11	a histopathological image of CLASSNAME.
12	a histopathological photograph of CLASSNAME.
13	a histopathological photograph showing CLASSNAME.
14	shows CLASSNAME.
15	presence of CLASSNAME.
16	CLASSNAME is present.
17	an H&E stained image of CLASSNAME.
18	an H&E stained image showing CLASSNAME.
19	an H&E image showing CLASSNAME.
20	an H&E image of CLASSNAME.
21	CLASSNAME, H&E stain.
22	CLASSNAME, H&E.
23	Close-up view of CLASSNAME.
24	Detailed image capturing CLASSNAME.
25	Microscopic analysis reveals CLASSNAME.
26	CLASSNAME under magnification.
27	The structure of CLASSNAME is visible.
28	Diagnosing CLASSNAME.
29	Typical appearance of CLASSNAME.
30	Zoomed image of CLASSNAME.
31	CLASSNAME in detail.
32	CLASSNAME at high magnification.
33	CLASSNAME in a clinical sample.
34	Clinical representation of CLASSNAME.
35	Pathological review of CLASSNAME.
36	Characteristics of CLASSNAME observed.
37	CLASSNAME identified.
38	Diagnosis: CLASSNAME.
39	Specimen showing CLASSNAME.
40	View of CLASSNAME with immunohistochemistry.
41	CLASSNAME with special staining.
42	Observation of CLASSNAME with fluorescent staining.

Supplementary Table 34: Class prompts for Breast Metastasis Detection.

Task	Class	CLASSNAME
Breast Metastasis Detection	Tumor	metastatic cancer lymph node with metastatic cancer metastatic breast cancer in lymph node tumor
	Normal	non-metastatic lymph node without metastatic cancer non-metastatic lymph node normal

Supplementary Table 35: Class prompts of PANDA for Prostate ISUP grading.

Task	Class	CLASSNAME
Prostate ISUP grading	0	benign tissue, healthy tissue, non-cancerous tissue, normal tissue
	1	Gleason score 6, ISUP grade 1, low-grade cancer, Gleason pattern 3+3
	2	Gleason score 7 (3+4), ISUP grade 2, moderately differentiated cancer, Gleason pattern 3+4
	3	Gleason score 7 (4+3), ISUP grade 3, moderately differentiated cancer, Gleason pattern 4+3
	4	Gleason score 8, ISUP grade 4, high-grade cancer, Gleason pattern 4+4, 3+5, or 5+3
	5	Gleason score 9 or 10, ISUP grade 5, high-grade aggressive cancer, Gleason pattern 4+5, 5+4, or 5+5

Supplementary Table 36: Class prompts of UBC-OCEAN for Ovarian Cancer Subtyping.

Task	Class	CLASSNAME
Ovarian Cancer Subtyping	HGSC	high-grade serous carcinoma, ovarian high-grade serous carcinoma, high-grade serous carcinoma of ovary
	LGSC	low-grade serous carcinoma, ovarian low-grade serous carcinoma, low-grade serous carcinoma of ovary
	EC	endometrioid carcinoma, ovarian endometrioid carcinoma, endometrioid carcinoma of ovary
	CC	clear cell carcinoma, ovarian clear cell carcinoma, clear cell carcinoma of ovary
	MC	mucinous carcinoma, ovarian mucinous carcinoma, mucinous carcinoma of ovary

Supplementary Table 37: Class prompts of BCNB for ER Prediction.

Task	Class	CLASSNAME
ER Prediction	Positive	ER positive, ER+, ER positive breast cancer, Estrogen Receptor positive, ER+ breast cancer, ER positive carcinoma, Estrogen Receptor positive breast cancer
	Negative	ER negative, ER- ER negative breast cancer, Estrogen Receptor negative, ER- breast cancer, ER negative carcinoma, Estrogen Receptor negative breast cancer

Supplementary Table 38: Class prompts of BCNB for PR Prediction.

Task	Class	CLASSNAME
PR Prediction	Positive	PR positive, PR+, PR positive breast cancer, Progesterone Receptor positive, PR+ breast cancer, PR positive carcinoma, Progesterone Receptor positive breast cancer
	Negative	PR negative, PR-, PR negative breast cancer, Progesterone Receptor negative, PR- breast cancer, PR negative carcinoma, Progesterone Receptor negative breast cancer

Supplementary Table 39: Class prompts of BCNB for HER2 Prediction.

Task	Class	CLASSNAME
HER2 Prediction	Positive	HER2 positive, HER2+, HER2 positive breast cancer, HER2 overexpression, HER2+ breast cancer, HER2 positive carcinoma, Human Epidermal growth factor Receptor 2 positive, Human Epidermal growth factor Receptor 2 overexpression
	Negative	HER2 negative, HER2-, HER2 negative breast cancer, no HER2 overexpression, HER2- breast cancer, HER2 negative carcinoma, Human Epidermal growth factor Receptor 2 negative

Supplementary Table 40: Source of datasets for 97 oncological tasks.

No.	Application	Task	Dataset	URL/Source
1	Pathological Diagnosis	Pathological Subtyping	BRCA-PathSubtype	https://portal.gdc.cancer.gov/
2	Pathological Diagnosis	Pathological Subtyping	GBMLGG_PathSubtype	https://portal.gdc.cancer.gov/
3	Pathological Diagnosis	Pathological Subtyping	HANCOCK_PathSubtype	https://hancock.research.fau.eu/download
4	Pathological Diagnosis	Pathological Subtyping	TCGA-NSCLC	https://portal.gdc.cancer.gov/
5	Pathological Diagnosis	Pathological Subtyping	EBrains_PathSubtype	https://www.ebrains.eu/
6	Pathological Diagnosis	Pathological Subtyping	NFGC_Lauren	NFH
7	Pathological Diagnosis	Pathological Subtyping	NFGC_PathSubtype	NFH
8	Pathological Diagnosis	Pathological Subtyping	YN1_PathSubtype	YN1
9	Pathological Diagnosis	Pathological Subtyping	YN3_Lauren	YN3
10	Pathological Diagnosis	Pathological Subtyping	YN3_PathSubtype	YN3
11	Pathological Diagnosis	Metastasis Detection	CAMELYON	https://camelyon16.grand-challenge.org/Data/
12	Pathological Diagnosis	Metastasis Detection	NF_Metastatic	NFH
13	Pathological Diagnosis	Metastasis Detection	NF_Metastatic.Fine	NFH
14	Pathological Diagnosis	Metastasis Detection	QFS_Metastatic	QFS
15	Pathological Diagnosis	Metastasis Detection	QFS_Metastatic.Fine	QFS
16	Pathological Diagnosis	Morphology Prediction	NFGC_Perineural	NFH
17	Pathological Diagnosis	Morphology Prediction	NFGC_Vascular	NFH
18	Pathological Diagnosis	Morphology Prediction	YN3_Perineural	YN3
19	Pathological Diagnosis	Morphology Prediction	YN3_Vascular	YN3
20	Pathological Diagnosis	Pathological Grading	PANDA	https://www.kaggle.com/c/prostate-cancer-grade-assessment/data
21	Pathological Diagnosis	Pathological Staging	HANCOCK-TSstage	https://hancock.research.fau.eu/download
22	Molecular Prediction	Mutation Prediction	BRCA-GATA3	https://portal.gdc.cancer.gov/
23	Molecular Prediction	Mutation Prediction	BRCA-PIK3CA	https://portal.gdc.cancer.gov/
24	Molecular Prediction	Mutation Prediction	BRCA-TP53	https://portal.gdc.cancer.gov/
25	Molecular Prediction	Mutation Prediction	BRCA-TTN	https://portal.gdc.cancer.gov/
26	Molecular Prediction	Mutation Prediction	CRC-APC	https://portal.gdc.cancer.gov/
27	Molecular Prediction	Mutation Prediction	GBM-EGFR	https://portal.gdc.cancer.gov/
28	Molecular Prediction	Mutation Prediction	GBM-TP53	https://portal.gdc.cancer.gov/
29	Molecular Prediction	Mutation Prediction	HNSC-TP53	https://portal.gdc.cancer.gov/
30	Molecular Prediction	Mutation Prediction	LGG-CIC	https://portal.gdc.cancer.gov/
31	Molecular Prediction	Mutation Prediction	LUAD-EGFR	https://portal.gdc.cancer.gov/
32	Molecular Prediction	Mutation Prediction	LUAD-KRAS	https://portal.gdc.cancer.gov/
33	Molecular Prediction	Mutation Prediction	LUSC-TP53	https://portal.gdc.cancer.gov/
34	Molecular Prediction	Mutation Prediction	NSCLC-TMB	https://portal.gdc.cancer.gov/
35	Molecular Prediction	Mutation Prediction	SKCM-BRAF	https://portal.gdc.cancer.gov/
36	Molecular Prediction	Mutation Prediction	SKCM-DNAH5	https://portal.gdc.cancer.gov/
37	Molecular Prediction	Mutation Prediction	UCEC-ARID1A	https://portal.gdc.cancer.gov/
38	Molecular Prediction	Mutation Prediction	UCEC-PTEN	https://portal.gdc.cancer.gov/
39	Molecular Prediction	Mutation Prediction	UCEC-TTN	https://portal.gdc.cancer.gov/
40	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_PIK3CA	https://proteomics.cancer.gov/programs/cptac
41	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_TP53	https://proteomics.cancer.gov/programs/cptac
42	Molecular Prediction	Mutation Prediction	CPTAC_BRCA_TTN	https://proteomics.cancer.gov/programs/cptac
43	Molecular Prediction	Mutation Prediction	CPTAC_LUAD_KRAS	https://proteomics.cancer.gov/programs/cptac
44	Molecular Prediction	Mutation Prediction	CPTAC_LUAD_EGFR	https://proteomics.cancer.gov/programs/cptac
45	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_ER	https://portal.gdc.cancer.gov/
46	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_HER2	https://portal.gdc.cancer.gov/
47	Molecular Prediction	IHC Biomarker Prediction	TCGA_BRCA_PR	https://portal.gdc.cancer.gov/
48	Molecular Prediction	IHC Biomarker Prediction	IHC_NF1_CK7	ZJ1
49	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_HER2_Level	ZJ1
50	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_CK5	ZJ1
51	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_ER_Level	ZJ1
52	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_HER2	ZJ1
53	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_PR	ZJ1
54	Molecular Prediction	IHC Biomarker Prediction	IHC_ZJ1_ER	ZJ1
55	Molecular Prediction	Molecular Subtyping	BRCA_MolSubtype	https://portal.gdc.cancer.gov/
56	Molecular Prediction	Molecular Subtyping	CRC_MolSubtype	https://portal.gdc.cancer.gov/
57	Molecular Prediction	Molecular Subtyping	GBMLGG_MolSubtype	https://portal.gdc.cancer.gov/
58	Molecular Prediction	Molecular Subtyping	TCGA_HNSC_HPV	https://portal.gdc.cancer.gov/
59	Molecular Prediction	Molecular Subtyping	EBrains_MolSubtype	https://www.ebrains.eu/
60	Molecular Prediction	Molecular Subtyping	HANCOCK_HPV	https://hancock.research.fau.eu/download
61	Molecular Prediction	Molecular Subtyping	ZJ1_Breast_MolSubtype	ZJ1

Supplementary Table 40: (Continuous Table) Source of datasets for 97 oncological tasks.

No.	Application	Task	Dataset	URL
62	Survival Prediction	Overall Survival	OS_BRCA	https://portal.gdc.cancer.gov/
63	Survival Prediction	Overall Survival	OS_CRC	https://portal.gdc.cancer.gov/
64	Survival Prediction	Overall Survival	OS_GBMLGG	https://portal.gdc.cancer.gov/
65	Survival Prediction	Overall Survival	OS_HNSC	https://portal.gdc.cancer.gov/
66	Survival Prediction	Overall Survival	OS_KIRC	https://portal.gdc.cancer.gov/
67	Survival Prediction	Overall Survival	OS_LUAD	https://portal.gdc.cancer.gov/
68	Survival Prediction	Overall Survival	OS_LUSC	https://portal.gdc.cancer.gov/
69	Survival Prediction	Overall Survival	OS_SKCM	https://portal.gdc.cancer.gov/
70	Survival Prediction	Overall Survival	OS_UCEC	https://portal.gdc.cancer.gov/
71	Survival Prediction	Disease-Free Survival	DFS_BRCA	https://portal.gdc.cancer.gov/
72	Survival Prediction	Overall Survival	OS_HANCOCK	https://hancock.research.fau.eu/download
73	Survival Prediction	Overall Survival	OS_ZJ1	ZJ1
74	Survival Prediction	Disease-Free Survival	DFS_YN1	YN1
75	Survival Prediction	Disease-Free Survival	DFS_ZJ1	ZJ1
76	Survival Prediction	Overall Survival	OS_NFCRC	NFH
77	Survival Prediction	Recurrence-Free Survival	RFS_HANCOCK	https://hancock.research.fau.eu/download
78	Multimodal Fusion	Overall Survival	OS_BRCA	https://portal.gdc.cancer.gov/
79	Multimodal Fusion	Overall Survival	OS_CRC	https://portal.gdc.cancer.gov/
80	Multimodal Fusion	Overall Survival	OS_GBMLGG	https://portal.gdc.cancer.gov/
81	Multimodal Fusion	Overall Survival	OS_HNSC	https://portal.gdc.cancer.gov/
82	Multimodal Fusion	Overall Survival	OS_KIRC	https://portal.gdc.cancer.gov/
83	Multimodal Fusion	Overall Survival	OS_LUAD	https://portal.gdc.cancer.gov/
84	Multimodal Fusion	Overall Survival	OS_LUSC	https://portal.gdc.cancer.gov/
85	Multimodal Fusion	Overall Survival	OS_SKCM	https://portal.gdc.cancer.gov/
86	Multimodal Fusion	Overall Survival	OS_UCEC	https://portal.gdc.cancer.gov/
87	Vision-Language	Zero-shot Slide Classification	CAMELYON	https://camelyon16.grand-challenge.org/Data/
88	Vision-Language	Zero-shot Slide Classification	PANDA	https://www.kaggle.com/c/prostate-cancer-grade-assessment/data
89	Vision-Language	Zero-shot Slide Classification	UBC-OCEAN	https://www.kaggle.com/competitions/UBC-OCEAN/data
90	Vision-Language	Zero-shot Slide Classification	BCNB-ER	https://bcnb.grand-challenge.org/
91	Vision-Language	Zero-shot Slide Classification	BCNB-PR	https://bcnb.grand-challenge.org/
92	Vision-Language	Zero-shot Slide Classification	BCNB-HER2	https://bcnb.grand-challenge.org/
93	Vision-Language	Zero-shot Slide Retrieval	TCGA	https://portal.gdc.cancer.gov/
94	Vision-Language	Zero-shot Slide Retrieval	Breast&Lung	NFH, ZJ1
95	Vision-Language	Report Generation	TCGA	https://portal.gdc.cancer.gov/
96	Vision-Language	Report Generation	Nanfang	NFH
97	Vision-Language	Report Generation	ZJ-First	ZJ1