

Supplementary Data Tables

Table S1: Classification performance of the MOT on each cancer label

	Cancers	precision	recall	f1-score	support
	ACC	0.91	0.88	0.89	24
	BLCA	0.99	0.98	0.98	89
	BRCA	1.00	1.00	1.00	255
	CESC	0.98	0.95	0.96	55
	CHOL	1.00	0.86	0.92	7
	COAD	0.92	0.86	0.89	118
	DLBC	1.00	1.00	1.00	7
	ESCA	0.92	0.97	0.94	34
	GBM	0.95	0.91	0.93	132
	HNSC	1.00	0.98	0.99	111
	KICH	0.96	1.00	0.98	22
	KIRC	0.98	0.97	0.98	145
	KIRP	0.93	0.96	0.94	71
	LAML	0.97	0.97	0.97	40
	LGG	0.96	1.00	0.98	105
	LIHC	0.99	1.00	0.99	86
	LUAD	0.91	0.95	0.93	128
	LUSC	0.94	0.90	0.92	115
	MESO	0.93	1.00	0.96	13
	OV	0.97	0.95	0.96	122
	PAAD	1.00	0.98	0.99	50
	PCPG	0.97	0.97	0.97	37
	PRAD	0.99	1.00	1.00	106
	READ	0.47	0.62	0.54	24
	SARC	0.95	0.98	0.97	58
	SKCM	0.99	0.99	0.99	87
	STAD	1.00	0.96	0.98	96
	TGCT	1.00	1.00	1.00	24
	THCA	0.99	1.00	1.00	113
	THYM	0.96	1.00	0.98	22
	UCEC	0.94	0.96	0.95	129
	UCS	0.60	0.75	0.67	8
	UVM	1.00	1.00	1.00	18
accuracy				0.96	2451
macro avg		0.94	0.95	0.94	2451
weighted avg		0.96	0.96	0.96	2451

Table S3: Study Abbreviations

Study Abbreviation	Study Name
ACC	Adrenocortical carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	Cholangiocarcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
ESCA	Esophageal carcinoma
GBM	Glioblastoma multiforme
HNSC	Head and Neck squamous cell carcinoma
KICH	Kidney Chromophobe
KIRC	Kidney renal clear cell carcinoma
KIRP	Kidney renal papillary cell carcinoma
LAML	Acute Myeloid Leukemia
LGG	Brain Lower Grade Glioma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung adenocarcinoma
LUSC	Lung squamous cell carcinoma
MESO	Mesothelioma
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular Germ Cell Tumors
THYM	Thymoma
THCA	Thyroid carcinoma
UCEC	Uterine Corpus Endometrial Carcinoma
UCS	Uterine Carcinosarcoma
UVM	Uveal Melanoma

Table S2: Classification performance of the MOT on each cancer label with all the 5 omics views available

	Cancers	precision	recall	f1-score	support
	ACC	1.00	1.00	1.00	9
	BLCA	0.99	0.97	0.98	72
	BRCA	1.00	1.00	1.00	125
	CESC	0.93	0.96	0.95	27
	CHOL	1.00	0.67	0.80	3
	COAD	0.92	0.94	0.93	51
	DLBC	0.86	1.00	0.92	6
	ESCA	0.94	0.94	0.94	17
	GBM				
	HNSC	1.00	1.00	1.00	60
	KICH	1.00	1.00	1.00	15
	KIRC	1.00	1.00	1.00	44
	KIRP	1.00	1.00	1.00	44
	LAML				
	LGG	1.00	1.00	1.00	82
	LIHC	0.97	1.00	0.99	38
	LUAD	0.95	0.97	0.96	64
	LUSC	0.93	0.93	0.93	40
	MESO	1.00	1.00	1.00	9
	OV				
	PAAD	0.96	1.00	0.98	26
	PCPG	1.00	0.95	0.97	19
	PRAD	1.00	1.00	1.00	57
	READ	0.71	0.56	0.63	9
	SARC	1.00	1.00	1.00	46
	SKCM	1.00	1.00	1.00	59
	STAD	1.00	0.98	0.99	48
	TGCT	1.00	1.00	1.00	15
	THCA	1.00	1.00	1.00	68
	THYM	1.00	1.00	1.00	18
	UCEC	0.97	0.97	0.97	64
	UCS	0.71	0.71	0.71	7
	UVM	1.00	1.00	1.00	2
accuracy				0.98	1144
macro avg		0.96	0.95	0.95	1144
weighted avg		0.98	0.98	0.98	1144

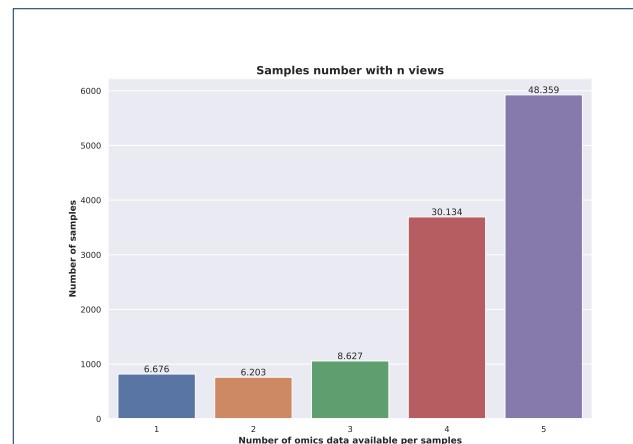


Figure S1: Number of samples available with (1) omic view, (2) omic view, (3) omic view, (4) omic view and (5) omic view

Table S4: Best MOT model parameters

data_size	2000
dataset_views_to_consider	all
exp_type	data_aug
activation	relu
batch_size	256
d_ff_enc_dec	512
d_input_enc	2000
d_model_enc_dec	128
dropout	0.13968749409625048
early_stopping	True
loss	ce
lr	0.000388670623884558
lr_scheduler	cosine_with_restarts
n_epochs	300
n_heads_enc_dec	8
n_layers_dec	6
n_layers_enc	6
nb_classes_dec	33
optimizer	Adam
weight_decay	0.008807626405326077
seed	42
class_weights	[4.03557312 ,0.85154295 ,0.30184775 ,1.18997669 ,8.25050505 ,0.72372851 ,7.73484848 ,1.81996435 ,0.62294082 ,0.61468995 ,4.07992008 ,0.49969411 ,1.07615283 ,1.85636364 ,0.7018388 ,0.84765463 ,0.60271547 ,0.62398778 ,4.26750261 ,0.61878788 ,1.89424861 ,1.98541565 ,0.65595888 ,2.05123054 ,1.37001006 ,0.77509964 ,0.76393565 ,2.67102681 ,0.64012539 ,2.94660895 ,0.64012539 ,6.51355662 ,4.64090909]

Table S5: Number of samples available for the 33 cancers

Omics Data Combination	Count
cnv	305
protein	36
rna	110
mirna	42
methyl	325
rna.protein	81
cnv.methyl	48
cnv.protein	153
cnv.rna	93
methyl.protein	1
methyl.rna	41
mirna.protein	2
mirna.rna	261
cnv.mirna	74
methyl.mirna	6
cnv.methyl.protein	61
cnv.methyl.rna	36
cnv.methyl.mirna	28
cnv.mirna.protein	113
cnv.mirna.rna	315
cnv.rna.protein	90
methyl.mirna.protein	1
methyl.mirna.rna	389
methyl.rna.protein	5
mirna.rna.protein	19
cnv.methyl.rna.protein	87
cnv.mirna.rna.protein	956
cnv.methyl.mirna.protein	43
cnv.methyl.mirna.rna	2510
methyl.mirna.rna.protein	96
cnv.methyl.mirna.rna.protein	5925

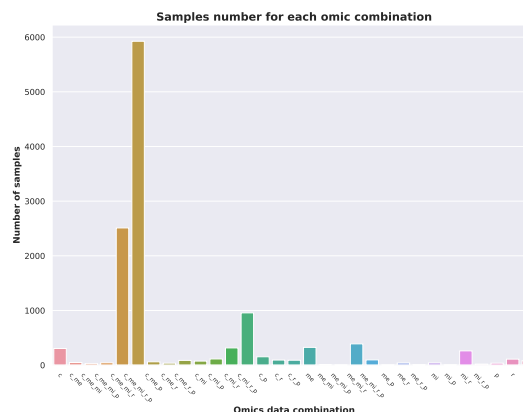


Figure S2: Number of samples available for each combination for all the 5 omics views. C=CNVs, me=Methyl, mi=miRNA, r=RNA, p=protein