Journal Article	Dataset used	ML model
Deep Learning–Based Multi-Omics Integration Robustly Predicts Survival in Liver Cancer Kumardeep Chaudhary, Olivier B. Poirion, Liangqun Lu and Lana X. Garmire Clin Cancer Res March 15 2018 (24) (6) 1248-1259; DOI: 10.1158/1078-0432.CCR-17-0853	TCGA HCC omics datasets of 360 samples	"We used the TCGA data in two steps: The first step is to obtain the labels of survival-risk classes, using the whole TCGA dataset; the second is to train a Support Vector Machine (SVM) model by splitting the samples 60%/40% to training

		and held-out testing data (detailed in "Data partitioning and robustness assessment" subsection). We used five additional confirmation datasets to evaluate the prediction accuracy of the DL-based prognosis model."
Xie, G., Dong, C., Kong, Y., Zhong, J. F., Li, M., & Wang, K. (2019). Group Lasso Regularized Deep Learning for Cancer	TCGA datasets were downloaded from Broad GDAC	Group Lasso

Prognosis from Multi-Omics and Clinical Features. Genes, 10(3), 240. https://doi.org/10.3390/genes10030240	(Genome Data Analysis Center) Firehose (https://gdac.broadinstitute.org/) and TCGA data portal (https://cancergenome.nih.gov/)	Neural Networks Concordance index(c-index)
Lee D, Park Y, Kim S. Towards multi-omics characterization of tumor heterogeneity: a comprehensive review of statistical and machine learning approaches. Brief Bioinform. 2020 Aug 25:bbaa188. doi: 10.1093/bib/bbaa188. Epub ahead of print. PMID: 32838412.		
Patel-Murray, N. L., Adam, M., Huynh, N., Wassie, B. T., Milani, P., & Fraenkel, E. (2020). A Multi-Omics Interpretable Machine Learning Model Reveals Modes of Action of Small Molecules. Scientific reports, 10(1), 954. https://doi.org/10.1038/s41598-020-57691-7		
https://journals.sagepub.com/doi/full/10.1177/1177932219899051		
https://www.nature.com/articles/srep37237/figures/3		