Table S2: Tools employing multi-omics data to predict diagnostic, prognostic, predictive, and personalized markers.

Tools	Description	URL	Pro/Con	Ref
Diagnostic Biomarker-based Tools				
HCCPred	Machine learning prediction models predict and differentiate the liver hepatocellular carcinoma and normal liver samples based on a three-genes (*CLEC1B, PRC1,* and *FCN3*) biomarker. This biomarker validated on 4 external datasets.	http://webs.iiitd.edu.in/raghava/hccpred/	**Pro:** Simple web-based machine prediction tool based on very large cohort of nearly 4,000 samples.	[55]
CancerLSP	Predicts the early and late stage of liver cancer samples using transcriptomics and epigenomics biomarkers. Here, prediction models developed using 21 methylation CpG sites, 30 RNA transcripts and 51 hybrid features (include both 21 methylation CpG sites and 30 RNA transcripts), independently.	http://webs.iiitd.edu.in/raghava/cancerlsp/	**Pro:** Simple web-based machine prediction tool. **Con:** It is based on only TCGA-LIHC data.	[66]

CancerCSP	ML-based model predicts the early and late-stage ccRCC patients using gene expression-based signatures. Prediction module integrated in the webserver based the key signature genes sets, i.e. 64 and 38 genes.	https://webs.iiitd.edu.in/raghava/cancercsp/	**Pro:** Simple web-based machine prediction tool. **Con:** It is based on only TCGA dataset.	[65]
CancerTSP	ML-based model predicts the early and late-stage of papillary thyroid carcinoma using RNA expression profiles of signature 36 RNA transcripts. These 36 RNA transcripts signature identified based on 500 samples of TCGA dataset.	http://webs.iiitd.edu.in/raghava/cancertsp/	**Pro:** Simple web-based machine learning prediction tool. Prediction models also validated on independent dataset.	[51]
CancerSPP	Predicts skin cutaneous melanoma progression using multi-omics signatures. Here, different panels of biomarker sets (17 RNA, 32miRNAs, 38 methylation features) that can classify samples into primary and metastatic categories independently implementing various machine learning algorithms.	https://webs.iiitd.edu.in/raghava/cancerspp/	**Pro:** Simple web-based machine learning prediction tool. **Con:** It is based on only TCGA dataset	[57]

CancerUBM	Web-bench for predicting the cancer status from proteomic data.	https://webs.iiitd.edu.in/raghava/cancerubm/	**Pro:** Simple web-based machine learning prediction tool. **Con:** Insufficient data for patients.	[67]
BBcancer	An expression atlas of the blood-based biomarker for early diagnosis of cancers. It contains expression data of the six RNA types (19,612 mRNAs, 10,918 lncRNAs, 60,306 circRNAs, 2568 miRNAs, 1231 piRNAs and 43,459 tRFRNAs) from 5040 normal and tumor blood samples across 15 cancer types.	http://bbcancer.renlab.org/	**Pro:** It is one of the largest blood sample resource for cancer biomarker research.	[68]
Prognostic Biomarker-based Tools				
OScc	Assess and evaluate the prognostic biomarker potential in cervical cancer based on 690 patients.	http://bioinfo.henu.edu.cn/CESC/	**Pro:** User will get output in the form of Kaplan - Meier survival curves with log-rank p-value and hazard ratio for given gene.	[69]

OSluca	Server to evaluate the prognostic biomarkers for lung cancer	http://bioinfo.henu.edu.cn/LUCA/	**Pro:** They evaluated 104 previously reported prognostic biomarkers for lung carcinoma	[63]
SKCMhrp	A web-bench for stratification of patients in high/low-risk groups using HLA-superallele and clinical characteristics for SKCM patients. Here, they identified 14 HLA superalleles and three clinical and demographic factors using survival analysis and machine methods based on 401 SKCM samples from the TCGA data	https://webs.iiitd.edu.in/raghava/skcmhrp/	**Pro:** Simple web-based prediction tool based on HLA superalleles and clinical factors. It is also validated on independent dataset. **Con:** Signatures derived from the low-resolution HLA alleles.	[56]
CMcrpred	Predict risk in cutaneous melanoma patients based on clinical features (TNM staging, Breslow Thickness and Ulceration status) of patients.	http://webs.iiitd.edu.in/raghava/cmcrpred/	**Pro:** Simple web-based prediction tool based on clinical characteristics of patients. **Con:** It is not validated on independent dataset.	[54]
CRCRpred	Stratify patients in high/low-risk	https://webs.iiitd.	**Pro:** Simple web-based	[53]

	cohorts using proteomic profiles of mitochondrial apoptotic proteins [one or upto five apoptotic proteins (Bak, Bax, Bcl2, BclXL or Mcl1) and clinical data for colorectal cancer.	edu.in/raghava/crcrpred/	prediction tool based on expression of 5 apoptotic proteins. **Con:** Prediction model not validated on independent dataset.	
OSbrca	Breast cancer prognostic biomarker investigation with massive data from tens of cohorts. Here, authors employed gene expression data of 7,400 patients obtained from the TCGA and GEO.	http://bioinfo.henu.edu.cn/BRCA/	**Pro:** It integrates 48 cohorts that contain more than 7,400 patients with RNA-sequencing and gene microarray data. **Con**: The loss of different platform integration, lacking noncoding gene information.	[70]
PROGgene	Integrative tools for prognostic biomarker identification from 134 cohorts among 21 cancer types. It gives a facility for the users to select	http://www.compbio.iupui.edu/proggene	**Pro:** It allows performing Survival analysis based on a) single gene b) multiple	[71]

	gene signatures of interest from nearly 10,000 published or curated gene signatures compiled from the molecular signature database.		genes as a signature, c) ratio of expression of two genes, and d) curated/published gene signatures. **Con:** Website is unstable and currently unavailable.	
SurvExpress	A resource encompassing nearly 20,000 samples and 130 datasets with censored clinical information covering tumors over 20 tissues. It provides tools for risk assessment and survival analysis.	http://bioinforma tica.mty.itesm.m x/SurvExpress	**Pro:** User-friendly interface to analyze prognostic potential of genes among cancer different cohorts. **Con:** It is not updated after the development in 2013.	[72]
PRECOG	Web resource encompasses genomic and clinical data for nearly 18,000 human tumors samples across 39 malignancies. Associated tools facilitate to delineate prognostic genes and leukocyte	http://precog.stan ford.edu	**Pro:** large number of cohorts used prognostic potential of genes. Besides, prognostic potential of 22 immune subset signatures	[73]

subsets within and across cancers.		elucidated among 25 cancer types. **Con:** It is not updated after the development in 2015.	
PrognoScan	It is a webresource that encompass 40 publicly available datasets with clinical annotation for 9 cancer types, as well as 2) a tool for assessing the prognostic potential of markers.	http://gibk21.bse.kyutech.ac.jp/PrognoScan/index.html	**Con:** Website is not stable and database was not updated.	[74]
GSCAlite	Webserver integrating various modules that offer different types of data analyses including differential gene expression, overall survival, single nucleotide variation, copy number variation, methylation, pathway analyses, miRNA regulation, and drug sensitivity, etc. It holds multi-omics data from different resources, i.e. 11,160 samples for 33 cancer types from	http://bioinfo.life.hust.edu.cn/web/GSCALite/	**Pro:** One of the most comprehensive tool for multi-omics data analyses to scrutinize signatures.	[75]

	TCGA, 746 drug data from Genomics of Drug Sensitivity in Cancer (GDSC) and Cancer Therapeutics Response Portal (CTRP) (Drug Sensitivity), and normal tissue expression data of 11 688 samples from GTEx.			
CaPSSA	A platform for detection of the prognostic potential of a patient subgroup based on gene expression and mutation data. It also allows association of patient group with clinical factors and annotated molecular types.	https://github.com/yjjang/capssa	**Pro:** User-friendly interactive platform.	[76]
MEXPRESS	Webtool for analysis and visualization of gene expression, methylation, and patient survival data from the TCGA.	https://mexpress.be	**Pro:** It provides facility to analyze DNA methylation data w.r.t. to its genomic location and other omics data, which is unique for this resource. **Con**: It has only TCGA	[77]

				data.	
PROGmiR	A platform for the exploration of prognostic potential of 1054 miRNA in a total of 3117 pan-cancer samples across 16 major cancer types.	http://www.compbio.iupui.edu/progmir	**Pro:** It allows users to study overall survival in form of prognostic plots using miRNA expression data from several publically available patient series.	[78]
SurvMicro	Assessment of prognostic potential of miRNA using multivariate analysis. It encompasses >40 cohorts in different tissues and have a web tool to execute quick survival analyses.	http://bioinformatica.mty.itesm.mx/SurvMicro	**Pro:** User-friendly webtool for quick prognostic analyses of miRNA. **Con:** It not updated after it's development.	[79]
OncoLnC	Interactive tool for assessing the survival correlation for lncRNA, miRNA, and mRNA on 21 cancer types. It encompasses survival data for 8,647 patients from 21 cancer studies performed by the TCGA.	http://www.oncolnc.org	**Pro:** It is the resource that uses modern gene definitions for TCGA mRNA and miRNA data, and a single resource for survival	[80]

			analysis of MiTranscriptome beta lncRNAs. **Con:** It is based on only TCGA Data	
TCPAv3.0	A comprehensive resource for the accessing, visualizing, and analyzing functional proteomics of tumor samples. Tool for exploring the survival correlation of mutation, SCNA, mRNA, miRNA, methylation, protein RPPA data for ~8,000 patient samples of 32 cancer types.	https://bioinformatics.mdanderson.org/public-software/tcpa/	**Pro:** It is an interactive platform to explore and analyze TCGA pan-cancer RPPA-based protein expression data. **Con:** It holds the c pan-cancer RPPA data for nearly 260 protein markers.	[81]
TRGAted	An open-source survival analysis tool for 31 cancer type based on protein RPPA data.	https://github.com/ncborcherding/TRGAted	**Pro:** It is an interactive web application that provides a graphical user interface combining survival information and reverse-phase protein array data from the TCGA.	[82]

Predictive/ Drug Biomarker-based Tools				
CancerDP	Predicts priority/potency of an anticancer drug against the cancer cell line using its genomic features. The drug sensitivity information for 504 cell lines was captured from CCLE browse data section. The data includes IC50 (μM) for 24 anticancer drugs on 504 cell lines.	https://webs.iiitd.edu.in/raghava/cancerdp/	**Pro:** A simple webserver-based tool for anticancer drug prioritization, which is a initial step towards personalized drug therapy for cancer. **Con**: It is based on cell line data.	[83]
CancerTOPE	A platform for designing genome-based immunotherapy or vaccine against the cancer cell. It hold a wide various epitopes including B-cell, CD8+ T-cell, HLA class I, HLA class II against 60 cancer-specific vaccine antigens. It has two major modules: (1) The database-specific service maintains neoepitopes examined in 905 cancer cell lines; (2) neoepitope-based database facilitates a demonstration for guiding the	https://webs.iiitd.edu.in/raghava/cancertope/	**Pro:** A simple web-based platform for predicting vaccine candidates effective against cancer. **Con:** It contains only predicted epitopes, which requires experimental validation.	[84]

	generation of neoepitopes against a tumor from its whole-genome.			
SCLC-CellMiner	Tool for prioritization of drugs for small cell lung cancer based on transcriptomics and methylation pattern. It integrates drug sensitivity and genomic data, methylomics and transcriptomics data from 118 patient-derived small cell lung cancer (SCLC) cell lines.	https://discover.nci.nih.gov/SclcCellMinerCDB/	**Pro:** It provides a unique resource of patient derived SCLC cell lines characterized comprehensively using multi-omics and drug sensitivity **Con:** It is based on cell line data only.	[85]
CancerDR	A resource for exploring the pharmacological profiling of anticancer drugs against 952 cancer cell lines. It holds information of 148 anti-cancer drugs, and their pharmacological profiling across 952 cancer cell lines. It provides comprehensive information, i.e. sequence of natural variants, mutations, tertiary structure, and alignment profile of mutants/variants	https://webs.iiitd.edu.in/raghava/cancerdr/	**Pro:** CancerDR is integrated with a user-friendly interface for extracting vital information from the database. **Con:** All the data is derived from cell lines only.	[86]

	about each drug target.			